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OM protein - protein search, using sw model

Run on: January 9, 2006, 15:51:24 ; Search time 90.4923 Seconds  
(without alignments)  
82.542 Million cell updates/sec

Title: US-10-759-832-18

Perfect score: 103  
Sequence: 1 EGPWLEEEBESSPPPPC 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*  
9: Geneseq2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	103	100.0	17	8	ADH89223	Adh89223 Gastrin G
2	87.5	85.0	16	2	AAR74295	Aar74295 Human gas
3	87.5	85.0	16	3	AAV49309	Aay49309 Human hep
4	87.5	85.0	16	6	ABP73035	Abp73035 Peptide s
5	79	76.7	15	2	AAR74297	Aar74297 Human gas
6	62.5	60.7	12	2	AAR06246	Aar06246 Antigenic
7	62.5	60.7	12	3	AAV49303	Aay49303 Human hep
8	62.5	60.7	12	3	AAV51309	Aay51309 Human gas
9	62.5	60.7	12	6	ABP73032	Abp73032 Peptide s
10	62.5	60.7	12	9	ADY37660	Ady37660 Human G17
11	60.5	58.7	14	2	AAR06249	Aar06249 Antigenic
12	60.5	58.7	14	9	ADY37666	Ady37666 Human G17
13	60	58.3	27	9	AEC05676	Aec05676 Gastrin T
14	59	57.3	11	9	ADW00245	Adw00245 Human wil
15	59	57.3	12	2	AAR06245	Aar06245 Antigenic
16	59	57.3	13	9	ADY37657	Ady37657 Human G17
17	59	57.3	17	2	AAW65184	Aaw65184 Gastrin f
18	59	57.3	17	2	AAW24398	Aaw24398 Carboxy-a
19	59	57.3	17	4	Aau05580	Aau05580 Human Jan
20	59	57.3	17	4	AAB91246	Aab91246 Gastrin r
21	59	57.3	17	4	AAB59273	Aab59273 K52-pepti
22	59	57.3	17	5	AAU76504	Aau76504 Protein k
23	59	57.3	17	7	ADF72769	Adf72769 Chemocele
24	59	57.3	17	8	ADF72934	Adf72934 Biotinyla

25	59	57.3	17	8	ADH10240	Adh10240 Peptide s
26	59	57.3	17	8	ADH89206	Adh89206 Gastrin G
27	59	57.3	17	8	ADK00577	Adk00577 Immunogen
28	59	57.3	17	8	ADL02105	Adl02105 Phosphope
29	59	57.3	17	8	ADN03334	Adn03334 Exemplary
30	59	57.3	17	8	ADR42169	Adr42169 Gastrin r
31	59	57.3	17	8	ADT49596	Adt49596 Human mat
32	59	57.3	17	8	ADU48550	Adu48550 Gastrin-1
33	59	57.3	17	8	ADU48549	Adu48549 Gastrin-1
34	59	57.3	17	9	ADV16301	Adv16301 Human gas
35	59	57.3	17	9	ADV16302	Adv16302 Human gas
36	59	57.3	17	9	ADW00243	Adw00243 Human var
37	59	57.3	17	9	ADW00242	Adw00242 Human wil
38	59	57.3	17	9	ADW71906	Adw71906 Non-phosp
39	59	57.3	17	9	AEA08308	Aea08308 PTK domai
40	59	57.3	17	9	AEA36970	Aea36970 Phosphoty
41	59	57.3	17	9	AEA52649	Aea52649 Kinase b1
42	59	57.3	17	9	AE825345	Aeb25345 Peptide u
43	59	57.3	17	9	AE877639	Aeb77639 Gastrin-1
44	59	57.3	17	9	AEC05671	Aec05671 Gastrin p
45	59	57.3	18	2	AAW24397	Aaw24397 Glycine-e

ALIGNMENTS

RESULT 1	
ADH89223	
ID	ADH89223 standard; peptide; 17 AA.
XX	
AC	ADH89223;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Gastrin G-17 peptide G17DT, SEQ ID 18.
XX	
KW	Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;
KW	gastrin G-34; gonadotropin releasing hormone; GnRH;
KW	chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;
KW	thyroid cancer; lung cancer; reproductive system cancer.
XX	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 1
FT	Modified-site 17 /note= "Pyroglutamic acid"
FT	Modified-site 17 /note= "This residue is covalently linked to the carrier molecule Diphtheria toxoid (DT) through the sulfhydryl group on this residue by reacting with heterobifunctional linker molecule to the epsilon-amino groups of the lysine residues present on the carrier protein"
XX	
XX	WO2004004687-A2.
XX	
XX	15-JAN-2004.
PF	03-JUL-2003; 2003WO-US021176.
XX	
XX	03-JUL-2002; 2002US-0394179P.
PR	
PA	(APHT-) APHTON CORP.
PA	(YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PI	
XX	Michaeli D, Grimes S, Barenholz Y, Even-Chen S;
XX	WPI; 2004-099340/10.
DR	
XX	
PT	Injectable liposomal composition for delivery of a water-soluble substance e.g. vaccine for preventing pregnancy, comprises several liposomal vesicles comprising a high weight ratio of lipid to encapsulated water-soluble substance.
PT	
XX	

Tue Jan 10 09:41:49 2006

Claim 39; SEQ ID NO 18; 73pp; English.

XX The present invention relates to injectable liposomal compositions (I) for delivery of a water-soluble substance e.g. immunomimetic peptides. (I) comprises several liposomal vesicles comprising a high weight ratio of a lipid to an encapsulated water-soluble substance so as to achieve a high efficiency of encapsulation. The immunomimetic peptide is chosen from gastrin G-17 (ADH89206 to ADH89213 and ADH89223), gastrin G-34 (ADH89217-ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89220 and ADH89222 and ADH89225). (I) comprising vaccines directed against hormone or hormone cognate receptors, where the vaccine comprises at least one: treating gastrointestinal malignancy, and non-gastrointestinal tumors such as thyroid and lung cancer; or GnRH or hCG immunomimetic peptide is useful as contraceptive and for treating cancers in male and female reproductive systems. The present sequence comprises a G17 peptide linked to a spacer peptide at the C-terminal end.

Sequence 17 AA;

Query Match 100.0%; Score 103; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEESSPPPPC 17  
Db 1 EGPWLEEEESSPPPPC 17

RESULT 2  
AAR74295  
ID AAR74295 standard; peptide; 16 AA.

XX AAR74295;

XX 10-JAN-1996 (first entry)

XX Human gastrin 17 antigenic peptide hG17(1-9)-Ser9.

XX Human gastrin 17; antigenic peptide hG17(1-9)-Ser9; immunisation; treatment; gastro-oesophageal reflux disease; gastric; duodenal; ulceration; cancer.

XX Synthetic.

XX WO9513297-A2.

XX 18-MAY-1995.

XX 10-NOV-1994; 94WO-US013205.

XX 12-NOV-1993; 93US-00151219.

XX (APHT-) APHTON CORP.

XX Gevas PC, Grimes S, Karr SL, Michaeli D, Scibienki R;

XX WPI, 1995-194034/25.

XX Immunogenic compen. for producing anti-human gastrin 17 antibodies - used for treating e.g. gastro-oesophageal reflux disease, gastric and duodenal ulceration or cancer.

XX Claim 1; Page 14; 17pp; English.

XX AAR74295 and AAR74297 are human gastrin 17 (hG17) antigenic peptides, used to produce anti-hG17 antibodies (Abs). The Abs can be induced in a patient, or used for passive immunisation, for the treatment of diseases in which hG17 is involved, e.g. gastric and duodenal ulceration; gastro-oesophageal reflux disease and cancer

XX Sequence 16 AA;

Query Match 85.0%; Score 87.5; DB 2; Length 16;  
Best Local Similarity 94.1%; Pred. No. 0.00022;  
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17  
Db 1 EGPWL-EEESSPPPPC 16

RESULT 3

AAY49309

ID AAY49309 standard; peptide; 16 AA.

XX AAY49309;

XX 06-MAR-2000 (first entry)

XX Human heptadecagastrin (G17) immunomimic with carboxy terminal spacer.

XX Gastroesophageal reflux disease; GERD; gastrin; anti-gastrin antibody; histamine H<sub>2</sub>; proton pump inhibitor; acid output; stomach; therapy; esophagitis; immunogen; human; heptadecagastrin; immunomimic; G17.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 1

XX /label= pGlu

XX /note= "pyroglutamate"

XX Peptide 10..16

XX /note= "carboxy-terminal spacer"

XX WO959612-A1.

XX 25-NOV-1999.

XX 14-MAY-1999; 99WO-US010734.

XX 15-MAY-1998; 98US-0085610P.

XX (APHT-) APHTON CORP.

XX Gevas PC, Grimes S, Karr S, Michaeli D;

XX WPI, 2000-062378/05.

XX Method for treatment of gastroesophageal reflux disease (GERD).

XX Example 5; Page 13; 24pp; English.

XX The invention relates to the treatment of gastroesophageal reflux disease (GERD) that comprises administering to a patient an immunogenic composition which generates anti-gastrin antibodies, which bind to gastrin, in a patient; and administering histamine H<sub>2</sub> antagonist or a proton pump inhibitor. The method provides a more effective method for controlling acid output by the stomach. The therapy is less costly. High gastrin levels associated with standard therapies are neutralized and undesirable side effects are reduced. The method permits a reduced dosage of acid reducing agent both at the acid producing level as well as the acid production stimulating level (gastrin). Reduction of dosages is desirable for prolonged treatment of GERD. In a combination therapy with H<sub>2</sub> agonists or proton pump inhibitors, anti-gastrin 17 antibody titers can be maintained by occasional booster shots while gastric acid inhibitor dosing is reduced. Immunization allows a sufficient time for the esophagitis to completely heal and no surgery is required. The present sequence represents a human heptadecagastrin (G17) immunomimic followed by a carboxy-terminal spacer

XX Sequence 16 AA;

Query Match 85.0%; Score 87.5; DB 3; Length 16;

```

Best Local Similarity 94.1%; Pred. No. 0.00022;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17
    ||||| ||||| |||||
DB 1 EGPWL-EEESSPPPPC 16

RESULT 4
ABP73035
ID ABP73035 standard; peptide; 16 AA.
XX
AC ABP73035;
XX
DT 03-JUN-2003 (first entry)
XX
DE Peptide specific for the induction of immune response to G17.
XX
KW Cancer; lung; oesophagus; liver; immunogen; hormone; gastrin 17; G17;
KW gastrin receptor; cholecystokinin-B; CCK-B; Barrett's condition;
KW gastrin-induced tumour; immune response.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT Peptide /note= "pyroglutamic acid"
FT /note= "spacer"
XX
PN WO2003005955-A2.
XX
PD 23-JAN-2003.
XX
PF 09-JUL-2002; 2002WO-US021768.
XX
PR 09-JUL-2001; 2001US-0303868P.
XX
PA (APHT-) APHTON CORP.
XX
PI Gevas PC, Michaeli D, Grimes S;
XX
DR WPI; 2003-229433/22.
XX
PT Treating cancerous or pre-cancerous conditions of the lung, esophagus or
PT liver, by administering an immunogen which induces antibodies in the
PT patient against G17 and/or cholecystokinin-B/gastrin receptors.
XX
PS Example 1; Page 7; 27pp; English.
XX
CC The specification describes a method of treating a cancerous or pre-
CC cancerous condition of the lung, oesophagus or liver. The method involves
CC administering to a patient an immunogen which induces antibodies in the
CC patient against peptide hormone gastrin 17 (G17) and/or a gastrin
CC receptor, e.g. cholecystokinin (CCK)-B. The method is useful for treating
CC cancerous or pre-cancerous condition of lung, oesophagus or liver, where
CC the condition is cancer, or Barrett's condition. The treatment prevents
CC or delays progression of the Barrett's oesophagus to a cancerous state.
CC The method is also useful for treating the growth of a gastrin-induced
CC tumour or pre-cancerous lesion of the lung, liver or oesophagus. ABP73032
CC -35 represent peptides which induce specific immune responses to G17. The
CC peptides comprise an amino terminal fragment of G17 and a carboxy-
CC terminal spacer
XX
SQ Sequence 16 AA;

Query Match 85.0%; Score 87.5; DB 6; Length 16;
Best Local Similarity 94.1%; Pred. No. 0.00022;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17
    ||||| ||||| |||||
DB 1 EGPWL-EEESSPPPPC 16

RESULT 5
AAR74297
ID AAR74297 standard; peptide; 15 AA.
XX
AC AAR74297;
XX
DT 10-JAN-1996 (first entry)
XX
DE Human gastrin 17 antigenic peptide hG17(1-9)-Arg9.
XX
KW Human gastrin 17; antigenic peptide hG17(1-9)-Arg9; immunisation;
KW treatment; gastro-oesophageal reflux disease; gastric; duodenal;
KW ulceration; cancer.
XX
OS Synthetic.
XX
PN WO9513297-A2.
XX
PD 18-MAY-1995.
XX
PF 10-NOV-1994; 94WO-US013205.
XX
PR 12-NOV-1993; 93US-00151219.
XX
PA (APHT-) APHTON CORP.
XX
PI Gevas PC, Grimes S, Karr SL, Michaeli D, Scibienski R;
XX
DR WPI; 1995-194034/25.
XX
PT Immunogenic compen. for producing anti-human gastrin 17 antibodies - used
PT for treating e.g. gastro-oesophageal reflux disease, gastric and duodenal
PT ulceration or cancer.
XX
PS Example 1; Page 3; 17pp; English.
XX
CC AAR74295 and AAR74297 are human gastrin 17 (hG17) antigenic peptides,
CC used to produce anti-hG17 antibodies (Abs). The Abs can be induced in a
CC patient, or used for passive immunisation, for the treatment of diseases
CC in which hG17 is involved, e.g. gastric and duodenal ulceration; gastro-
CC oesophageal reflux disease and cancer
XX
SQ Sequence 15 AA;

Query Match 76.7%; Score 79; DB 2; Length 15;
Best Local Similarity 82.4%; Pred. No. 0.0025;
Matches 14; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17
    ||||| ||||| |||||
DB 1 EGPWLEEEER--PPPPC 15

RESULT 6
AAR06246
ID AAR06246 standard; protein; 12 AA.
XX
AC AAR06246;
XX
DT 09-JAN-2003 (revised)
DT 07-DEC-1990 (first entry)
XX
DE Antigenic peptide fragment selected from the 12 N-terminal AAs of
DE heptadecagastrin (G17).
XX
KW Gastrin; tumours; peptic ulcers; diphtheria toxoid; tetanus toxin.
XX
OS Unidentified.
XX
PN EP380230-A.

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Tue Jan 10 09:41:49 2006

Example 4; Page 11; 24pp; English.

PS The invention relates to the treatment of gastroesophageal reflux disease  
 CC (GERD) that comprises administering to a patient an immunogenic  
 CC composition which generates anti-gastrin antibodies, which bind to  
 CC gastrin, in a patient; and administering histamine H<sub>2</sub> antagonist or a  
 CC proton pump inhibitor. The method provides a more effective method for  
 CC controlling acid output by the stomach. The therapy is less costly. High  
 CC gastrin levels associated with the standard therapies are neutralized and  
 CC undesirable side effects are reduced. The method permits a reduced dosage  
 CC of acid reducing agent both at the acid producing level as well as the  
 CC acid production stimulating level (gastrin). Reduction of dosages is  
 CC desirable for prolonged treatment of GERD. In a combination therapy with  
 CC H<sub>2</sub> agonists or proton pump inhibitors, anti-gastrin 17 antibody titers  
 CC can be maintained by occasional booster shots while gastric acid  
 CC inhibitor dosing is reduced. Immunization allows a sufficient time for  
 CC the esophagitis to completely heal and no surgery is required. Sequences  
 CC AAY49303-306 represent human heptadecagastrin (G17) immunogenic peptides  
 CC  
 XX Sequence 12 AA;  
 XX

Query Match 60.7%; Score 62.5; DB 3; Length 12;  
 Best Local Similarity 64.7%; Pred. No. 0.27; 1; Indels 5; Gaps 1;  
 Matches 11; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

QY 1 EGPWLEEESSPPPPC 17  
 |||||  
 DB 1 EGPWLER-----PPPPC 12

RESULT 8  
 AAY51309  
 ID AAY51309 standard; peptide; 12 AA.

XX AAY51309;  
 AC

DT 14-APR-2000 (first entry)

DE Human gastrin G17 derived immunogen hg17(6).

XX Immunogenic; treatment; hypergastrinemia; gastrin G17; gastrin G34;  
 KW pernicious anemia; anti-ulcer; proton pump inhibitor; colorectal disease.

XX Homo sapiens.

PN WO9959631-A1.

PD 25-NOV-1999.

XX 14-MAY-1999; 99WO-US010751.

XX 15-MAY-1998; 98US-0085714P.

XX (APHT-) APHTON CORP.

XX Gevas PC, Grimes S, Karr S, Michaeli D, Watson S;

XX WPI; 2000-116301/10.

XX Treating or preventing hypergastrinemia comprising administration of,  
 FT e.g. anti-gastrin antibodies.

XX Example 3; Page 18; 44pp; English.

XX This invention describes a novel method for the treatment or preventing  
 CC hypergastrinemia by administering to a patient a gastrin G17 and/or G34  
 CC peptide fragment linked by an amino acid spacer to an immunogenic  
 CC carrier. The methods are used to treat hypergastrinemic patients,  
 CC particularly those with pernicious anemia, those receiving treatment with  
 CC anti-ulcer agents such as proton pump inhibitors (particularly omeprazole  
 CC or lansoprazole) or H<sub>2</sub> receptor blocking agents or antagonists, or those  
 CC having colorectal disorders or diseases. This sequence represents a human  
 CC gastrin G17 derived immunogen which is used to illustrate the method of

PS Claim 8; Page 19; 32pp; English.

XX Antigenic fragments may be attached to an immunogenic carrier and used to  
 CC raise Abs to a specific single form of Gastrin 16, G17 or G34. Peptide  
 CC fragments capable of binding to these Abs are useful in neutralising anti  
 CC -gastrin Abs in vivo. (Updated on 09-JAN-2003 to add missing OS field.)

XX Sequence 12 AA;  
 XX

Query Match 60.7%; Score 62.5; DB 2; Length 12;  
 Best Local Similarity 64.7%; Pred. No. 0.27;  
 Matches 11; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

QY 1 EGPWLEEESSPPPPC 17  
 |||||  
 DB 1 EGPWLER-----PPPPC 12

RESULT 7

AAY49303  
 ID AAY49303 standard; peptide; 12 AA.

XX AAY49303;  
 AC

DT 06-MAR-2000 (first entry)

DE Human heptadecagastrin (G17) immunogenic peptide 1.

XX Gastroesophageal reflux disease; GERD; gastrin; anti-gastrin antibody;  
 KW histamine H<sub>2</sub>; proton pump inhibitor; acid output; stomach; therapy;  
 KW esophagitis; immunogen; human; heptadecagastrin; G17.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 1  
 FT /label= pglu  
 FT /note= "pyroglutamate"

XX WO9959612-A1.

XX 25-NOV-1999.

XX 14-MAY-1999; 99WO-US010734.

XX 15-MAY-1998; 98US-0085610P.

XX (APHT-) APHTON CORP.

XX Gevas PC, Grimes S, Karr S, Michaeli D;

XX WPI; 2000-062378/05.

XX Method for treatment of gastroesophageal reflux disease (GERD).

Query Match 60.7%; Score 62.5; DB 6; Length 12;

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Query Match          60.7%; Score 62.5; DB 9; Length 12;
Best Local Similarity 64.7%; Pred. No. 0.27;
Matches 11; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17
   |||||
Db 1 EGPWLEER-----PPPPC 12

RESULT 11
AAR06249
ID AAR06249 standard; protein; 14 AA.
XX
AC AAR06249;
XX
DT 09-JAN-2003 (revised)
DT 07-DEC-1990 (first entry)
XX
DE Antigenic peptide fragment selected from the 12 N-terminal AAs of
DE heptadecagastrin (G17).
XX
KW Gastrin; tumours; peptic ulcers; diphtheria toxoid; tetanus toxin.
XX
OS Unidentified.
XX
PN EP380230-A.
XX
PD 01-AUG-1990.
XX
PF 17-JAN-1990; 90EP-00300456.
XX
PR 24-JAN-1989; 89US-00301353.
PR 12-MAY-1989; 89US-00351193.
XX
PA (APHT-) APHTON CORP.
XX
PI Gevas PC, Grimes S, Karr SL, Littenberg RL;
XX
WPI; 1990-233029/31.
XX
PT Immunogens against gastrin peptide(s) - used to induce antibodies that
PT specifically neutralise single form of gastrin, G17 or G34.
XX
PS Claim 8; Page 19; 32pp; English.
XX
CC Antigenic fragments may be attached to an immunogenic carrier and used to
CC raise Abs to a specific single form of Gastrin ie. G17 or G34. Peptide
CC fragments capable of binding to these Abs are useful in neutralising anti
CC -gastrin Abs in vivo. (Updated on 09-JAN-2003 to add missing OS field.)
XX
SQ Sequence 14 AA;

Query Match          58.7%; Score 60.5; DB 2; Length 14;
Best Local Similarity 68.8%; Pred. No. 0.56;
Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 1 EGPWLEEEESSPPPP 16
   |||||
Db 1 EGPWLEEKR---PPPP 13

RESULT 12
ADY37666
ID ADY37666 standard; peptide; 14 AA.
XX
AC ADY37666;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human G17 (1-7) peptide.
XX
KW Cytostatic; Gastrointestinal-Gen.; Antiulcer; Vaccine; pharmaceutical;

hormone; gastrin; heptadecagastrin; ulcer; duodenal ulcer; stomach ulcer;
tumor.
KW
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key
FH Peptide
FT Modified-site 1
FT /note= "Residues 1-7 of human G17"
FT /note= "Pyroglutamic acid"
FT Peptide
FT /note= "Spacer peptide"
XX
PN US6861510-B1.
XX
PD 01-MAR-2005.
XX
PF 06-JUN-1995; 95US-00465917.
XX
PR 24-JAN-1989; 89US-00301353.
PR 12-MAY-1989; 89US-00351193.
PR 23-JAN-1990; 90US-00721638.
PR 23-JAN-1990; 90WO-US000520.
PR 19-APR-1991; 91US-00679212.
PR 30-MAR-1994; 94US-00219773.
XX
PA (APHT-) APHTON CORP.
XX
PI Gevas PC, Karr SL, Grimes S, Littenberg RL;
XX
WPI; 2005-201185/21.
XX
PT New pharmaceutical composition for passive immunization comprising anti-
PT human gastrin G34 or anti-hunt gastrin G17 monoclonal antibodies, useful
PT for preventing or treating ulcers or tumors.
XX
PS Example 5; Col 15-16; 24pp; English.
XX
CC The present invention relates to novel pharmaceutical compositions for
CC passive immunization. The compositions comprise monoclonal antibodies for
CC the human hormone gastrin (G17 and G34) which selectively bind and
CC neutralize gastrin, and a pharmaceutical inert carrier. The hormone
CC gastrin has two main functions: stimulation of acid secretion and
CC stimulation of gastrointestinal tract cell growth, and exists in two
CC forms: heptadecagastrin (G17) and tetratriacontagastrin (G34). The
CC compositions are useful for preventing or treating ulcers, e.g. duodenal
CC and gastric ulcers or tumors whose growth is dependent on or stimulated
CC by gastrin hormones. The present sequence is a fusion peptide comprising
CC a fragment of human G17 and a spacer peptide. This sequence was used to
CC demonstrate that a polymerised peptide immunogen can be constructed and
CC used to reduce anti-G17 antibody responses. This peptide comprises a
CC unique epitope for G17 (residues 1-7) and residues that can bind to
CC crosslinking agents (residues 8 and 14).
XX
SQ Sequence 14 AA;

Query Match          58.7%; Score 60.5; DB 9; Length 14;
Best Local Similarity 68.8%; Pred. No. 0.56;
Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 1 EGPWLEEEESSPPPP 16
   |||||
Db 1 EGPWLEEKR---PPPP 13

RESULT 13
AEC05676
ID AEC05676 standard; peptide; 27 AA.
XX
AC AEC05676;
XX
DT 20-OCT-2005 (first entry)

```

XX Gastrin TDK 2 peptide.  
 XX Vaccine; development; antibody production; immunogenicity; gastrin;  
 KW hormone.  
 XX Synthetic.  
 OS Unidentified.  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "Pyroglutamic acid"  
 FT Misc-difference 13  
 FT Misc-difference 26 /note= "D-form residue"  
 FT Modified-site 27 /note= "D-form residue"  
 FT /note= "C-terminal amide"  
 XX EP1564554-A1.  
 XX 17-AUG-2005.  
 XX 12-FEB-2004; 2004EP-00075439.  
 XX 12-FEB-2004; 2004EP-00075439.  
 XX (PEPS-) PEPSCAN SYSTEMS BV.  
 PA (UYUT-) UNIV UTRECHT HOLDING BV.  
 XX Akresteiijn GJ, Hensen EJ, Scibelli A, Van Der Most RG, Meloen RH;  
 PI Turkstra JA;  
 XX WPI; 2005-573732/59.  
 XX Affinity-binding assay for selecting antigen specific immune cells, by  
 PT contacting cell having four copies of target molecule with two labeled  
 PT binding molecules, detecting cells staining with each label, selecting  
 PT cells binding both labels.  
 XX Example 3; Page 6; 45pp; English.  
 PS The present invention relates to an affinity-binding assay for selecting  
 CC antigen specific immune cells. The method involves contacting particle  
 CC such as a cell having four copies of target molecule with two binding  
 CC molecules specific for the target molecule, where first of the binding  
 CC molecules is associated with a first label and a second of the binding  
 CC molecules is associated with a second label, detecting cells staining  
 CC with each label and selecting cells binding both labels. The invention  
 CC also provides a method for detection of early B cell populations in  
 CC vaccine development. The invention is useful for the preparation of an  
 CC antibody. The present sequence is a gastrin TDK 2 peptide. This sequence  
 CC is an immunogenic peptide used as a vaccine.  
 XX Sequence 27 AA;  
 SQ  
 Query Match 58.3%; Score 60; DB 9; Length 27;  
 Best Local Similarity 68.8%; Pred. No. 1.2;  
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEESSPPPP 16  
 DB |||||  
 1 EGPWLEEEEEKYKQGP 16  
 RESULT 14  
 ADW00245  
 ID ADW00245 standard; peptide; 11 AA.  
 XX ADW00245;  
 XX 24-MAR-2005 (first entry)  
 DT  
 XX

DE Human wild type gastrin-17 peptide aa 1-11.  
 XX antidiabetic; gastrin receptor; cholecystokinin receptor;  
 KW gastrin receptor modulator; CCK receptor modulator; gastrin; diabetes;  
 KW fasting blood glucose; insulin.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "pyroglutamic acid"  
 FT US2004266682-A1.  
 XX 30-DEC-2004.  
 XX 21-NOV-2003; 2003US-00719450.  
 XX 22-OCT-2002; 2002US-0420187P.  
 PR 22-OCT-2002; 2002US-0420399P.  
 PR 21-NOV-2002; 2002US-0428100P.  
 PR 22-NOV-2002; 2002US-0428562P.  
 PR 03-DEC-2002; 2002US-0430590P.  
 PR 22-OCT-2003; 2003US-00691123.  
 PR 14-NOV-2003; 2003US-0519933P.  
 XX (CRUZ/) CRUZ A.  
 XX Cruz A;  
 XX WPI; 2005-074216/08.  
 XX Pharmaceutical composition useful for treating diabetes, comprises a  
 PT gastrin compound having an extended activity upon administration to a  
 PT subject in comparison with native gastrin.  
 PS Claim 1; Page; 25pp; English.  
 XX The invention relates to a pharmaceutical composition (I) comprising a  
 CC gastrin compound (C1) having an extended activity upon administration to  
 CC a subject in comparison with native gastrin. (I) or C1 is useful for  
 CC treating a subject having diabetes, which involves administering C1 or a  
 CC modified gastrin capable of covalently reacting with a serum protein,  
 CC where the frequency of administering the gastrin compound is less than  
 CC frequency of administration of a native gastrin. The method further  
 CC involves measuring a physiological indicator of islet neogenesis,  
 CC measuring fasting blood glucose (FPG), and decreasing insulin dependency.  
 CC The modified gastrin comprises a sequence of native gastrin capable of  
 CC binding to the gastrin/CCK receptor and an amino terminal cysteine or  
 CC lysine. (I) or C1 is useful for maintaining for an extended period of  
 CC time an increased gastrin serum level compared with the serum level of a  
 CC peptide having an amino acid sequence of a native gastrin, which involves  
 CC administering C1. (I) Contains gastrin compositions having longer active  
 CC function than native gastrin peptides, and has a longer half-life in  
 CC circulation in a subject. This sequence corresponds to amino acids 1-11  
 CC of the wild type gastrin-17 peptide used in the invention. (Note: this  
 CC sequence is not given in the specification but is generated using  
 CC information given by the inventors in the Claims section).  
 XX Sequence 11 AA;  
 SQ  
 Query Match 57.3%; Score 59; DB 9; Length 11;  
 Best Local Similarity 90.9%; Pred. No. 0.69;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEES 11  
 DB |||||  
 1 EGPWLEEEESA 11  
 RESULT 15  
 AAR06245  
 ID AAR06245 standard; peptide; 12 AA.

XX  
AC AAR06245;  
XX  
DT 09-JAN-2003 (revised)  
DT 07-DEC-1990 (first entry)  
XX  
DE Antigenic peptide fragment selected from the 12 N-terminal AAs of  
DE heptadecagastrin (G17).  
XX  
KW Gastrin; tumours; peptic ulcers; diphtheria toxoid; tetanus toxin.  
XX  
OS Unidentified.  
XX  
PN EP380230-A.  
XX  
PD 01-AUG-1990.  
XX  
PF 17-JAN-1990; 90EP-00300456.  
XX  
PR 24-JAN-1989; 89US-00301353.  
PR 12-MAY-1989; 89US-00351193.  
XX  
PA (APHT-) APHTON CORP.  
XX  
PI Gevas PC, Grimes S, Karr SL, Littenberg RL;  
XX  
DR WPI; 1990-233029/31.  
XX  
PT Immunogens against gastrin peptide(s) - used to induce antibodies that  
PT specifically neutralise single form of gastrin, G17 or G34.  
XX  
PS Claim 6; Page 19; 32pp; English.  
XX  
CC Antigenic fragments may be attached to an immunogenic carrier and used to  
CC raise Abs to a specific single form of Gastrin ie. G17 or G34. Peptide  
CC fragments capable of binding to these Abs are useful in neutralising anti  
CC -gastrin Abs in vivo. (Updated on 09-JAN-2003 to add missing OS field.)  
XX  
SQ Sequence 12 AA;  
  
Query Match 57.3%; Score 59; DB 2; Length 12;  
Best Local Similarity 90.9%; Pred. No. 0.75;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 EGPWLEEEES 11  
Db 1 EGPWLEEEEA 11

Search completed: January 9, 2006, 16:09:03  
Job time : 92.4923 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 9, 2006, 15:52:14 ; Search time 17.5231 Seconds  
(without alignments)  
93.345 Million cell updates/sec

Title: US-10-759-832-18  
Perfect score: 103  
Sequence: 1 EGPWLEEEESSPPPPC 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80\*  
1: Pirl:.\*  
2: Pirl2:.\*  
3: Pirl3:.\*  
4: Pirl4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	54.4	101	1 GKHUB	gastrin precursor
2	54	52.4	104	1 GMPGB	gastrin precursor
3	52	50.5	548	2 S52735	Cw17R protein - mo
4	52	50.5	639	2 G02919	transcription fact
5	51	49.5	645	2 G01205	TVL protein - huma
6	50	48.5	33	2 A60506	big gastrin - Nort
7	50	48.5	104	1 GNCIT	gastrin precursor
8	50	48.5	238	2 T46166	MTB27 protein - Ar
9	50	48.5	315	2 A84565	hypothetical prote
10	50	48.5	472	2 A60330	protein A precursor
11	50	48.5	535	2 T52098	probable nuclear t
12	49.5	48.1	4005	2 T09070	probable tenascin
13	48	46.6	17	2 A60071	gastrin - rhesus m
14	48	46.6	104	1 GMDG	gastrin precursor
15	48	46.6	395	2 T30048	hypothetical prote
16	48	46.6	457	2 T21063	hypothetical prote
17	48	46.6	736	2 D90574	hypothetical prote
18	48	46.6	995	2 H59432	RhoGAP protein hom
19	47	45.6	17	1 GMSH	gastrin - sheep
20	47	45.6	34	2 JS0426	big gastrin - goat
21	47	45.6	104	1 GMB0	gastrin precursor
22	47	45.6	152	2 T09283	late embryonic abu
23	47	45.6	254	2 D64540	signal-transducing
24	47	45.6	267	2 A46122	homeotic protein H
25	47	45.6	268	2 S18814	homeotic protein H
26	47	45.6	532	2 T52102	probable nuclear t
27	47	45.6	532	2 T52268	Importin alpha t
28	47	45.6	543	2 A38093	transformation-sen
29	47	45.6	850	2 T13352	stn-A protein - fr

ALIGNMENTS

RESULT 1

GKHUB

gastrin precursor [validated] - human  
N;Contains: big gastrin; cryptagastrin; gastrin; gastrin-17  
C;Species: Homo sapiens (man)  
C;Date: 24-Apr-1984 #sequence revision 30-Jun-1987 #text change 09-Jul-2004  
C;Accession: A93997; A94473; A94473; A9152; A91628; A18854; A40869; A32487; B32487; C3  
R;Ito, R.; Sato, K.; Helmer, T.; Jay, G.; Agarwal, K.  
Proc. Natl. Acad. Sci. U.S.A. 81, 4662-4666, 1984  
A;Title: Structural analysis of the gene encoding human gastrin: the large intron conta  
A;Reference number: A93997; MUID:84272693; PMID:6087340  
A;Accession: A93997  
A;Molecule type: DNA  
A;Residues: 1-101 <TO>  
A;Cross-references: UNIPROT:P01350; UNIPARC:UPI000012B0F4; GB:K01254; GB:J00147; NID:91  
R;Kato, K.; Hayashizaki, Y.; Takahashi, Y.; Himeno, S.; Matsuura, K.  
Nucleic Acids Res. 11, 8197-8203, 1983  
A;Title: Molecular cloning of the human gastrin gene.  
A;Reference number: A93497; MUID:84169471; PMID:6324077  
A;Accession: A93497  
A;Molecule type: DNA  
A;Residues: 1-101 <KAT>  
A;Cross-references: UNIPARC:UPI000012B0F4; GB:K00183; NID:g31648; PIDN:CAA25005.1; PID  
R;Harris, J.I.; Kenner, E.W.  
unpublished results, cited by Gregory, R.A., and Tracy, H.J., in Gastrointestinal Hormo

T20H2.17 protein -  
hypothetical prote  
Lsd1 protein homol  
myb protein - rice  
transcription regu  
hypothetical prote  
hypothetical prote  
hypothetical prote  
gene VGF protein -  
amyloid precursor-  
probable magnesium  
VGF8a protein prec  
mating type A alph  
conserved hypotet  
calcium channel al

A;Cross-references: UNIPARC:UPI000014A9F1  
A;Note: the gastrin was isolated from human Zollinger-Ellison pancreatic tumor  
R;Wiborg, O.; Berglund, L.; Boel, E.; Norris, K.; Renfeld, J.F.; Marcker, K.  
Proc. Natl. Acad. Sci. U.S.A. 81, 1067-1069, 1984  
A;Title: Structure of a human gastrin gene.

A;Cross-references: UNIPARC:UPI000014A9F1  
A;Note: the gastrin was isolated from human Zollinger-Ellison pancreatic tumor  
R;Wiborg, O.; Berglund, L.; Boel, E.; Norris, K.; Renfeld, J.F.; Marcker, K.  
Proc. Natl. Acad. Sci. U.S.A. 81, 1067-1069, 1984  
A;Title: Structure of a human gastrin gene.

Tue Jan 10 09:41:49 2006

A;Reference number: A18854; MUID:84144842; PMID:6322186  
A;Accession: A18854  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-101 <WIB>  
A;Cross-references: UNIPARC:UPI000012B0F4; GB:K01254; GB:J00147; NID:g182987; PIDN:AA859  
R;Huebner, V.D.; Jiang, R.; Lee, T.D.; Legesse, K.; Walsh, J.H.; Shively, J.E.; Chew, P.  
J. Biol. Chem. 266, 12223-12227, 1991  
A;Title: Purification and structural characterization of progastrin-derived peptides from  
A;Reference number: A40869; MUID:91286236; PMID:2061307  
A;Accession: A40869  
A;Status: Preliminary  
A;Molecule type: protein  
A;Residues: 22-51 <HUE>  
A;Cross-references: UNIPARC:UPI0000173596  
R;Higashimoto, Y.; Himeno, S.; Shinomura, Y.; Nagao, K.; Tamura, T.; Tarui, S.  
Biochem. Biophys. Res. Commun. 160, 1364-1370, 1989  
A;Title: Purification and structural determination of urinary NH-2-terminal big gastrin  
A;Reference number: A32487; MUID:89273602; PMID:2730647  
A;Accession: A32487  
A;Molecule type: protein  
A;Residues: 59-67 <HI2>  
A;Cross-references: UNIPARC:UPI000014A9EF  
A;Experimental source: urine  
A;Note: this urinary fragment of big gastrin was designated peak Ia  
A;Accession: B32487  
A;Molecule type: protein  
A;Residues: 59-66 <HI3>  
A;Cross-references: UNIPARC:UPI0000173597  
A;Experimental source: urine  
A;Note: this urinary fragment of big gastrin was designated peak Ib  
A;Accession: C32487  
A;Molecule type: protein  
A;Residues: 59-68 <HI4>  
A;Cross-references: UNIPARC:UPI0000173598  
A;Experimental source: urine  
A;Note: this urinary fragment of big gastrin was designated peak II  
R;Higashimoto, Y.; Shinomura, Y.; Nagao, K.; Yasunaga, Y.; Tamura, T.; Tarui, S.  
Biochem. Biophys. Res. Commun. 172, 1392-1399, 1990  
A;Title: Purification of N-terminal hexapeptide of big gastrin from human urine.  
A;Reference number: A36249; MUID:91058586; PMID:2244519  
A;Accession: A36249  
A;Molecule type: protein  
A;Residues: 59-64 <HIG>  
A;Cross-references: UNIPARC:UPI0000173599  
A;Note: this urinary fragment of big gastrin was designated peak III  
R;Boel, E.; Vuust, J.; Norris, F.; Norris, K.; Wind, A.; Rehfeld, J.F.; Marcker, K.A.  
Proc. Natl. Acad. Sci. U.S.A. 80, 2866-2869, 1983  
A;Title: Molecular cloning of human gastrin cDNA: evidence for evolution of gastrin by 9  
A;Reference number: I37408; MUID:83221503; PMID:6574456  
A;Accession: I37408  
A;Molecule type: mRNA  
A;Residues: 1-101 <RES>  
A;Cross-references: UNIPARC:UPI000012B0F4; EMBL:V00511; NID:g31654; PIDN:CAA23769.1; PID  
R;Rehfeld, J.F.; Johnsen, A.H.  
Eur. J. Biochem. 223, 765-773, 1994  
A;Title: Identification of gastrin component I as gastrin-71. The largest possible bios  
A;Reference number: S48183; MUID:94333379; PMID:8055952  
A;Accession: S48183  
A;Status: Preliminary  
A;Molecule type: protein  
A;Residues: 22-40 <REH>  
A;Cross-references: UNIPARC:UPI000017359A  
R;Kariya, Y.; Kato, K.; Hayashizaki, Y.; Himeno, S.; Tarui, S.; Matsubara, K.  
Gene 50, 345-352, 1986  
A;Title: Expression of human gastrin gene in normal and gastrinoma tissues.  
A;Reference number: I54006; MUID:87219893; PMID:3034736  
A;Accession: I54006  
A;Status: translated from GB/ENBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-101 <KAR>  
A;Cross-references: UNIPARC:UPI000012B0F4; GB:M15958; NID:g182990; PIDN:AAAS2520.1; PID:  
R;Rehfeld, J.F.; Hansen, C.P.; Johnsen, A.H.

EMBO J. 14, 389-396, 1995  
A;Title: Post-poly(Glu) cleavage and degradation modified by O-sulfated tyrosine: a novel  
A;Reference number: S54350; MUID:95137019; PMID:7530658  
A;Accession: S54350  
A;Molecule type: protein  
A;Residues: 76-92 <REW>  
A;Cross-references: UNIPARC:UPI000014A9F1  
A;Note: gastrin-6 isolated from gastric mucosa and blood is fully active; sulfation of 1  
C;Genetics:  
A;Gene: GDB:GAS  
A;Cross-references: GDB:119261; OMIM:137250  
A;Map position: 17q-17q  
A;Intons: 71/1  
C;Superfamily: gastrin  
C;Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-56/Product: cryptogastrin (amino-terminal propeptide) #status experimental <PRO>  
F;59-92/Product: big gastrin #status experimental <BGN>  
F;76-92/Product: gastrin #status experimental <SGN>  
F;87-92/Product: gastrin-6 #status experimental <GN6>  
F;59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #link BGN #statu  
F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #link SGN #statu  
F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 54.4%; Score 56; DB 1; Length 101;  
Best Local Similarity 81.8%; Pred. No. 1.3;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPWLEEEES 11  
DB 76 QGPWLEEEEA 86

RESULT 2  
GNPGB  
Gastrin precursor [validated] - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 17-Dec-1982 #sequence revision 17-Dec-1982 #text change 09-Jul-2004  
C;Accession: A93903; B94473; A93148; I46622; A60070; A01618  
R;Yoo, O.J.; Powell, C.T.; Agarwal, K.L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1049-1053, 1982  
A;Title: Molecular cloning and nucleotide sequence of full-length cDNA coding for porc  
A;Reference number: A93903; MUID:82174533; PMID:6951161  
A;Accession: A93903  
A;Molecule type: mRNA  
A;Residues: 1-104 <YOO>  
A;Cross-references: UNIPROT:P01351; UNIPARC:UPI000012B0F6; GB:V01303; GB:J00651; NID:gl.  
R;Harris, J.I.; Kenner, E.W.  
unpublished results, cited by Gregory, R.A., and Tracy, H.J., in Gastrointestinal Hormo  
A;Reference number: A94473  
A;Accession: B94473  
A;Molecule type: protein  
A;Residues: 59-64 'HPP', 68-92 <HAR>  
A;Cross-references: UNIPARC:UPI000017359B  
A;Note: Tyr-87 is sulfated in two-thirds of the molecules  
A;Note: this peptide was extracted from the antral mucosa  
R;Gregory, H.; Hardy, P.M.; Jones, D.S.; Kenner, G.W.; Sheppard, R.C.  
Nature 204, 931-933, 1964  
A;Title: The antral hormone gastrin.  
A;Reference number: A93148  
A;Accession: A93148  
A;Molecule type: protein  
A;Residues: 76-92 <GRE>  
A;Cross-references: UNIPARC:UPI000017359C  
R;Anderson, J.C.; Barton, M.A.; Gregory, R.A.; Hardy, P.M.; Kenner, G.W.; MacLeod, J.K.  
Nature 204, 933-934, 1964  
A;Reference number: A93149  
A;Contents: annotation; synthesis  
R;Agarwal, K.L.; Noyes, B.E.  
Ann. N. Y. Acad. Sci. 343, 433-442, 1980  
A;Title: Studies on gastrin mRNA structure using an oligonucleotide probe.  
A;Reference number: I46622; MUID:80240380; PMID:6930858

A;Accession: I46622  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 56-82 <AGA>  
A;Cross-references: UNIPARC:UPI000016C6EA; GB:M25036; NID:g164626; PIDN:AAA31111.1; PID:  
R;Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.  
Regul. Pept. 25, 223-233, 1989  
A;Title: The constitution and properties of phosphorylated and unphosphorylated C-termin  
A;Reference number: A60070; MUID:89331947; PMID:2756156  
A;Accession: A60070  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 97-104 <DES>  
A;Cross-references: UNIPARC:UPI000017359D  
C;Superfamily: gastrin  
C;Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-56/Domain: amino-terminal propeptide #status predicted <PRO>  
F;59-92/Product: big gastrin #status experimental <BGN>  
F;76-92/Product: gastrin #status experimental <SGN>  
F;59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen  
F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen  
F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly  
F;96/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 52.4%; Score 54; DB 1; Length 104;  
Best Local Similarity 72.7%; Pred. No. 2.5;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11  
|||:|||||:  
Db 76 QGPWMEEEEA 86

RESULT 3  
S52735  
C;Species: Mus musculus (house mouse)  
C;Date: 19-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 05-Nov-1999  
C;Accession: S52735  
R;Schmitt-Wrede, H.P.; Wrehlke, C.; Qiao, Z.D.; Heischkamp, H.; Bente, W.P.M.; Wunderli  
submitted to the EMBL Data Library, March 1995  
A;Description: Testosterone-induced immunosuppression of Plasmodium chabaudi malaria: di  
A;Reference number: S52735  
A;Accession: S52735  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-548 <SCH>  
A;Cross-references: UNIPARC:UPI000016D1C4; EMBL:X85802; NID:g1332610; PIDN:CAA59797.1; H

Query Match 50.5%; Score 52; DB 2; Length 548;  
Best Local Similarity 42.9%; Pred. No. 26;  
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 PWLEEEESGPPPP 16  
|||:|||||:  
Db 499 PWQQQQQPPPPPP 512

RESULT 4  
G02919  
C;Species: Homo sapiens (man)  
C;Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 09-Jul-2004  
C;Accession: G02919; I54371; I68667; I68669  
R;Breviario, P.  
submitted to GenBank, December 1995  
A;Reference number: H01954  
A;Accession: G02919  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-639 <BRE>

A;Cross-references: UNIPROT:Q15637; UNIPARC:UPI0000072211; GB:L49380; NID:g1405420; PID:  
R;Toda, T.; Iida, A.; Miwa, T.; Nakamura, Y.; Imai, T.  
Hum. Mol. Genet. 3, 465-470, 1994  
A;Title: Isolation and characterization of a novel gene encoding nuclear protein at a l  
A;Reference number: I54371; MUID:94282041; PMID:7912130  
A;Accession: I54371  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-268, 'G', 270-347, 'A', 349-376, 'W', 378-586, 'RSIECLLCLLSLTQLPLPLPKPGQDPSRR  
A;Cross-references: UNIPARC:UPI0000073986; GB:D26120; NID:g785995; PIDN:BAA05116.1; PID  
A;Accession: I68667  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-268, 'G', 270-347, 'A', 349-376, 'W', 378-527, 'RSLPAAAM', 536, 'RAMRVRTFRAHW' <R  
A;Cross-references: UNIPARC:UPI00000703C3; GB:D26120; NID:g785995; PIDN:BAA05116.1; PID  
A;Accession: I68669  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 116-138 <RE3>  
A;Cross-references: UNIPARC:UPI000006D50F; GB:D26122; NID:g473832; PIDN:BAA05119.1; PID  
C;Genetics:  
A;Gene: GDB:ZNF162; ZPM1  
A;Cross-references: GDB:320035; OMIM:601516  
A;Map position: 11q13-11q13  
A;Introns: 528/1

Query Match 50.5%; Score 52; DB 2; Length 639;  
Best Local Similarity 42.9%; Pred. No. 31;  
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 PWLEEEESGPPPP 16  
|||:|||||:  
Db 499 PWQQQQQPPPPPP 512

RESULT 5  
G01205  
TYL protein - human  
C;Species: Homo sapiens (man)  
C;Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 09-Jul-2004  
C;Accession: G01205  
R;Perletti, L.  
submitted to the EMBL Data Library, July 1996  
A;Reference number: H00608  
A;Accession: G01205  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-645 <PER>  
A;Cross-references: UNIPROT:Q15673; UNIPARC:UPI00000700C6; EMBL:X99688; NID:g1480102  
C;Genetics:  
A;Gene: TVL

Query Match 49.5%; Score 51; DB 2; Length 645;  
Best Local Similarity 37.8%; Pred. No. 42;  
Matches 11; Conservative 3; Mismatches 3; Indels 12; Gaps 2;

QY 1 EGPWLE--BEES-----SPPPPC 17  
|||:|||||:  
Db 96 DGPWTQGESEAEARAKLAPGREPPSPC 124

RESULT 6  
A60506  
big gastrin - North American opossum  
N;Contains: gastrin  
C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opos  
C;Date: 19-Mar-1993 #sequence\_revision 19-Mar-1993 #text\_change 09-Jul-2004  
C;Accession: A60506  
R;Shinomura, Y.; Eng, J.; Rattan, S.C.; Yalow, R.S.  
Comp. Biochem. Physiol. B 96, 239-242, 1990  
A;Title: Opossum (Didelphis virginiana) "little" and "big" gastrins.  
A;Reference number: A60506; MUID:90298616; PMID:2361360  
A;Accession: A60506

Tue Jan 10 09:41:49 2006

A;Molecule type: protein  
A;Residues: 1-33 <SH1>  
A;Cross-references: UNIPROT:P33713; UNIPARC:UPI000012B0F1  
C;Superfamily: Gastrin  
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; sulfoprotein  
F;1-33/Product: big gastrin #status experimental <MATB>  
F;18-33/Product: gastrin #status experimental <MATL>  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;1/Binding site: sulfatate (Tyr) (covalent) (partial) #status experimental  
F;28/Modified site: amidated carboxyl end (Phe) #status experimental  
F;33/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 48.5%; Score 50; DB 2; Length 33;  
Best Local Similarity 88.9%; Pred. No. 2.4;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9  
Db 18 QGPWLEEEE 26  
:|||||

RESULT 7  
GMCT  
gastrin precursor [validated] - cat  
N;Contains: big gastrin (gastrin-34); gastrin  
C;Species: Felis silvestris catus (domestic cat)  
C;Date: 13-Jun-1983 #sequence revision 02-Jun-1994 #text\_change 09-Jul-2004  
C;Accession: S14401, A01621; A61074  
R;Kim, S.-J.; Uhm, K.N.; Kang, Y.K.; Yoo, O.J.  
DNA Seq. 1, 181-187, 1991  
A;Title: Bovine and feline gastrin cDNA sequences and the amino acid and nucleotide sequence  
A;Reference number: S14400, MUID:92127058; PMID:1773057  
A;Accession: S14401  
A;Molecule type: mRNA  
A;Residues: 1-104 <IM>  
A;Cross-references: UNIPROT:P01354; UNIPARC:UPI000012B0F2; EMBL:X16582; NID:G1099; PIDN:  
R;Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.  
J. Am. Chem. Soc. 91, 3096-3097, 1969  
A;Title: Feline gastrin. An example of peptide sequence analysis by mass spectrometry.  
A;Reference number: A01621; MUID:69206035; PMID:5784957  
A;Accession: A01621  
A;Molecule type: protein  
A;Residues: 76-92 <AGA>  
A;Cross-references: UNIPARC:UPI00001735A3  
R;Eng, J.; Du, B.H.; Johnson, G.F.; Kanakamedala, S.; Samuel, S.; Raufman, J.P.; Straus,  
Regul. Pept. 37, 9-13, 1992  
A;Title: Cat gastrinoma and the sequence of cat gastrins.  
A;Reference number: A61074; MUID:92262853; PMID:1585019  
A;Accession: A61074  
A;Molecule type: protein  
A;Residues: 59-92 <ENG>  
A;Cross-references: UNIPARC:UPI00001735A4  
C;Superfamily: gastrin  
C;Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;59-92/Product: big gastrin #status experimental <BNAT>  
F;76-92/Product: gastrin #status experimental <MAT>  
F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental  
F;87/Binding site: sulfatate (Tyr) (covalent) (partial) #status experimental  
F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 48.5%; Score 50; DB 1; Length 104;  
Best Local Similarity 88.9%; Pred. No. 8.2;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9  
Db 76 QGPWLEEEE 84  
:|||||

RESULT 8  
T46166  
MYB27 protein - Arabidopsis thaliana  
N;Alternate names: protein T4D2.130

C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 31-Dec-2004  
C;Accession: T46166  
R;Nakatani, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;  
submitted to the Protein Sequence Database, December 1999  
A;Reference number: 223025  
A;Accession: T46166  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-238 <NYA>  
A;Cross-references: UNIPROT:Q9SCP1; UNIPARC:UPI0000000CSAE; EMBL:AL132958  
A;Experimental source: cultivar Columbia; BAC clone T4D2  
C;Genetics:  
A;Map position: 3  
A;Introns: 42/1; 85/2; 119/1  
A;Note: T4D2.130  
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 48.5%; Score 50; DB 2; Length 238;  
Best Local Similarity 88.9%; Pred. No. 20;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPWLEEEE 10  
Db 12 GPWLEEEE 20  
:|||||

## RESULT 9

A84565  
Hypothetical protein At2g18500 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: A84565  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: A84565  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-315 <STO>  
A;Cross-references: UNIPROT:Q9ZU65; UNIPARC:UPI0000000BE2B; GB:AE002093; NID:G4218008; PID:  
C;Genetics:  
A;Gene: At2g18500  
A;Map position: 2

Query Match 48.5%; Score 50; DB 2; Length 315;  
Best Local Similarity 75.0%; Pred. No. 27;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LEEESSESPPPP 16  
Db 191 IEESSESSSPPP 202  
:|||||

## RESULT 10

protein A precursor - Treponema denticola  
C;Species: Treponema denticola  
C;Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000  
C;Accession: A60330  
R;Miyamoto, M.; Noji, S.; Kokeguchi, S.; Kato, K.; Kurihara, H.; Murayama, Y.; Taniguchi,  
Infect. Immun. 59, 1941-1947, 1991  
A;Title: Molecular cloning and sequence analysis of antigen gene tdpA of Treponema dent  
A;Reference number: A60330; MUID:91244433; PMID:2037356  
A;Accession: A60330  
A;Molecule type: DNA  
A;Residues: 1-472 <MIY>  
A;Cross-references: UNIPARC:UPI000017047A; GB:D00598; NID:G217165; PIDN:BAAA00474.1; PID:  
C;Genetics:  
A;Gene: tdpA

C;Superfamily: Treponema denticola protein A  
 C;Keywords: lipoprotein; membrane protein  
 F;1-16/Domain: signal sequence #status predicted <SIG>  
 F;17-472/Product: protein A #status predicted <MAT>

Query Match 48.5%; Score 50; DB 2; Length 472;  
 Best Local Similarity 50.0%; Pred. No. 41;  
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EGPWLEEESSPPPP 16  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 438 ENKWFNEYETATPPP 453

## RESULT 11

T52098  
 Probable nuclear transport factor importin alpha [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004  
 C;Accession: T52098  
 R;Schledz, M.; Leclerc, D.; Neuhaus, G.; Merkle, T.  
 submitted to the EMBL Data Library, August 1997  
 A;Reference number: Z25951  
 A;Accession: T52098  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-535 <SCH>  
 A;Cross-references: UNIPROT:O49600; UNIPARC:UPI000000ACF1C; EMBL:Y14615; P1DN:CAA74965.1  
 A;Experimental source: ecotype Columbia; vegetative tissue; 3 weeks old  
 C;Genetics:  
 A;Gene: Impa-2  
 C;Superfamily: pendulin

Query Match 48.5%; Score 50; DB 2; Length 535;  
 Best Local Similarity 72.7%; Pred. No. 47;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 WLEEESSPP 14  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 499 WLEEEETLPP 509

## RESULT 12

T09070  
 Probable tenascin X - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
 C;Accession: T09070  
 R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; So  
 submitted to the EMBL Data Library, October 1997  
 A;Description: Sequence of the mouse major histocompatibility locus class III region.  
 A;Reference number: Z16543  
 A;Accession: T09070  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-4006 <ROW>  
 A;Cross-references: UNIPROT:O35452; UNIPARC:UPI000002A159; EMBL:AF030001; NID:G2564945;  
 C;Genetics:  
 A;Gene: TNX  
 A;Map position: 17  
 A;Intons: 124/1; 735/1; 773/3; 826/1; 914/1; 1037/1; 1135/1; 1232/1; 1329/1; 1440/1; 15  
 019/1; 3115/1; 3208/1; 3302/1; 3405/1; 3517/1; 3558/1; 3606/1; 3646/1; 3694/1; 3737/3; 3  
 C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin ty  
 C;Keywords: extracellular matrix  
 F;422-448/Domain: EGF homology <EGF>  
 F;826-906/Domain: fibronectin type III repeat homology <3PR>  
 F;3789-3997/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 48.1%; Score 49.5; DB 2; Length 4006;  
 Best Local Similarity 43.5%; Pred. No. 4.6e+02;  
 Matches 10; Conservative 1; Mismatches 5; Indels 7; Gaps 1;

Qy 1 EGPWLEEE-----ESSPPPP 16

Db 986 EGPWAHELLPGDVQQAALVPPPP 1008  
 | | | | | | | | | | | | | | | | | | | | | |  
 | | | | | | | | | | | | | | | | | | | | | |

## RESULT 13

A60071  
 Gastrin - rhesus macaque  
 C;Species: Macaca mulatta (rhesus macaque)  
 C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 09-Jul-2004  
 C;Accession: A60071  
 R;Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.  
 Regul. Pept. 32, 39-45, 1991  
 A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences  
 A;Reference number: A60071; MUID:91164506; PMID:2003150  
 A;Accession: A60071  
 A;Molecule type: protein  
 A;Residues: 1-17 <YUA>  
 A;Cross-references: UNIPROT:P33714; UNIPARC:UPI0000012B0F5  
 C;Superfamily: gastrin  
 C;Keywords: amidated carboxyl end; hormone; intestine; pyroglutamic acid; sulfoprotein  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;12/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
 F;17/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 46.6%; Score 48; DB 2; Length 17;  
 Best Local Similarity 77.8%; Pred. No. 2.2;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9  
 : | | | | | | | | | | | | | | | | | | | | | |  
 Db 1 QGPMWEEEE 9

## RESULT 14

GMDG  
 Gastrin precursor [validated] - dog  
 N;Contains: big gastrin; gastrin  
 C;Species: Canis lupus familiaris (dog)  
 C;Date: 13-Jun-1983 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
 C;Accession: B61053; A61053; JS0425; A01620; B60070  
 R;Gantz, I.; Takeuchi, T.; Yamada, T.  
 Digestion 46, 99-104, 1990  
 A;Title: Cloning of canine gastrin cDNA's encoding variant amino acid sequences.  
 A;Reference number: A61053; MUID:91085716; PMID:2262079  
 A;Accession: B61053  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-104 <GAN>  
 A;Cross-references: UNIPROT:P01353; UNIPARC:UPI0000012B0ED  
 A;Accession: A61053  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-84, T', 86-104 <GA2>  
 A;Cross-references: UNIPARC:UPI0000017359E  
 A;Note: It is unclear whether the sequence difference results from polymorphism, multi

R;Bonato, C.; Eng, J.; Hulmes, J.D.; Miedel, M.; Pan, Y.C.E.; Yalow, R.S.  
 Peptides 7, 689-693, 1986  
 A;Title: Sequences of gastrins purified from a single antrum of dog and of goat.  
 A;Reference number: JS0425; MUID:87016557; PMID:3763441  
 A;Accession: JS0425  
 A;Molecule type: protein  
 A;Residues: 59-92 <BON>  
 A;Cross-references: UNIPARC:UPI0000017359F  
 A;Experimental source: antral mucosa  
 A;Note: about 10% of gastrin is sulfated  
 R;Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.  
 Experientia 25, 346-348, 1969  
 A;Title: Structure and synthesis of canine gastrin.  
 A;Reference number: A01620; MUID:69253357; PMID:5799207  
 A;Accession: A01620  
 A;Molecule type: protein  
 A;Residues: 76-82, 'A', '84', 'E', '86-92 <AGA>  
 A;Cross-references: UNIPARC:UPI000001735A0

R;Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.  
Regul. Pept. 25, 223-233, 1989  
A;Title: The constitution and properties of phosphorylated and unphosphorylated C-termin  
A;Reference number: A60070; MUID:89331947; PMID:2756156  
A;Accession: B60070  
A;Molecule type: protein  
A;Residues: 96-104 <DES>  
A;Cross-references: UNIPARC:UPI00001735A1  
C;Comment: Big gastrin constitutes only about 5% of antral gastrin.  
C;Superfamily: Gastrin  
C;Keywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic acid;  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;59-92/Product: big gastrin #status experimental <MAT>  
F;76-92/Product: gastrin #status experimental <MA1>  
F;59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen  
F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen  
F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
F;92/Modified site: amidated carboxyl end (phe) (amide in mature form from following gly  
F;96/Binding site: phosphate (Ser) (covalent) (partial) #status experimental

Query Match 46.6%; Score 48; DB 1; Length 104;  
Best Local Similarity 77.1%; Pred. No. 15;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGFWLEEEE 9  
DB 76 QGFWMEEEE 84

RESULT 15  
T30048  
hypothetical protein K06C4.6 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000  
C;Accession: T30048  
R;Miller, N.; Bradshaw, H.  
submitted to the EMBL Data Library, July 1996  
A;Description: The sequence of C. elegans cosmid K06C4.  
A;Reference number: Z20728  
A;Accession: T30048  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-395 <MIL>  
A;Cross-references: UNIPARC:UPI000017799B; EMBL:U64843; PIDN:AAB04848.1; GSPDB:GN000023;  
A;Experimental source: strain Bristol N2; clone K06C4  
C;Genetics:  
A;Gene: CESP:K06C4.6  
A;Map position: 5  
A;Introns: 28/3; 65/2; 106/3; 264/1; 298/2; 327/3; 341/3; 378/3  
C;Superfamily: acetylcholine receptor

Query Match 46.6%; Score 48; DB 2; Length 395;  
Best Local Similarity 57.1%; Pred. No. 61;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 PWLEEEESSPPPP 16  
DB 337 FLIEMRSTSPPPP 350

Search completed: January 9, 2006, 16:10:20  
Job time : 18.5231 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2006, 15:38:08 ; Search time 96.2462 Seconds  
(without alignments)  
124.618 Million cell updates/sec

Title: US-10-759-832-18

Perfect score: 103

Sequence: 1 EGPWLEEEERSPPPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	56.3	839	1 APBA1 RAT	Q35430 rattus norv
2	56	54.4	101	1 GAST HUMAN	P01350 homo sapien
3	56	54.4	200	2 Q5XJ22 BRARE	Q5XJ22 brachydanio
4	56	54.4	212	2 Q5RGW2 BRARE	Q5RGW2 brachydanio
5	55	53.4	298	2 Q7S888 NEUCR	Q7S888 neurospora
6	55	53.4	336	2 Q5JMG8 ORYSA	Q5JMG8 oryza sativ
7	55	53.4	543	2 Q6P302 XENTR	Q6P302 xenopus tro
8	54	52.4	104	1 GAST PIG	P01351 sus scrofa
9	54	52.4	204	2 Q5CZ84 HUMAN	Q5CZ84 homo sapien
10	54	52.4	217	2 Q5JS24 HUMAN	Q5JS24 homo sapien
11	54	52.4	224	1 CHIC1 HUMAN	Q5VXU3 homo sapien
12	54	52.4	265	2 Q7QKK0 ANOGA	Q7QKK0 anopheles g
13	54	52.4	492	2 Q4WZ06 ASPFU	Q4WZ06 aspergillus
14	54	52.4	812	2 Q73M73 TREDE	Q73M73 treponema d
15	53	51.5	254	2 Q82H29 STRAW	Q82H29 streptomyce
16	53	51.5	309	2 Q6DHS9 BRARE	Q6DHS9 brachydanio
17	53	51.5	515	2 Q4IF73 GIBZE	Q4IF73 gibberella
18	53	51.5	1151	2 Q6R7F1 GHERP	Q6R7F1 ostrleid her
19	52.5	51.0	218	2 Q7PY87 ANOGA	Q7PY87 anopheles g
20	52.5	51.0	267	2 Q4WND3 ASPFU	Q4WND3 aspergillus
21	52	50.5	182	2 Q5TV37 ANOGA	Q5TV37 anopheles g
22	52	50.5	211	2 Q76123 ORYSA	Q76123 oryza sativ
23	52	50.5	231	2 Q6Z730 ORYSA	Q6Z730 oryza sativ
24	52	50.5	320	2 Q6L9K2 ARATH	Q6L9K2 arabidopsis
25	52	50.5	450	2 Q6MYW6 ASPFU	Q6MYW6 aspergillus
26	52	50.5	455	2 Q4WS76 ASPFU	Q4WS76 aspergillus
27	52	50.5	502	2 Q66HH6 RAT	Q66HH6 rattus norv
28	52	50.5	530	2 Q4T6W3 TETNG	Q4T6W3 tetraodon n
29	52	50.5	542	2 Q5RKM3 BRARE	Q5RKM3 brachydanio
30	52	50.5	543	2 Q7ZWU1 XENLA	Q7ZWU1 xenopus lae
31	52	50.5	550	2 Q4X1P5 ASPFU	Q4X1P5 aspergillus

32	52	50.5	612	2 Q8N3W1 HUMAN	Q8N3W1 homo sapien
33	52	50.5	613	2 Q8IXT9 HUMAN	Q8IXT9 homo sapien
34	52	50.5	614	2 Q96C34 HUMAN	Q96C34 homo sapien
35	52	50.5	633	2 Q5VJK7 RAT	Q5VJK7 rattus norv
36	52	50.5	639	1 SP01 HUMAN	Q15637 homo sapien
37	52	50.5	650	1 APLP1 HUMAN	P51693 homo sapien
38	52	50.5	653	1 SF01_MOUSE	Q64213 mus musculu
39	52	50.5	962	2 Q9EB08_VIRU	Q9EB08 sesbania mo
40	52	50.5	1059	2 Q5VJW4 RAT	Q5VJW4 rattus norv
41	52	50.5	1234	2 Q4WEL2 ASPFU	Q4WEL2 aspergillus
42	52	50.5	1424	2 Q5XJV6_MOUSE	Q5XJV6 mus musculu
43	52	50.5	1424	2 Q52KF1_MOUSE	Q52KF1 mus musculu
44	51.5	50.0	1688	2 Q4TBX6_TETNG	Q4TBX6 tetraodon n
45	51	49.5	227	1 CHIC1_MOUSE	Q8CBW7 mus musculu

#### ALIGNMENTS

RESULT 1  
APBA1 RAT STANDARD; PRT; 839 AA.  
AC Q35430;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Anyloid beta A4 precursor protein-binding family A member 1 (Neuron-specific X11 protein) (Neuronal Munc18-1-interacting protein 1) (Mint-1) (Adapter protein X11alpha).  
DE 1)  
GN Name=Apbal; Synonyms=Mint1, X11;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OC NCBI\_TaxID=10116;  
OX [1]  
RN NUCLEOTIDE SEQUENCE.  
RP TISSUE=Brain;  
RC MEDLINE=98058933; PubMed=9395480; DOI=10.1074/jbc.272.50.31459;  
RX Okamoto M., Suedhof T.C.;  
RA "Mintc, Munc18-interacting proteins in synaptic vesicle exocytosis."; J. Biol. Chem. 272:31459-31464(1997).  
RL [2]  
RN INTERACTIONS WITH CASK AND LIN7.  
RC TISSUE=Testis;  
MEDLINE=98424246; PubMed=9753324; DOI=10.1016/S0092-8674(00)81736-5;  
RX Butz S., Okamoto M., Suedhof T.C.;  
RA "A tripartite protein complex with the potential to couple synaptic vesicle exocytosis to cell adhesion in brain."; Cell 94:773-782(1998).  
RL [1]  
RN FUNCTION: Putative function in synaptic vesicle exocytosis by binding to Munc18-1, an essential component of the synaptic vesicle exocytotic machinery. May modulate processing of the beta-amyloid precursor protein (APP) and hence formation of beta-APP.  
CC SUBUNIT: Part of a multimeric complex containing Munc18-1 and synaptotagmin-1. Also part of the brain-specific heterotrimeric complex LIN-10/X11-alpha, LIN-2/CASK, and LIN7. Binds to the cytoplasmic domain of amyloid protein (APP) (By similarity).  
CC TISSUE SPECIFICITY: Brain. Detected in the cerebellum, hippocampus, olfactory system, piriform and entorhinal cortex, suproptic nucleus of the hypothalamus, substantia nigra, and other mesencephalic areas.  
CC -1- DOMAIN: Composed of an N-terminal domain that binds Munc18-1 and LIN-2/CASK, a middle phosphotyrosine-binding domain (PID/PTB) that mediates binding with the cytoplasmic domain of the beta-amyloid precursor protein, and two C-terminal PDZ domains thought to attach proteins to the plasma membrane (By similarity).  
CC -1- SIMILARITY: Contains 2 PDZ (DHR) domains.  
CC -1- SIMILARITY: Contains 1 PID domain.

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CC use as long as its content is in no way modified and this statement is not removed.

CC -----  
CC EMBL; AF029105; AAC05303.1; -; mRNA.  
CC HSSP; Q02410; IAQC.  
CC DR Ensembl; ENSRNOG00000014928; Rattus norvegicus.  
CC DR RGD; 620844; Apbal.  
CC DR GO; GO:0005886; C:plasma membrane; IDA.  
CC DR GO; GO:0005546; F:phosphatidylinositol-4,5-bisphosphate binding; IDA.  
CC DR GO; GO:0005515; F:protein binding; IDA.  
CC DR GO; GO:0016079; P:synaptic vesicle exocytosis; TAS.  
CC DR InterPro; IPR001478; PDZ.  
CC DR InterPro; IPR011993; PH type.  
CC DR InterPro; IPR006020; PTB\_PID.  
CC DR Pfam; PF00595; PDZ; 2.  
CC DR Pfam; PF00640; PID; 1.  
CC DR SMART; SM00228; PDZ; 2.  
CC DR SMART; SM00462; PTB; 1.  
CC DR PROSITE; PS01106; PID; 2.  
CC DR PROSITE; PS01179; PID; 1.  
CC DR Protein transport; Repeat; Transport.  
KW DOMAIN 459 645 PID.  
FT DOMAIN 658 744 PDZ 1.  
FT DOMAIN 749 824 PDZ 2.  
FT REGION 227 315 Munc-18-1 binding.  
FT REGION 375 438 LIN-2/CASK binding.  
FT COMPIAS 40 65 Pro-rich.  
FT COMPIAS 67 71 Poly-Glu.  
FT COMPIAS 295 331 Pro-rich.  
FT COMPIAS 370 454 Pro-rich.  
SQ SEQUENCE 839 AA; 92654 MW; 57F6EEA458376CAD CRC64;  
  
Query Match 56.3%; Score 58; DB 1; Length 839;  
Best Local Similarity 62.5%; Pred. No. 66;  
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 EGPWLREEEESSPPPP 16  
Db 30 EHPEVEEQSPSPPP 45  
| : ||| : ||||  
| : ||| : ||||  
  
RESULT 2  
GAST\_HUMAN STANDARD; PRT; 101 AA.  
AC -GAST\_HUMAN STANDARD; PRT; 101 AA.  
ID P01350; P78463; P78464;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 23-OCT-1986 (Rel. 02, Last sequence update)  
DE Gastrin precursor [Contains: Gastrin 71 (Component I); Gastrin 52; Big  
DE Gastrin (Gastrin 34) (Component II); Gastrin (Gastrin 17) (Component  
DE III); Gastrin 14; Gastrin 6].  
GN Name=GAST; Synonyms=GAS;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=87219893; PubMed=3034736; DOI=10.1016/0378-1119(86)90338-0;  
RA Kariya Y., Kato K., Hayaishizaki Y., Himeno S., Tarui S., Matsubara K.;  
RT "Expression of human gastrin gene in normal and gastrinoma tissues.";  
RL Gene 50:345-352(1986).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=84272693; PubMed=6087340;  
RA Ito R., Sato K., Helmer T., Jay G., Agarwal K.L.;  
RT "Structural analysis of the gene encoding human gastrin: the large  
RT intron contains an Alu sequence.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:4662-4666(1984).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=84169471; PubMed=6324077;

RA Kato K., Hayaishizaki Y., Takahashi Y., Himeno S., Matsubara K.;  
RT "Molecular cloning of the human gastrin gene.";  
RN Nucleic Acids Res. 11:8197-8203(1983).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=83221503; PubMed=6574456;  
RA Boel E., Vuust J., Norris F., Norris K., Wind A., Rehfeld J.F.,  
RA Marcker K.A.;  
RT "Molecular cloning of human gastrin cDNA: evidence for evolution of  
RT gastrin by gene duplication.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:2866-2869(1983).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=84144842; PubMed=6322186;  
RA Wiborg O., Berglund L., Boel E., Norris F., Norris K., Rehfeld J.F.,  
RA Marcker K.A., Vuust J.;  
RT "Structure of a human gastrin gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:1067-1069(1984).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=84159488; PubMed=6689486; DOI=10.1016/0378-1119(83)90035-5;  
RA Kato K., Himeno S., Takahashi Y., Wakabayashi T., Tarui S.,  
RA Matsubara K.;  
RT "Molecular cloning of human gastrin precursor cDNA.";  
RN Gene 26:53-57(1983).  
RN [7]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [8]  
RP PROTEIN SEQUENCE OF 22-101, AND CHARACTERIZATION OF GASTRIN 71.  
RC TISSUE=Antral mucosa;  
RX MEDLINE=94333379; PubMed=8055952;  
RA Rehfeld J.F., Johnsen A.H.;  
RT "Identification of gastrin component I as gastrin-71. The largest  
RT possible bioactive progastrin product.";  
RL Eur. J. Biochem. 223:765-773(1994).  
RN [9]  
RP PROTEIN SEQUENCE OF 76-92.  
RX MEDLINE=67021327; PubMed=5921183;  
RA Bentley P.H., Kenner G.W., Sheppard R.C.;  
RT "Structures of human gastrins I and II.";  
RL Nature 209:583-585(1966).  
RN [10]  
RP PROTEIN SEQUENCE OF 59-68.  
RX MEDLINE=89273602; PubMed=2730647;  
RA Higashimoto Y., Himeno S., Shinomura Y., Nagao K., Tamura T.,  
RA Tarui S.;  
RT "Purification and structural determination of urinary NH2-terminal big  
RT gastrin fragments.";  
RL Biochem. Biophys. Res. Commun. 160:1364-1370(1989).  
RN [11]  
RP PROTEIN SEQUENCE OF 76-92.  
RX MEDLINE=69298172; PubMed=5822140;

RA Gregory R.A., Tracy H.J., Agarwal K.L., Grosseman M.I.;  
 RT "Aminoacid constitution of two gastrins isolated from Zollinger-  
 RL Ellison tumour tissue.";  
 RL Gut 10:603-608(1969).  
 RN [12]  
 RP CHARACTERIZATION OF GASTRIN 6, AND SULFATION OF TYR-87.  
 RX MEDLINE=95137019; PubMed=7530658;  
 RA Rehfeld J.F., Hansen C.P., Johnsen A.H.;  
 RT "Post-poly(Glu) cleavage and degradation modified by O-sulfated  
 RL tyrosine: a novel post-translational processing mechanism.";  
 RL EMBO J. 14:389-396(1995).  
 RN [13]  
 RP PROCRESSING, AND SULFATION OF TYR-87.  
 RX MEDLINE=20508341; PubMed=11052986;  
 RA Palmes Hansen C., Stadil F., Rehfeld J.F.;  
 RT "Metabolism and acid secretory effect of sulfated and nonsulfated  
 RL gastrin-6 in humans.";  
 RL Am. J. Physiol. 279:G903-G909(2000).  
 CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and  
 CC secrete hydrochloric acid and the pancreas to secrete its  
 CC digestive enzymes. It also stimulates smooth muscle contraction  
 CC and increases blood circulation and water secretion in the stomach  
 CC and intestine.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: Two different processing pathways probably exist in antral G-  
 CC cells. In the dominant pathway progastrin is cleaved at three  
 CC sites resulting in two major bioactive gastrins, gastrin-34 and  
 CC gastrin-17. In the putative alternative pathway, progastrin may be  
 CC processed only at the most C-terminal dibasic site resulting in  
 CC the synthesis of gastrin-71.  
 CC -1- PTM: Sulfation of Tyr-87 blocks peptide degradation and enhances  
 CC activity.  
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; X00183; CAA25005.1; -; Genomic DNA.  
 CC EMBL; X00183; CAA25006.1; -; Genomic DNA.  
 CC EMBL; X00183; CAA25007.1; -; Genomic DNA.  
 CC EMBL; X00511; CAA23769.1; -; mRNA.  
 CC EMBL; M15958; AAS2520.1; -; Genomic DNA.  
 CC EMBL; X01254; AAB59533.1; -; Genomic DNA.  
 CC EMBL; BC069724; AAB69724.1; -; mRNA.  
 CC EMBL; BC069762; AAB69762.1; -; mRNA.  
 CC PIR; A93997; GMHUB.  
 CC Ensembl; ENSG00000184502; Homo sapiens.  
 CC HGNC; HGNC:4164; GAST.  
 CC MIM; 137250; -.  
 CC GO; GO:0005179; F: hormone activity; TAS.  
 CC GO; GO:0007165; P: signal transduction; NAS.  
 CC InterPro; IPR001651; Gastrin.  
 CC Pfam; PF00918; Gastrin, 1.  
 CC SMART; SM00029; Gastrin, 1.  
 CC PROSITE; PS00259; GASTRIN; 1.  
 CC Amidation; Cleavage on pair of basic residues;  
 CC Direct protein sequencing; Hormone; Phosphorylation;  
 CC Pyrolydione carboxylic acid; Signal; Sulfation.  
 FT SIGNAL 1 21  
 FT PEPTIDE 22 92 Gastrin 71.  
 FT PEPTIDE 41 92 Gastrin 52.  
 FT PEPTIDE 59 92 Big gastrin.  
 FT PEPTIDE 76 92 Gastrin.  
 FT PEPTIDE 79 92 Gastrin 14.  
 FT PEPTIDE 87 92 Gastrin 6.  
 FT PROPEP 96 101 Removed in mature form.  
 FT SITE 40 41 Cleavage.  
 FT SITE 58 59 Cleavage.  
 FT SITE 75 76 Cleavage.  
 FT SITE 95 95 Cleavage.

FT MOD\_RES 59 59 Pyrrolidone carboxylic acid.  
 FT MOD\_RES 76 76 Pyrrolidone carboxylic acid.  
 FT MOD\_RES 87 87 Sulfotyrosine (partial).  
 FT MOD\_RES 92 92 Phenylalanine amide (G-93 provides amide  
 group).  
 FT MOD\_RES 96 96 Phosphoserine (By similarity).  
 SQ SEQUENCE 101 AA; 11394 MW; A03C847CFE7216C CRC64;  
 Query Match 54.4%; Score 56; DB 1; Length 101;  
 Best Local Similarity 81.8%; Pred. No. 12;  
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEES 11  
 Db 76 QGPWLEEEEA 86  
 :|||||:  
 76 QGPWLEEEEA 86  
 RESULT 3  
 Q5XJP2 BRARE PRELIMINARY; PRT; 200 AA.  
 ID Q5XJP2 BRARE PRELIMINARY;  
 AC Q5XJP2;  
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)  
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)  
 DE Zgc:101717.  
 GN ORFNames=zgc:101717;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 CC Cyprinidae; Danio.  
 CC NCBI\_TaxID=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=olfactory epithelium;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Sapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueclin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=olfactory epithelium;  
 RA Director MGC Project;  
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; BC083256; AAB83256.1; -; mRNA.  
 RL ZFIN; ZDB-GENE-041010-168; zgc:101717.  
 DR GO; GO:0005622; C: intracellular; IEA.  
 DR GO; GO:0005515; P: protein binding; IEA.  
 DR GO; GO:0042981; P: regulation of apoptosis; IEA.  
 DR GO; GO:0007165; P: signal transduction; IEA.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR000488; Death.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00531; Death; 1.  
 DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00005; DEATH; 1.  
 DR PROSITE; PS50209; CARD; 1.

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DR PROSITE, PS50017; DEATH_DOMAIN; 1.
SQ SEQUENCE 200 AA; 22744 MW; 367283BEF02AF5FF CRC64;

Query Match 54.4%; Score 56; DB 2; Length 200;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 10; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 3 PWLEE-----EEESSPPPP 16
DB 81 FWIRDKLQLNEEESPPPP 100

RESULT 4
Q5RCW2 BRARE
ID Q5RCW2_BRARE PRELIMINARY; PRT; 212 AA.
AC Q5RCW2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel protein similar to vertebrate CASP2 and RIPK1 domain containing
DE adaptor with death domain (CRADD) (Fragment).
GN Name=ORTDARP0000007994; ORFNames=DKEYP-30A8.3-001;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hunter G.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX649503; CAI21366.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR004488; Death.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00531; Death; 1.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00005; DEATH; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
FT NON_TER 1
SQ SEQUENCE 212 AA; 23985 MW; 8FBC690938DCE624 CRC64;

Query Match 54.4%; Score 56; DB 2; Length 212;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 10; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 3 PWLEE-----EEESSPPPP 16
DB 93 FWIRDKLQLNEEESPPPP 112

RESULT 5
Q7S8S8 NEUCR
ID Q7S8S8_NEUCR PRELIMINARY; PRT; 298 AA.
AC Q7S8S8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU08806.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Koche G.O., Jedd K., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmami S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Naevig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAE0100024; EAA32757.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003684; F:damaged DNA binding; IEA.
DR GO; GO:0008094; F:DNA-dependent ATPase activity; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR GO; GO:0006281; P:DNA repair; IEA.
DR InterPro; IPR001553; RecA.
DR PROSITE; PS50162; RECA_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 298 AA; 32241 MW; 6B4C133470E7F791 CRC64;

Query Match 53.4%; Score 55; DB 2; Length 298;
Best Local Similarity 61.5%; Pred. No. 52;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 WLEEEESSPPPP 16
DB 149 WQEEDEAVPPPP 161

RESULT 6
Q5JMG8 ORYSA
ID Q5JMG8_ORYSA PRELIMINARY; PRT; 336 AA.
AC Q5JMG8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Copper chaperone (CCH)-related protein-like.
GN Name=P050504.41; Synonyms=P0423A12.20;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Kobayashi N., Kono I.,
RA Karasawa W., Katagiri S., Kikuta A., Kihara Y., Kikuchi Y.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojibori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AF003272; BAD87339.1; -; Genomic_DNA.
DR EMBL; AF003246; BAD87164.1; -; Genomic_DNA.
```

DR GO: GO:0046872; F-metal ion binding; IEA.  
 DR GO: GO:0030001; P-metal ion transport; IEA.  
 DR InterPro: IPR006121; HeavyMe\_transpt.  
 DR Pfam: PF00403; HMA; 1.  
 DR PROSITE: PS00846; HMA\_2; 1.  
 SQ SEQUENCE 336 AA; 36847 MW; 250A05788588236F CRC64;

Query Match 53.4%; Score 55; DB 2; Length 336;  
 Best Local Similarity 57.1%; Pred. No. 59;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 PWLEEEESSPPPP 16  
 |||||:::||||  
 Db 76 PWPEEPKQQPPPP 89

## RESULT 7

Q6P302 XENTR  
 ID Q6P302 XENTR PRELIMINARY; PRT; 543 AA.  
 AC Q6P302  
 DT 03-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein MGC76181.  
 GN Name:MGC76181;  
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodinae; Xenopus; Silurana.  
 OC NCBI\_TaxID=8364;  
 OX NCBI\_TaxID=8364;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.

## NUCLEOTIDE SEQUENCE.

RC TISSUE=Embryo;  
 RC Klein S., Gerhard D.S.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; BC064232; AAH64232.1; -; mRNA.  
 DR SMR; Q6P302; 2-118, 223-349.  
 DR InterPro: IPR006636; STIL\_HS\_bd.  
 DR InterPro: IPR001440; TPR.  
 DR InterPro: IPR011990; TPR-like\_helical.  
 DR Pfam; PF00515; TPR 1; 8.  
 DR SMART; SM00727; STIL; 2.  
 DR SMART; SM00028; TPR; 9.  
 DR PROSITE; PS50005; TPR; 9.  
 DR PROSITE; PS50293; TPR\_REGION; 2.  
 KW Hypothetical protein; Repeat; TPR repeat.  
 SQ SEQUENCE 543 AA; 62323 MW; C1BCECBF4F7987E3 CRC64;

Query Match 53.4%; Score 55; DB 2; Length 543;

Best Local Similarity 75.0%; Pred. No. 1e+02;  
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 LREERESSPPPP 16  
 :|||||:||||  
 Db 190 VBEEDTTPPPP 201

## RESULT 8

GAST\_PIG  
 ID GAST\_PIG STANDARD; PRT; 104 AA.  
 AC P01351;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].  
 GN Name-GAST; Synonyms-GAS;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
 OC Sus.  
 OC NCBI\_TaxID=9823;  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=82174533; PubMed=6951161;  
 RA Yoo O.J., Powell C.T., Agarwal K.L.;  
 RT "Molecular cloning and nucleotide sequence of full-length of cDNA  
 RT coding for porcine gastrin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1049-1053(1982).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE OF 56-82.  
 RX MEDLINE=80240380; PubMed=6930858;  
 RA Agarwal K.L., Noyes B.E.;  
 RT "Studies on gastrin mRNA structure using an oligonucleotide probe.";  
 RL Ann. N. Y. Acad. Sci. 343:433-442(1980).  
 RN [3]  
 RP PROTEIN SEQUENCE OF 76-92.  
 RX PubMed=14248711;  
 RA Gregory H., Hardy P.M., Jones D.S., Kenner G.W., Sheppard R.C.;  
 RT "The antral hormone gastrin.";  
 RL Nature 204:931-933(1964).  
 RN [4]  
 RP SYNTHESIS.  
 RX PubMed=14248712;  
 RA Anderson J.C., Barton M.A., Gregory R.A., Hardy P.M., Kenner G.W.,  
 RA McLeod J.K., Preston J., Sheppard R.C., Morley J.S.;  
 RT "Synthesis of gastrin.";  
 RL Nature 204:933-934(1964).  
 CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and  
 CC secrete hydrochloric acid and the pancreas to secrete its  
 CC digestive enzymes. It also stimulates smooth muscle contraction  
 CC and increases blood circulation and water secretion in the stomach  
 CC and intestine.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL; V01303; CAA24610.1; -; mRNA.  
 DR EMBL; M25036; AAA31111.1; -; mRNA.  
 DR PIR; A93903; GMFGB.  
 DR InterPro: IPR001651; Gastrin.  
 DR Pfam; PF00918; Gastrin; 1.  
 DR SMART; SM00029; GASTRIN; 1.  
 DR PROSITE; PS00259; GASTRIN; 1.  
 DR Amidation; Cleavage on pair of basic residues;  
 KW Direct protein sequencing; Hormone; Phosphorylation;  
 KW Pyrolydione carboxylic acid; Signal; Sulfation.  
 FT SIGNAL 1 21

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FT PROPEP      22 58
FT PEPTIDE     59 92
FT PEPTIDE     76 92
FT PROPEP      96 104
FT MOD_RES     59 59
FT MOD_RES     76 76
FT MOD_RES     87 87
FT MOD_RES     92 92
FT MOD_RES     96 96
FT SEQUENCE    104 AA; 11558 MW; B0BD1D7E05304B79 CRC64;

Query Match      52.4%; Score 54; DB 1; Length 104;
Best Local Similarity 72.7%; Pred. No. 22;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEERES 11
   :|||:||||:
Db 76 QGPWMEEREA 86

RESULT 9
Q5C284 HUMAN
ID Q5C284_HUMAN PRELIMINARY; PRT; 204 AA.
AC Q5C284;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein DKFZp686F2342.
GN Name=DKFZp686F2342;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Amysdata;
RG The German CDNA Consortium;
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP936642; CAI56782.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 204 AA; 23151 MW; 8DC30451DD3335E03 CRC64;

Query Match      52.4%; Score 54; DB 2; Length 204;
Best Local Similarity 81.8%; Pred. No. 46;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 EEEESSPPPP 16
   ||||:||||
Db 63 EEEEEAPPPP 73

RESULT 10
Q5JSZ4 HUMAN
ID Q5JSZ4_HUMAN PRELIMINARY; PRT; 217 AA.
AC Q5JSZ4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Cysteine-rich hydrophobic domain 1.
GN Name=CHIC1; ORFNames=RP11-108A15.1-001;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bird C.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AL358796; CAI41484.1; -; Genomic DNA.
DR EMBL; AL356513; CAI41484.1; JOINED; Genomic DNA.
SQ SEQUENCE 217 AA; 24847 MW; 9F9D29AB93FE36E1 CRC64;

Query Match      52.4%; Score 54; DB 2; Length 217;
Best Local Similarity 81.8%; Pred. No. 50;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 EEEESSPPPP 16
   ||||:||||
Db 56 EEEEEAPPPP 66

RESULT 11
CHIC1 HUMAN
ID CHIC1_HUMAN STANDARD; PRT; 224 AA.
AC Q5VXU3;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cysteine-rich hydrophobic domain 1 protein (Brain X-linked protein).
GN Name=CHIC1; Synonyms=BRX;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
RA Wray P.;
RX Pubmed=9321471; DOI=10.1007/s00359900561;
RA Simmler M.-C., Heard E., Rougeulle C., Cruaud C., Weissenbach J.,
RA Avner P.;
RT "Localization and expression analysis of a novel conserved brain
RT expressed transcript, Brx/BRX, lying within the Xic/Xic candidate
RT region."
RL Mamm. Genome 8:760-766(1997).
CC -!- SURCELLULAR LOCATION: Plasma membrane associated and also present
CC at a Golgi-like vesicular compartment and at scattered vesicles
CC (By similarity).
CC -!- TISSUE SPECIFICITY: Equally expressed in various parts of the
CC brain.
CC -!- PTM: Palmitoylated (By similarity).
CC -!- SIMILARITY: Belongs to the CHIC family.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-8 is the initiator.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; AL356513; CAH70034.1; ALT INIT; Genomic DNA.
DR EMBL; AL358796; CAH70034.1; JOINED; Genomic DNA.
DR HGNC; HGNC:1934; CHIC1.
KW Coiled coil; Lipoprotein; Membrane; Palmitate.
FT COILED 42 70 Potential.
FT COMPIAS 16 24 Poly-Glu.
FT COMPIAS 28 39 Ser-rich.
FT COMPIAS 45 68 Poly-Glu.
FT COMPIAS 147 165 Cys-rich.
SQ SEQUENCE 224 AA; 25616 MW; ED6438E3B379F7E6 CRC64;

Query Match      52.4%; Score 54; DB 1; Length 224;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 EEEESSPPPP 16
   ||||:||||
Db 63 EEEEEAPPPP 73

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RESULT 12
Q7QKKO ANOQA PRELIMINARY; PRT; 265 AA.
ID Q7QKKO
AC Q7QKKO
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP00000011537.
GN ORFNames=ENSANG00000011048;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL "Anopheles gambiae re-annotation.";
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL: AAB01008794; EAA03561.2; -: Genomic_DNA.
DR InterPro: IPR006631; DUF DM4_12.
DR SMART: SM00718; DM4_12; I.
SQ SEQUENCE 265 AA; 29542 MW; A3E7F5B3D3836BB2 CRC64;

Query Match 52.4%; Score 54; DB 2; Length 265;
Best Local Similarity 56.2%; Pred. No. 62;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGPWLEEEESSPPPP 16
Db 130 DQGWQLDTSLSPPPP 145

RESULT 13
Q4WZ06 ASPFU PRELIMINARY; PRT; 492 AA.
ID Q4WZ06
AC Q4WZ06
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Afu3g14900;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RG Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bernejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
RA Penava M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,

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RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.,
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL: AAHF01000002; EAL92097.1; -: Genomic_DNA.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 492 AA; 55585 MW; 9BD8957726F0222E CRC64;

Query Match 52.4%; Score 54; DB 2; Length 492;
Best Local Similarity 47.1%; Pred. No. 1.2e+02;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGPWLEEEESSPPPP 17
Db 206 QQFWSEQAEADPPLYC 222

RESULT 14
Q73M73 TREDE PRELIMINARY; PRT; 812 AA.
ID Q73M73
AC Q73M73
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Surface antigen, putative.
GN OrderedLocuNames=TDE1636;
OS Treponema denticola.
OC Bacterii; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 35405 / DSM 14222;
RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebregeorgis E., Geer K., Tsagaye G., Malek J.A., Ayodeji B.,
RA Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).
DR EMBL: AE017251; AAS12153.1; -: Genomic_DNA.
DR TIGR; TDE1636; -.
KW Complete proteome.
SQ SEQUENCE 812 AA; 89462 MW; AF91AE6967BC4F62 CRC64;

Query Match 52.4%; Score 54; DB 2; Length 812;
Best Local Similarity 56.2%; Pred. No. 2.1e+02;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGPWLEEEESSPPPP 16
Db 435 ENKWFKEYESATPPP 450

RESULT 15
Q82H29 STRAW PRELIMINARY; PRT; 254 AA.
ID Q82H29
AC Q82H29
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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Tue Jan 10 09:41:49 2006

```
DE Hypothetical protein.
GN OrderedLocusNames=SAV3359;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22609306; PubMed=12692562; DOI=10.1038/nbt820;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RL microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
DR EMBL; BA000030; BAC71070.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 254 AA; 27256 MW; C2F2EA022BD978B5 CRC64;

Query Match 51.5%; Score 53; DB 2; Length 254;
Best Local Similarity 57.1%; Pred. No. 79;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 PWLEEEESSPPPP 16
Db |||||: :|||
135 PWLPEEDVAAPPEP 148

Search completed: January 9, 2006, 16:03:06
Job time : 98.2462 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 9, 2006, 15:56:09 ; Search time 25.6308 Seconds  
(without alignment)  
54.836 Million cell updates/sec

Title: US-10-759-832-18  
Perfect score: 103  
Sequence: 1 EGPWLEEEESSPPPC 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues  
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87.5	85.0	16	1	US-08-151-219-1
2	87.5	85.0	16	4	PCT-US94-13205-1
3	79	76.7	15	1	US-08-151-219-4
4	79	76.7	15	4	PCT-US94-13205-4
5	59	57.3	12	1	US-08-652-971-10
6	59	57.3	12	1	US-08-991-258A-10
7	59	57.3	12	2	US-08-769-399-10
8	59	57.3	12	2	US-08-991-953A-10
9	59	57.3	17	2	US-09-174-216-4
10	59	57.3	17	2	US-09-623-548A-422
11	59	57.3	17	2	US-09-657-276-422
12	56	54.4	12	1	US-08-446-692-75
13	56	54.4	12	1	US-08-488-351A-75
14	56	54.4	17	1	US-08-446-692-74
15	56	54.4	17	1	US-08-488-351A-74
16	56	54.4	17	2	US-09-079-372-17
17	56	54.4	18	2	US-09-079-372-10
18	56	54.4	18	2	US-09-079-372-15
19	56	54.4	21	2	US-09-079-372-12
20	56	54.4	33	2	US-10-360-101-170
21	56	54.4	34	1	US-08-446-692-69
22	56	54.4	34	1	US-08-488-351A-69
23	56	54.4	34	2	US-09-079-372-9
24	56	54.4	34	2	US-09-079-372-16
25	56	54.4	34	2	US-09-623-548A-423
26	56	54.4	34	2	US-09-657-276-423
27	56	54.4	35	2	US-09-079-372-8

28	56	54.4	47	1	US-08-446-692-100	Sequence 100, App
29	56	54.4	47	1	US-08-488-351A-100	Sequence 100, App
30	56	54.4	52	1	US-08-446-692-99	Sequence 99, Appl
31	56	54.4	52	1	US-08-488-351A-99	Sequence 99, Appl
32	56	54.4	69	1	US-08-446-692-95	Sequence 95, Appl
33	56	54.4	69	1	US-08-488-351A-95	Sequence 95, Appl
34	56	54.4	74	2	US-09-079-372-7	Sequence 7, Appl
35	56	54.4	100	2	US-09-079-372-14	Sequence 14, Appl
36	56	54.4	122	2	US-09-949-016-11739	Sequence 11739, A
37	54	52.4	17	2	US-09-174-263-2	Sequence 2, Appl
38	53	51.5	9	1	US-08-151-219-2	Sequence 2, Appl
39	53	51.5	9	4	PCT-US94-13205-2	Sequence 2, Appl
40	52	50.5	623	2	US-09-949-016-6530	Sequence 6530, Ap
41	52	50.5	693	2	US-09-949-016-7806	Sequence 7806, Ap
42	51.5	50.0	168	2	US-09-902-540-12003	Sequence 12003, A
43	51	49.5	419	2	US-10-237-551-198	Sequence 198, App
44	51	49.5	614	2	US-09-902-540-14372	Sequence 14372, A
45	51	49.5	724	2	US-09-949-016-9953	Sequence 9953, Ap

ALIGNMENTS

RESULT 1  
US-08-151-219-1  
; Sequence 1, Application US/08151219  
; Patent No. 5468494  
; GENERAL INFORMATION:  
; APPLICANT: Gevas, Philip C.  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Karr, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Scibienski, Robert  
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dimitrios T. Drivas, White and Case  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 100036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/151,219  
; FILING DATE: 12-NOV-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Drivas, Dimitrios T.  
; REGISTRATION NUMBER: 32,218  
; REFERENCE/DOCKET NUMBER: 1102865-028  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 819-8286  
; TELEFAX: (212) 354-8113  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEetical: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
US-08-151-219-1

Query Match 85.0%; Score 87.5; DB 1; Length 16;  
Best Local Similarity 94.1%; Pred. No. 2e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 1 EGPWL-EEESSPPPPC 16

RESULT 2
PCT-US94-13205-1
; Sequence 1, Application PC/TUS9413205
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13205
; FILING DATE: 12-NOV-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; PCT-US94-13205-1

Query Match 85.0%; Score 87.5; DB 4; Length 16;
Best Local Similarity 94.1%; Pred. No. 2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17
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Db 1 EGPWL-EEESSPPPPC 16

RESULT 3
US-08-151-219-4
; Sequence 4, Application US/08151219
; Patent No. 5468494
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
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; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,219
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-151-219-4

Query Match 76.7%; Score 79; DB 1; Length 15;
Best Local Similarity 82.4%; Pred. No. 0.00025;
Matches 14; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17
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Db 1 EGPWLEEEER--PPPPC 15

RESULT 4
PCT-US94-13205-4
; Sequence 4, Application PC/TUS9413205
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13205
; FILING DATE: 12-NOV-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
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NAME: Drivas, Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-028  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 819-8286  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
PCT-US94-13205-4

Query Match 76.7%; Score 79; DB 4; Length 15;  
Best Local Similarity 82.4%; Pred. No. 0.00025;  
Matches 14; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy 1 EGPWLEEESSPPPPC 17  
Db 1 EGPWLEEEER--PPPPC 15

RESULT 5  
US-08-652-971-10  
; Sequence 10, Application US/08652971  
; Patent No. 5814507  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd.  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,971  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Ginger R.  
; REGISTRATION NUMBER: 33,055  
; REFERENCE/DOCKET NUMBER: P1033  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 952-9881  
; TELEFAX: (415) 952-9881  
; TELEX: 910 371-7168  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

Query Match 57.3%; Score 59; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 0.089;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEES 11  
Db 1 EGPWLEEESEA 11  
RESULT 6  
US-08-991-258A-10  
; Sequence 10, Application US/08991258A  
; Patent No. 5928887  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT, LLP  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/991,258A  
; FILING DATE: 17-DEC-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/652,971  
; FILING DATE: 24-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-63478-3/WH/MTK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-991-258A-10

Query Match 57.3%; Score 59; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 0.089;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEES 11  
Db 1 EGPWLEEESEA 11

RESULT 7  
US-08-769-399-10  
; Sequence 10, Application US/08769399  
; Patent No. 5976852  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd.

```
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,399
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1033
; TELEPHONE: (415) 225-3216
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-769-399-10

Query Match 57.3%; Score 59; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 0.089;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
DB 1 EGPWLEEEEA 11

RESULT 8
US-08-991-953A-10
; Sequence 10, Application US/08991953A
; Patent No. 6083748
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOERBACH, TEST, ALBRITTON & HERBERT, LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,953A
; FILING DATE: 16-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,971
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63478-3/WH/D/MTK
; TELECOMMUNICATION INFORMATION:

; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,953A
; FILING DATE: 16-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,971
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63478-3/WH/D/MTK
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-991-953A-10

Query Match 57.3%; Score 59; DB 2; Length 12;
Best Local Similarity 90.9%; Pred. No. 0.089;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
DB 1 EGPWLEEEEA 11

RESULT 9
US-09-174-216-4
; Sequence 4, Application US/09174216A
; Patent No. 6335176
; GENERAL INFORMATION:
; APPLICANT: Inglesse, James
; APPLICANT: Glickman, Joseph Fraser
; TITLE OF INVENTION: Incorporation of Phosphorylation Sites
; FILE REFERENCE: 1073.050
; CURRENT APPLICATION NUMBER: US/09/174,216A
; CURRENT FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed
; OTHER INFORMATION: peptide to act as kinase substrate
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; US-09-174-216-4

Query Match 57.3%; Score 59; DB 2; Length 17;
Best Local Similarity 90.9%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
DB 1 EGPWLEEEEA 11

RESULT 10
US-09-623-548A-422
; Sequence 422, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjugchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
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;; PRIOR APPLICATION NUMBER: 60/134,406  
;; PRIOR FILING DATE: 1999-05-17  
;; PRIOR APPLICATION NUMBER: 60/153,406  
;; PRIOR FILING DATE: 1999-09-10  
;; PRIOR APPLICATION NUMBER: 60/159,783  
;; PRIOR FILING DATE: 1999-10-18  
;; NUMBER OF SEQ ID NOS: 1617  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 422  
;; LENGTH: 17  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: Peptide  
US-09-623-548A-422

Query Match 57.3%; Score 59; DB 2; Length 17;  
Best Local Similarity 90.9%; Pred. No. 0.13;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEES 11  
Db 1 EGPWLEEEEA 11

RESULT 11  
US-09-657-276-422  
;; Sequence 422, Application US/09657276  
;; Patent No. 6887470  
;; GENERAL INFORMATION:  
;; APPLICANT: Conjuchem, Inc.  
;; APPLICANT: Bridon, Dominique  
;; APPLICANT: Ezrin, Alan  
;; APPLICANT: Milner, Peter  
;; APPLICANT: Holmes, Darren  
;; APPLICANT: Thibaudau, Karen  
;; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
;; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
;; TITLE OF INVENTION: COMPONENTS  
;; FILE REFERENCE: 2110  
;; CURRENT APPLICATION NUMBER: US/09/657,276  
;; CURRENT FILING DATE: 2000-09-07  
;; PRIOR APPLICATION NUMBER: 60/134,406  
;; PRIOR FILING DATE: 1999-05-17  
;; PRIOR APPLICATION NUMBER: 60/153,406  
;; PRIOR FILING DATE: 1999-09-10  
;; PRIOR APPLICATION NUMBER: 60/159,783  
;; PRIOR FILING DATE: 1999-10-18  
;; NUMBER OF SEQ ID NOS: 1617  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 422  
;; LENGTH: 17  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: Peptide  
US-09-657-276-422

Query Match 57.3%; Score 59; DB 2; Length 17;  
Best Local Similarity 90.9%; Pred. No. 0.13;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEES 11  
Db 1 EGPWLEEEEA 11

RESULT 12  
US-08-446-692-75  
;; Sequence 75, Application US/08446692  
;; Patent No. 5759551

;; GENERAL INFORMATION:  
;; APPLICANT: Ladd, Anna  
;; APPLICANT: Wang, Chang Yi  
;; APPLICANT: Zamb, Timothy  
;; TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
;; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
;; NUMBER OF SEQUENCES: 114  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Maria C.H. Lin  
;; STREET: 345 Park Avenue  
;; CITY: New York  
;; STATE: NY  
;; COUNTRY: US  
;; ZIP: 10154-0053  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/446,692  
;; FILING DATE: 7-JUN-1995  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Maria C.H. Lin  
;; REGISTRATION NUMBER: 29,323  
;; REFERENCE/DOCKET NUMBER: 1151-4146 US2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)415-8745  
;; TELEFAX: (516)751-8849  
;; INFORMATION FOR SEQ ID NO: 75:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 12 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-446-692-75

Query Match 54.4%; Score 56; DB 1; Length 12;  
Best Local Similarity 81.8%; Pred. No. 0.22;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEES 11  
Db 1 QGPWLEEEEA 11

RESULT 13  
US-08-488-351A-75  
;; Sequence 75, Application US/08488351A  
;; Patent No. 5843446  
;; GENERAL INFORMATION:  
;; APPLICANT: Ladd, Anna  
;; APPLICANT: Wang, Chang Yi  
;; APPLICANT: Zamb, Timothy  
;; TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
;; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
;; NUMBER OF SEQUENCES: 114  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Maria C.H. Lin  
;; STREET: 345 Park Avenue  
;; CITY: New York  
;; STATE: NY  
;; COUNTRY: US  
;; ZIP: 10154-0053  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/488,351A  
;; FILING DATE: 7-JUN-1995

us-10-759-832-18.ra1

Tue Jan 10 09:41:49 2006

LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-446-692-74

Query Match 54.4%; Score 56; DB 1; Length 17;  
Best Local Similarity 81.8%; Pred. No. 0.32; Indels 0; Gaps 0;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11  
Db 1 QGPWLEEEER 11

RESULT 15  
US-08-488-351A-74  
Sequence 74, Application US/08488351A  
Patent No. 5843446  
GENERAL INFORMATION:  
APPLICANT: Ladd, Anna  
APPLICANT: Wang, Chang Yi  
APPLICANT: Zamb, Timothy  
TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Maria C.H. Lin  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: US  
ZIP: 10154-0053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,351A  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/446,692  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/229,275  
FILING DATE: 14-APR-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,166  
FILING DATE: 27-APR-1992  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maria C.H. Lin  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4146 US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)415-8745  
TELEFAX: (516)751-6849  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-488-351A-74

Query Match 54.4%; Score 56; DB 1; Length 17;  
Best Local Similarity 81.8%; Pred. No. 0.32; Indels 0; Gaps 0;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/446,692  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/229,275  
FILING DATE: 14-APR-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,166  
FILING DATE: 27-APR-1992  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maria C.H. Lin  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4146 US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)415-8745  
TELEFAX: (516)751-6849  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-488-351A-75

Query Match 54.4%; Score 56; DB 1; Length 12;  
Best Local Similarity 81.8%; Pred. No. 0.22; Indels 0; Gaps 0;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11  
Db 1 QGPWLEEEER 11

RESULT 14  
US-08-446-692-74  
Sequence 74, Application US/08446692  
Patent No. 5759551  
GENERAL INFORMATION:  
APPLICANT: Ladd, Anna  
APPLICANT: Wang, Chang Yi  
APPLICANT: Zamb, Timothy  
TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Maria C.H. Lin  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: US  
ZIP: 10154-0053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,692  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maria C.H. Lin  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4146 US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)415-8745  
TELEFAX: (516)751-6849  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:

Qy 1 EGPWLEEEES 11  
:|||||:  
Db 1 QGPWLEEEEA 11

Search completed: January 9, 2006, 16:12:08  
Job time : 25.6308 secs

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OM protein - protein search, using sw model

Run on: January 9, 2006, 16:09:15 ; Search time 76.1077 Seconds  
(without alignments)  
93.330 Million cell updates/sec

Title: US-10-759-832-18

Perfect score: 103

Sequence: 1 EGPWLEEESSPPPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\_Main:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	100.0	17	4	US-10-613-377A-18
2	103	100.0	17	5	US-10-759-832-18
3	103	100.0	17	6	US-11-036-690-18
4	87.5	85.0	16	5	US-10-762-226-6
5	82.5	80.1	16	4	US-10-192-257-4
6	62.5	60.7	12	4	US-10-314-057-1
7	62.5	60.7	12	5	US-10-762-226-3
8	62.5	60.7	12	5	US-10-829-137-5
9	60.5	58.7	14	5	US-10-762-226-2
10	59	57.3	12	5	US-10-762-226-1
11	59	57.3	17	4	US-10-197-954-60
12	59	57.3	17	4	US-10-613-377A-1
13	59	57.3	17	4	US-10-372-917-13
14	59	57.3	17	5	US-10-759-832-1
15	59	57.3	17	5	US-10-760-085-60
16	59	57.3	17	5	US-10-813-336-1
17	59	57.3	17	5	US-10-206-081-2
18	59	57.3	17	5	US-10-770-712-61
19	59	57.3	17	6	US-11-036-690-1
20	59	57.3	17	6	US-11-066-697-422
21	59	57.3	18	4	US-10-613-377A-2
22	59	57.3	18	5	US-10-759-832-2
23	59	57.3	18	5	US-10-813-336-2
24	59	57.3	18	6	US-11-036-690-2
25	59	57.3	34	5	US-10-813-336-3
26	59	57.3	35	5	US-10-813-336-4
27	59	57.3	114	4	US-10-425-115-284097

28	58	56.3	10	4	US-10-613-377A-8	Sequence 8, Appli
29	58	56.3	10	5	US-10-759-832-8	Sequence 8, Appli
30	58	56.3	10	6	US-11-036-690-8	Sequence 8, Appli
31	58	56.3	659	4	US-10-227-490-11	Sequence 11, Appl
32	58	56.3	659	4	US-10-356-456-11	Sequence 11, Appl
33	58	56.3	839	4	US-10-227-490-9	Sequence 9, Appli
34	58	56.3	839	4	US-10-227-490-10	Sequence 10, Appl
35	58	56.3	839	4	US-10-356-456-9	Sequence 9, Appli
36	58	56.3	839	4	US-10-356-456-10	Sequence 10, Appl
37	57.5	55.8	12	4	US-10-192-257-1	Sequence 1, Appli
38	57	55.3	11	4	US-10-314-057-2	Sequence 2, Appli
39	57	55.3	11	5	US-10-762-226-4	Sequence 4, Appli
40	57	55.3	11	5	US-10-829-137-6	Sequence 6, Appli
41	56	54.4	17	5	US-10-839-017-3	Sequence 3, Appli
42	56	54.4	33	4	US-10-360-101-170	Sequence 170, App
43	56	54.4	33	5	US-10-728-082-1	Sequence 1, Appli
44	56	54.4	33	5	US-10-728-082-2	Sequence 2, Appli
45	56	54.4	33	5	US-10-719-450-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-10-613-377A-18  
; Sequence 18, Application US/10613377A  
; Publication No. US20040208920A1  
; GENERAL INFORMATION:  
; APPLICANT: Apton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059  
; CURRENT APPLICATION NUMBER: US/10/613,377A  
; CURRENT FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 18  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide of GnRH amino acid sequence linked to a spacer  
; OTHER INFORMATION: peptide  
US-10-613-377A-18

Query Match	100.0%	Score 103;	DB 4;	Length 17;
Best Local Similarity	100.0%	Pred. No. 5.2e-06;		
Matches	17;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;
Qy	1	EGPWLEEESSPPPPC 17		
Db	1	EGPWLEEESSPPPPC 17		
RESULT 2				
US-10-759-832-18				
; Sequence 18, Application US/10759832				
; Publication No. US20040247661A1				
; GENERAL INFORMATION:				
; APPLICANT: Apton Corporation				
; TITLE OF INVENTION: Liposomal Vaccine				
; FILE REFERENCE: 1102865-0059CIP				
; CURRENT APPLICATION NUMBER: US/10/759,832				
; CURRENT FILING DATE: 2004-01-15				
; PRIOR APPLICATION NUMBER: 60/394,179				
; PRIOR FILING DATE: 2002-07-03				
; PRIOR APPLICATION NUMBER: 10/613,377				
; PRIOR FILING DATE: 2003-07-03				
; NUMBER OF SEQ ID NOS: 20				
; SOFTWARE: Patentin version 3.2				
; SEQ ID NO 18				
; LENGTH: 17				

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; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of GnRH amino acid sequence linked to a spacer
; US-10-759-832-18

Query Match      100.0%; Score 103; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEESSPPPPC 17
   |||||
Db 1 EGPWLEEEESSPPPPC 17

RESULT 3
US-11-036-690-18
; Sequence 18, Application US/11036690
; Publication No. US20050169979A1
; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059C1P
; CURRENT APPLICATION NUMBER: US/11/036,690
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of GnRH amino acid sequence linked to a spacer
; US-11-036-690-18

Query Match      100.0%; Score 103; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEESSPPPPC 17
   |||||
Db 1 EGPWLEEEESSPPPPC 17

RESULT 4
US-10-762-226-6
; Sequence 6, Application US/10762226
; Publication No. US20050025770A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Karr, Stephen L.
; APPLICANT: Grimes, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Watson, Susan A.
; TITLE OF INVENTION: Immunological Methods for the Treatment of
; FILE REFERENCE: 1102865-0031
; CURRENT APPLICATION NUMBER: US/10/762,226
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/011,411
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Pyroglutamic acid residue
; US-10-762-226-6

Query Match      85.0%; Score 87.5; DB 5; Length 16;
Best Local Similarity 94.1%; Pred. No. 0.00041;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17
   |||||
Db 1 EGPWL-EEESSPPPPC 16

RESULT 5
US-10-192-257-4
; Sequence 4, Application US/10192257
; Publication No. US20030021786A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Condition
; FILE REFERENCE: 1102865-0057
; CURRENT APPLICATION NUMBER: US/10/192,257
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/303,868
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1):(1)
; OTHER INFORMATION: Xaa=pyroglutamic acid
; US-10-192-257-4

Query Match      80.1%; Score 82.5; DB 4; Length 16;
Best Local Similarity 93.8%; Pred. No. 0.0017;
Matches 15; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 GPWLEEEESSPPPPC 17
   |||||
Db 2 GPWL-EEESSPPPPC 16

RESULT 6
US-10-314-057-1
; Sequence 1, Application US/10314057
; Publication No. US20030068326A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip
; APPLICANT: Stephen, Grimes
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; TITLE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux Disease
; FILE REFERENCE: ACGIUSA
; CURRENT APPLICATION NUMBER: US/10/314,057
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/700,378
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: PCT/US99/10734
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/085,610
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
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; ORGANISM: human  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)-(1)  
; OTHER INFORMATION: pyroglutamic acid  
US-10-314-057-1

Query Match 60.7%; Score 62.5; DB 4; Length 12;  
Best Local Similarity 64.7%; Pred. No. 0.39;  
Matches 11; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

Qy 1 EGPWLEEESSPPPPC 17  
Db 1 EGPWLER-----PPPPC 12

## RESULT 7

US-10-762-226-3  
; Sequence 3, Application US/10762226  
; Publication No. US20050025770A1  
; GENERAL INFORMATION:  
; APPLICANT: Gevas, Philip C.  
; APPLICANT: Karr, Stephen L.  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Watson, Susan A.  
; TITLE OF INVENTION: Immunological Methods for the Treatment of  
; TITLE OF INVENTION: Gastrointestinal Cancer  
; FILE REFERENCE: 1102865-0031  
; CURRENT APPLICATION NUMBER: US/10/762,226  
; CURRENT FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: 60/011,411  
; PRIOR FILING DATE: 1996-02-08  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)-  
; OTHER INFORMATION: Pyroglutamic acid residue  
US-10-762-226-3

Query Match 60.7%; Score 62.5; DB 5; Length 12;  
Best Local Similarity 64.7%; Pred. No. 0.39;  
Matches 11; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

Qy 1 EGPWLEEESSPPPPC 17  
Db 1 EGPWLER-----PPPPC 12

## RESULT 8

US-10-829-137-5  
; Sequence 5, Application US/10829137  
; Publication No. US20050187152A1  
; GENERAL INFORMATION:  
; APPLICANT: Gevas, Philip  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Karr, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Watson, Susan  
; TITLE OF INVENTION: Prevention and Treatment of Hypergastrinemia  
; FILE REFERENCE: ACG2USA  
; CURRENT APPLICATION NUMBER: US/10/829,137  
; CURRENT FILING DATE: 2004-04-21  
; PRIOR APPLICATION NUMBER: US/09/700,329  
; PRIOR FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: PCT/US99/10751  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 60/085,714

; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: human gastrin peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)-(1)  
; OTHER INFORMATION: pyroglutamic acid  
US-10-829-137-5

Query Match 60.7%; Score 62.5; DB 5; Length 12;  
Best Local Similarity 64.7%; Pred. No. 0.39;  
Matches 11; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

Qy 1 EGPWLEEESSPPPPC 17  
Db 1 EGPWLER-----PPPPC 12

## RESULT 9

US-10-762-226-2  
; Sequence 2, Application US/10762226  
; Publication No. US20050025770A1  
; GENERAL INFORMATION:  
; APPLICANT: Gevas, Philip C.  
; APPLICANT: Karr, Stephen L.  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Watson, Susan A.  
; TITLE OF INVENTION: Immunological Methods for the Treatment of  
; TITLE OF INVENTION: Gastrointestinal Cancer  
; FILE REFERENCE: 1102865-0031  
; CURRENT APPLICATION NUMBER: US/10/762,226  
; CURRENT FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: 60/011,411  
; PRIOR FILING DATE: 1996-02-08  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)-  
; OTHER INFORMATION: Pyroglutamic acid residue  
US-10-762-226-2

Query Match 58.7%; Score 60.5; DB 5; Length 14;  
Best Local Similarity 68.8%; Pred. No. 0.79;  
Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

Qy 1 EGPWLEEESSPPPP 16  
Db 1 EGPWLEEKR---PPPP 13

## RESULT 10

US-10-762-226-1  
; Sequence 1, Application US/10762226  
; Publication No. US20050025770A1  
; GENERAL INFORMATION:  
; APPLICANT: Gevas, Philip C.  
; APPLICANT: Karr, Stephen L.  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Watson, Susan A.  
; TITLE OF INVENTION: Immunological Methods for the Treatment of  
; TITLE OF INVENTION: Gastrointestinal Cancer  
; FILE REFERENCE: 1102865-0031

us-10-759-832-18.rapbm

```

; CURRENT APPLICATION NUMBER: US/10/762,226
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/011,411
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Pyroglutamic acid residue
US-10-762-226-1

Query Match          57.3%; Score 59; DB 5; Length 12;
Best Local Similarity 90.9%; Pred. No. 1;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
Db 1 EGPWLEEEEA 11

RESULT 11
US-10-197-954-60
; Sequence 60, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K'ster, Hubert
; APPLICANT: Siddiqi, Suhail
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-197-954-60

Query Match          57.3%; Score 59; DB 4; Length 17;
Best Local Similarity 90.9%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
Db 1 EGPWLEEEEA 11

RESULT 12
US-10-613-377A-1
; Sequence 1, Application US/10613377A
; Publication No. US2004020820A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059
; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2004-01-15
; CURRENT APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT

; CURRENT APPLICATION NUMBER: US/10/762,226
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/011,411
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-613-377A-1

Query Match          57.3%; Score 59; DB 4; Length 17;
Best Local Similarity 90.9%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
Db 1 EGPWLEEEEA 11

RESULT 13
US-10-372-917-13
; Sequence 13, Application US/10372917
; Publication No. US2004020979A1
; GENERAL INFORMATION:
; APPLICANT: VASIOS, GEORGE
; TITLE OF INVENTION: JAK/STAT PATHWAY INHIBITORS AND THE USES THEREOF
; FILE REFERENCE: 5004C
; CURRENT APPLICATION NUMBER: US/10/372,917
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/177,872
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-372-917-13

Query Match          57.3%; Score 59; DB 4; Length 17;
Best Local Similarity 90.9%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
Db 1 EGPWLEEEEA 11

RESULT 14
US-10-759-832-1
; Sequence 1, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-759-832-1
Query Match      57.3%; Score 59; DB 5; Length 17;
Best Local Similarity 90.9%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEES 11
Db 1 EGPWLEEEEA 11

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RESULT 15
US-10-760-085-60
; Sequence 60, Application US/10760085
; Publication No. US20050042771A1
; GENERAL INFORMATION:
; APPLICANT: Hubert K"ster
; APPLICANT: Daniel Paul Little
; APPLICANT: Suhailb Mahmood Siddiqi
; APPLICANT: Matthew Peter Grealish
; APPLICANT: Subramaniam Marappan
; APPLICANT: Chester Frederick Haseman III
; APPLICANT: Ping Yip
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2309
; CURRENT APPLICATION NUMBER: US/10/760.085
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: 60/441,398
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-760-085-60
Query Match      57.3%; Score 59; DB 5; Length 17;
Best Local Similarity 90.9%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEES 11
Db 1 EGPWLEEEEA 11

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Search completed: January 9, 2006, 16:35:45  
Job time : 77.1077 secs

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# OM protein - protein search, using sw model

Run on: January 9, 2006, 16:10:30 ; Search time 9.15385 Seconds  
(without alignments)  
15.774 Million cell updates/sec

Title: US-10-759-832-18

Perfect score: 103

Sequence: 1 EGPWLEEEERSPPPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 61141 seqs, 8493638 residues

Total number of hits satisfying chosen parameters: 61141

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Published Applications AA New:  
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3: /cgn2\_6/ptodata/2/pubpa/US07\_NEW\_PUB\_PEP.\*  
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6: /cgn2\_6/ptodata/2/pubpa/US10\_NEW\_PUB\_PEP.\*  
7: /cgn2\_6/ptodata/2/pubpa/US11\_NEW\_PUB\_PEP.\*  
8: /cgn2\_6/ptodata/2/pubpa/US60\_NEW\_PUB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	57.3	17	6 US-10-985-023-10	Sequence 10, Appl
2	55	53.4	17	6 US-10-997-066-31	Sequence 31, Appl
3	55	53.4	19	7 US-11-145-566-38	Sequence 38, Appl
4	49.5	48.1	17	6 US-10-509-292-54	Sequence 54, Appl
5	49.5	48.1	17	6 US-10-509-292-60	Sequence 60, Appl
6	48.5	47.1	485	6 US-10-204-029-7	Sequence 7, Appl
7	47	45.6	17	6 US-10-509-292-58	Sequence 58, Appl
8	46	44.7	615	6 US-10-982-545-14	Sequence 14, Appl
9	46	44.7	616	6 US-10-982-545-5	Sequence 5, Appl
10	46	44.7	2161	7 US-11-126-313-31	Sequence 31, Appl
11	45.5	44.2	28	6 US-10-509-292-43	Sequence 43, Appl
12	45	43.7	7	6 US-10-509-292-39	Sequence 39, Appl
13	45	43.7	17	6 US-10-509-292-50	Sequence 50, Appl
14	45	43.7	17	6 US-10-509-292-52	Sequence 52, Appl
15	45	43.7	17	6 US-10-509-292-56	Sequence 56, Appl
16	45	43.7	27	6 US-10-509-292-46	Sequence 46, Appl
17	45	43.7	27	6 US-10-509-292-47	Sequence 47, Appl
18	45	43.7	27	6 US-10-509-292-49	Sequence 49, Appl
19	45	43.7	28	6 US-10-509-292-42	Sequence 42, Appl
20	44	42.7	572	6 US-10-821-234-1290	Sequence 1290, Ap
21	44	42.7	3375	7 US-11-044-111-23	Sequence 23, Appl
22	43.5	42.2	795	6 US-10-821-234-1002	Sequence 1002, Ap
23	43	41.7	353	6 US-10-131-826A-296	Sequence 296, App
24	43	41.7	432	7 US-11-140-417-4	Sequence 4, Appli
25	43	41.7	463	7 US-11-102-240-86	Sequence 86, Appl

Sequence 872, App  
Sequence 400, App  
Sequence 1, Appli  
Sequence 98, Appl  
Sequence 97, Appl  
Sequence 3231, Ap  
Sequence 96, Appl  
Sequence 2, Appli  
Sequence 3230, Ap  
Sequence 912, App  
Sequence 290, App  
Sequence 2, Appli  
Sequence 1, Appli  
Sequence 63, Appl  
Sequence 227, App  
Sequence 671, App  
Sequence 670, App  
Sequence 1155, Ap  
Sequence 809, App

26 43 41.7 463 7 US-11-000-463-872  
27 43 41.7 567 7 US-11-000-463-400  
28 42.5 41.3 3144 7 US-11-055-035-1  
29 42 40.8 271 6 US-10-667-295-98  
30 42 40.8 277 6 US-10-667-295-97  
31 42 40.8 290 7 US-11-054-515-3231  
32 42 40.8 296 6 US-10-667-295-96  
33 42 40.8 309 7 US-11-065-669-2  
34 42 40.8 309 7 US-11-054-515-3230  
35 42 40.8 410 6 US-10-821-234-912  
36 42 40.8 420 6 US-10-131-826A-290  
37 42 40.8 438 7 US-11-140-417-2  
38 42 40.8 445 7 US-11-115-564-1  
39 42 40.8 445 7 US-11-115-564-2  
40 42 40.8 467 7 US-11-037-243-63  
41 42 40.8 613 6 US-10-055-877-227  
42 42 40.8 4346 6 US-10-995-561-671  
43 42 40.8 4347 6 US-10-995-561-670  
44 42 40.8 4419 6 US-10-821-234-1155  
45 41.5 40.3 1375 6 US-10-995-561-809

## ALIGNMENTS

### RESULT 1

US-10-985-023-10  
; Sequence 10, Application US/10985023  
; Publication No. US2005028295A1  
; GENERAL INFORMATION:  
; APPLICANT: Currie, Kevin S.  
; APPLICANT: Desimone, Robert W.  
; APPLICANT: Pippin, Douglas A.  
; APPLICANT: Barrow, James W.  
; APPLICANT: Mitchell, Scott A.  
; TITLE OF INVENTION: Certain  
; TITLE OF INVENTION: Imidazo[1,2-a]pyrazin-8-ylamines, method of making, and  
; FILE REFERENCE: 09580-0003-02000  
; CURRENT APPLICATION NUMBER: US/10/985,023  
; CURRENT FILING DATE: 2004-11-10  
; PRIOR APPLICATION NUMBER: 60/519,311  
; PRIOR FILING DATE: 2003-11-11  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Biotinylated substrate  
US-10-985-023-10

Query Match 57.3%; Score 59; DB 6; Length 17;  
Best Local Similarity 90.9%; Pred. No. 0.02;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERS 11

Db 1 EGPWLEEEEREA 11

### RESULT 2

US-10-997-066-31  
; Sequence 31, Application US/10997066  
; Publication No. US20050244891A1  
; GENERAL INFORMATION:  
; APPLICANT: GRAHAM, RONALD J.  
; APPLICANT: LEE, LINDA G.  
; APPLICANT: SUN, HONGYE  
; TITLE OF INVENTION: LIGAND-CONTAINING MICELLES AND USES THEREOF  
; FILE REFERENCE: 375461-011US  
; CURRENT APPLICATION NUMBER: US/10/997,066

Tue Jan 10 09:41:49 2006

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; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/525,492
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/628,509
; PRIOR FILING DATE: 2004-11-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-997-066-31

Query Match      53.4%; Score 55; DB 6; Length 17;
Best Local Similarity 81.8%; Pred. No. 0.066;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
DB 1 KGPWLEEEEA 11

RESULT 3
US-11-145-566-38
; Sequence 38, Application US/11145566
; Publication No. US20050272083A1
; GENERAL INFORMATION:
; APPLICANT: SOMASEKAR SESHAGIRI
; TITLE OF INVENTION: EGFR Mutations
; FILE REFERENCE: 39766-0153
; CURRENT APPLICATION NUMBER: US/11/145,566
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,425
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/635,344
; PRIOR FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US 60/666,068
; PRIOR FILING DATE: 2005-03-28
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 38
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-145-566-38

Query Match      53.4%; Score 55; DB 7; Length 19;
Best Local Similarity 81.8%; Pred. No. 0.073;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
DB 3 KGPWLEEEEA 13

RESULT 4
US-10-509-292-54
; Sequence 54, Application US/10509292
; Publication No. US20050287159A1
; GENERAL INFORMATION:
; APPLICANT: Mercia Pharma LLC
; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Botaxin
; FILE REFERENCE: MERPH.001
; CURRENT APPLICATION NUMBER: US/10/509,292
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/367,591
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54

; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Botaxin epitope/Spacer
US-10-509-292-54

Query Match      48.1%; Score 49.5; DB 6; Length 17;
Best Local Similarity 57.1%; Pred. No. 0.34;
Matches 8; Conservative 3; Mismatches 0; Indels 3; Gaps 1;

QY 4 WLEEEESSPPPPC 17
DB 7 WV---QDSSPPPPC 17

RESULT 5
US-10-509-292-60
; Sequence 60, Application US/10509292
; Publication No. US20050287159A1
; GENERAL INFORMATION:
; APPLICANT: Mercia Pharma LLC
; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Botaxin
; FILE REFERENCE: MERPH.001
; CURRENT APPLICATION NUMBER: US/10/509,292
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/367,591
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Botaxin epitope/Spacer
US-10-509-292-60

Query Match      48.1%; Score 49.5; DB 6; Length 17;
Best Local Similarity 57.1%; Pred. No. 0.34;
Matches 8; Conservative 3; Mismatches 0; Indels 3; Gaps 1;

QY 4 WLEEEESSPPPPC 17
DB 7 WV---QDSSPPPPC 17

RESULT 6
US-10-204-029-7
; Sequence 7, Application US/10204029
; Publication No. US20050261487A1
; GENERAL INFORMATION:
; APPLICANT: Cully, Doris F.
; APPLICANT: Priest, Birgit
; APPLICANT: Yuan, Jeffrey
; APPLICANT: Zheng, Yingcong
; TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND-GATED ION
; FILE REFERENCE: 20615P
; CURRENT APPLICATION NUMBER: US/10/204,029
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/US01/06096
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/186645
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-204-029-7
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Query Match          47.1%; Score 48.5; DB 6; Length 485;
Best Local Similarity 34.8%; Pred. No. 9;
Matches 8; Conservative 4; Mismatches 4; Indels 7; Gaps 1;

Qy 1 EGPWLEEEES-----SPPPP 16
Db 407 DGPWIPQESRIILTPTIAPPPP 429

RESULT 7
US-10-509-292-58
; Sequence 58, Application US/10509292
; Publication No. US20050287159A1
; GENERAL INFORMATION:
; APPLICANT: Mercia Pharma LLC
; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Botaxin
; FILE REFERENCE: MERPH.001
; CURRENT APPLICATION NUMBER: US/10/509,292
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/367,591
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Eotaxin epitope/Spacer
US-10-509-292-58

Query Match          45.6%; Score 47; DB 6; Length 17;
Best Local Similarity 61.5%; Pred. No. 0.72;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 LEEEEEESPPPPP 17
Db 5 LAKDITSSPPPPC 17

RESULT 8
US-10-982-545-14
; Sequence 14, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Eotaxin epitope/Spacer
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Query Match          44.7%; Score 46; DB 6; Length 615;
Best Local Similarity 57.1%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 PWLEEEESPPPPP 16
Db 529 PWDREDEVYPPGP 542

RESULT 9
US-10-982-545-5
; Sequence 5, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: nerve growth factor inducible Neurosecretory
; OTHER INFORMATION: protein vaccinia virus growth factor (VGF)
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Tue Jan 10 09:41:49 2006

us-10-759-832-18.rapbn

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; OTHER INFORMATION: precursor
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(22)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (23)..(616)
; OTHER INFORMATION: biomarker peptide M3951.6, nerve growth factor
; OTHER INFORMATION: inducible Neurosecretory protein vaccinia virus
; OTHER INFORMATION: growth factor (VGF) mature peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (26)..(62)
; OTHER INFORMATION: biomarker peptide M3687.7, N-terminal fragment of
; OTHER INFORMATION: nerve growth factor inducible Neurosecretory
; OTHER INFORMATION: protein vaccinia virus growth factor (VGF)
US-10-982-545-5

Query Match 44.7%; Score 46; DB 6; Length 616;
Best Local Similarity 57.1%; Pred. No. 24;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 PWLEEESSPPPP 16
Db 529 PWDREDEVPPGP 542

RESULT 10
US-11-126-313-31
; Sequence 31, Application US/11126313
; Publication No. US20050288489A1
; GENERAL INFORMATION:
; APPLICANT: Hirsch, Joel
; TITLE OF INVENTION: VOLTAGE-DEPENDENT CALCIUM CHANNEL BETA SUBUNIT FUNCTIONAL CORE
; FILE REFERENCE: P-6758-US
; CURRENT APPLICATION NUMBER: US/11/126.313
; CURRENT FILING DATE: 2005-05-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 2161
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-126-313-31

Query Match 44.7%; Score 46; DB 7; Length 2161;
Best Local Similarity 58.3%; Pred. No. 72;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 EEEESSPPPPC 17
Db 810 EDEEDKDPYPPC 821

RESULT 11
US-10-509-292-43
; Sequence 43, Application US/10509292
; Publication No. US20050287159A1
; GENERAL INFORMATION:
; APPLICANT: Mercia Pharma LLC
; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Botaxin
; FILE REFERENCE: MERPH.001
; CURRENT APPLICATION NUMBER: US/10/509,292
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/367,591
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 28
; TYPE: PRT

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; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Botaxin epitope/Spacer
US-10-509-292-43

Query Match 44.2%; Score 45.5; DB 6; Length 28;
Best Local Similarity 32.0%; Pred. No. 1.7;
Matches 8; Conservative 4; Mismatches 2; Indels 11; Gaps 1;

QY 4 WLEEE-----EESSPPPPC 17
Db 4 WVQDSMKYLDQKSPTPKPSPPPPC 28

RESULT 12
US-10-509-292-39
; Sequence 39, Application US/10509292
; Publication No. US20050287159A1
; GENERAL INFORMATION:
; APPLICANT: Mercia Pharma LLC
; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Botaxin
; FILE REFERENCE: MERPH.001
; CURRENT APPLICATION NUMBER: US/10/509,292
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/367,591
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Spacer peptide
US-10-509-292-39

Query Match 43.7%; Score 45; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SSPPPPC 17
Db 1 SSPPPPC 7

RESULT 13
US-10-509-292-50
; Sequence 50, Application US/10509292
; Publication No. US20050287159A1
; GENERAL INFORMATION:
; APPLICANT: Mercia Pharma LLC
; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Botaxin
; FILE REFERENCE: MERPH.001
; CURRENT APPLICATION NUMBER: US/10/509,292
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/367,591
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
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; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Botaxin epitope/Spacer
US-10-509-292-50

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Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 11 SSPPPC 17  
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Db 11 SSPPPC 17

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US-10-509-292-52  
; Sequence 52, Application US/10509292  
; Publication No. US20050287159A1  
; GENERAL INFORMATION:  
; APPLICANT: Merckia Pharma LLC  
; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Eotaxin  
; FILE REFERENCE: MERPH.001  
; CURRENT APPLICATION NUMBER: US/10/509,292  
; CURRENT FILING DATE: 2004-09-23  
; PRIOR APPLICATION NUMBER: US 60/367,591  
; PRIOR FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 52  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Eotaxin epitope/Spacer  
US-10-509-292-52

Query Match 43.7%; Score 45; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 11 SSPPPC 17

RESULT 15  
US-10-509-292-56  
; Sequence 56, Application US/10509292  
; Publication No. US20050287159A1  
; GENERAL INFORMATION:  
; APPLICANT: Merckia Pharma LLC  
; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Eotaxin  
; FILE REFERENCE: MERPH.001  
; CURRENT APPLICATION NUMBER: US/10/509,292  
; CURRENT FILING DATE: 2004-09-23  
; PRIOR APPLICATION NUMBER: US 60/367,591  
; PRIOR FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 56  
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; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Eotaxin epitope/Spacer  
US-10-509-292-56

Query Match 43.7%; Score 45; DB 6; Length 17;  
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 11 SSPPPC 17

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OM protein - protein search, using sw model

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139	38	84.4	52	4	US-10-437-963-130889	Sequence 130889,	212	38	84.4	1329	3	US-09-918-715-295	Sequence 295, App
140	38	84.4	68	4	US-10-424-599-280270	Sequence 280270,	213	38	84.4	1329	4	US-10-474-794-191	Sequence 191, App
141	38	84.4	74	4	US-10-425-115-275828	Sequence 275828,	214	38	84.4	1329	4	US-10-474-794-295	Sequence 295, App
142	38	84.4	86	4	US-10-425-115-282850	Sequence 282850,	215	38	84.4	1329	5	US-10-979-159-191	Sequence 191, App
143	38	84.4	87	4	US-10-424-599-235360	Sequence 235360,	216	38	84.4	1329	5	US-10-979-159-295	Sequence 295, App
144	38	84.4	88	4	US-10-425-115-230840	Sequence 230840,	217	38	84.4	1346	4	US-10-437-963-201536	Sequence 201536,
145	38	84.4	93	4	US-10-425-115-313923	Sequence 313923,	218	38	84.4	1403	4	US-10-425-114-54518	Sequence 54518, A
146	38	84.4	94	4	US-10-424-599-237679	Sequence 237679,	219	38	84.4	1636	4	US-10-433-794-1	Sequence 1, Appli
147	38	84.4	97	4	US-10-425-115-204395	Sequence 204395,	220	38	84.4	1636	5	US-10-745-237-212	Sequence 212, App
148	38	84.4	98	4	US-10-424-599-156880	Sequence 156880,	221	38	84.4	6	4	US-10-192-257-5	Sequence 5, Appli
149	38	84.4	99	4	US-10-425-115-303949	Sequence 303949,	222	37	82.2	6	4	US-10-613-377A-9	Sequence 9, Appli
150	38	84.4	100	3	US-09-764-891-2875	Sequence 2875, Ap	223	37	82.2	6	5	US-10-759-832-9	Sequence 9, Appli
151	38	84.4	104	4	US-10-425-115-351470	Sequence 351470,	224	37	82.2	6	6	US-11-036-690-9	Sequence 9, Appli
152	38	84.4	109	4	US-10-425-115-361830	Sequence 361830,	225	37	82.2	8	4	US-10-613-377A-11	Sequence 11, Appli
153	38	84.4	111	4	US-10-437-963-136743	Sequence 136743,	226	37	82.2	8	5	US-10-759-832-11	Sequence 11, Appli
154	38	84.4	114	4	US-10-437-963-174703	Sequence 174703,	227	37	82.2	8	6	US-11-036-690-11	Sequence 11, Appli
155	38	84.4	117	4	US-10-425-115-246952	Sequence 246952,	228	37	82.2	9	3	US-09-823-240-7	Sequence 7, Appli
156	38	84.4	118	4	US-10-425-115-212228	Sequence 212228,	229	37	82.2	9	4	US-10-192-257-3	Sequence 3, Appli
157	38	84.4	126	4	US-10-424-599-247250	Sequence 247250,	230	37	82.2	10	4	US-10-314-057-3	Sequence 3, Appli
158	38	84.4	127	4	US-10-425-115-192963	Sequence 192963,	231	37	82.2	10	5	US-10-762-226-5	Sequence 5, Appli
159	38	84.4	129	4	US-10-767-701-39023	Sequence 39023, A	232	37	82.2	10	5	US-10-829-137-7	Sequence 7, Appli
160	38	84.4	136	4	US-10-437-963-190733	Sequence 190733,	233	37	82.2	11	4	US-10-192-257-2	Sequence 2, Appli
161	38	84.4	152	4	US-10-425-115-355471	Sequence 355471,	234	37	82.2	11	4	US-10-314-057-2	Sequence 2, Appli
162	38	84.4	155	4	US-10-437-963-124062	Sequence 124062,	235	37	82.2	11	4	US-10-133-128-208	Sequence 208, App
163	38	84.4	164	4	US-10-425-115-360442	Sequence 360442,	236	37	82.2	11	4	US-10-289-660-208	Sequence 208, App
164	38	84.4	167	4	US-10-425-115-303462	Sequence 303462,	237	37	82.2	11	4	US-10-693-057-349	Sequence 349, App
165	38	84.4	169	4	US-10-425-115-224853	Sequence 224853,	238	37	82.2	11	5	US-10-762-226-4	Sequence 4, Appli
166	38	84.4	175	4	US-10-425-115-360415	Sequence 360415,	239	37	82.2	11	5	US-10-693-056-349	Sequence 349, App
167	38	84.4	198	5	US-10-739-930-9678	Sequence 9678, Ap	240	37	82.2	11	5	US-10-840-723-349	Sequence 349, App
168	38	84.4	209	4	US-10-425-115-180125	Sequence 287125,	241	37	82.2	11	5	US-10-871-602-349	Sequence 349, App
169	38	84.4	210	4	US-10-437-963-180688	Sequence 180688,	242	37	82.2	11	5	US-10-971-679-349	Sequence 349, App
170	38	84.4	219	4	US-10-437-963-151867	Sequence 151867,	243	37	82.2	11	5	US-10-829-137-6	Sequence 6, Appli
171	38	84.4	230	6	US-11-097-143-9030	Sequence 9030, Ap	244	37	82.2	11	5	US-10-966-064A-235	Sequence 235, App
172	38	84.4	235	4	US-10-437-963-150753	Sequence 150753,	245	37	82.2	12	4	US-10-192-257-1	Sequence 1, Appli
173	38	84.4	241	4	US-10-104-047-2317	Sequence 2317, Ap	246	37	82.2	12	4	US-10-314-057-1	Sequence 1, Appli

247	37	82.2	12	4	US-10-314-057-4	Sequence 4, Appli	320	37	82.2	78	4	US-10-425-115-189993	Sequence 189993,
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252	37	82.2	12	5	US-10-829-137-5	Sequence 5, Appli	325	37	82.2	81	4	US-10-425-115-290824	Sequence 290824,
253	37	82.2	12	5	US-10-829-137-8	Sequence 8, Appli	326	37	82.2	82	4	US-10-001-843-116	Sequence 116, App
254	37	82.2	15	4	US-10-314-057-6	Sequence 6, Appli	327	37	82.2	82	6	US-11-005-609-116	Sequence 116, App
255	37	82.2	15	4	US-10-161-791-433	Sequence 433, App	328	37	82.2	83	4	US-10-425-115-241121	Sequence 241121,
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265	37	82.2	25	5	US-10-693-056-348	Sequence 348, App	338	37	82.2	87	4	US-10-437-963-157249	Sequence 157249,
266	37	82.2	25	5	US-10-801-990-345	Sequence 345, App	339	37	82.2	87	4	US-10-437-963-166572	Sequence 166572,
267	37	82.2	25	5	US-10-840-723-348	Sequence 348, App	340	37	82.2	87	4	US-10-425-115-238770	Sequence 238770,
268	37	82.2	25	5	US-10-871-602-348	Sequence 348, App	341	37	82.2	87	4	US-10-425-115-286370	Sequence 286370,
269	37	82.2	25	5	US-10-971-679-348	Sequence 348, App	342	37	82.2	88	3	US-09-833-245-342	Sequence 342, App
270	37	82.2	25	5	US-10-966-064B-234	Sequence 234, App	343	37	82.2	88	4	US-10-425-115-208743	Sequence 208743,
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426	37	82.2	119	4	US-10-425-115-198913	Sequence 198913,	499	37	82.2	153	4	US-10-424-599-245949	Sequence 245949,
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431	37	82.2	120	5	US-10-450-763-31206	Sequence 31206, A	504	37	82.2	156	4	US-10-437-963-191335	Sequence 191335,
432	37	82.2	121	4	US-10-424-599-254302	Sequence 254302,	505	37	82.2	157	4	US-10-425-115-229768	Sequence 229768,
433	37	82.2	121	4	US-10-437-963-115247	Sequence 115247,	506	37	82.2	157	4	US-10-425-115-242387	Sequence 242387,
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435	37	82.2	122	4	US-10-437-963-155563	Sequence 155563,	508	37	82.2	158	4	US-10-425-115-327671	Sequence 327671,
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456	37	82.2	133	4	US-10-437-963-147501	Sequence 147501,	529	37	82.2	177	4	US-10-437-963-170239	Sequence 170239,
457	37	82.2	133	4	US-10-425-115-293389	Sequence 293389,	530	37	82.2	178	4	US-10-425-115-258806	Sequence 258806,
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463	37	82.2	136	4	US-10-425-115-300135	Sequence 300135,	536	37	82.2	183	3	US-09-833-245-2225	Sequence 2225, Ap
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465	37	82.2	137	4	US-10-437-963-179424	Sequence 179424,	538	37	82.2	184	4	US-10-259-194A-158	Sequence 158, App

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544	37	82.2	187	4	US-10-425-115-218139	Sequence 218139,	617	37	82.2	252	3	US-09-800-729-133	Sequence 133, App
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546	37	82.2	188	4	US-10-437-963-171745	Sequence 171745,	619	37	82.2	252	5	US-10-450-763-33745	Sequence 33745, A
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553	37	82.2	190	3	US-09-525-302-647	Sequence 647, App	626	37	82.2	270	4	US-10-424-593-169724	Sequence 169724,
554	37	82.2	193	4	US-10-425-115-197497	Sequence 197497,	627	37	82.2	271	4	US-10-363-616-371	Sequence 371, App
555	37	82.2	193	4	US-10-425-115-261551	Sequence 261551,	628	37	82.2	277	4	US-10-017-161-2310	Sequence 2310, App
556	37	82.2	196	4	US-10-437-963-142125	Sequence 142125,	629	37	82.2	277	4	US-10-292-798-1956	Sequence 1956, App
557	37	82.2	196	4	US-10-425-115-238514	Sequence 238514,	630	37	82.2	277	4	US-10-437-963-130563	Sequence 130563
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559	37	82.2	198	4	US-10-425-114-49199	Sequence 49199, A	632	37	82.2	280	4	US-10-308-485-1	Sequence 1, Appli
560	37	82.2	198	4	US-10-425-114-64819	Sequence 64819, A	633	37	82.2	283	4	US-10-437-963-204521	Sequence 204521,
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570	37	82.2	205	4	US-10-425-114-39645	Sequence 39645, A	643	37	82.2	302	4	US-10-108-268A-3176	Sequence 3176, App
571	37	82.2	205	4	US-10-437-963-120755	Sequence 120755,	644	37	82.2	303	4	US-10-437-963-112671	Sequence 112671,
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573	37	82.2	207	4	US-10-425-115-303230	Sequence 303230,	646	37	82.2	306	4	US-10-437-963-137920	Sequence 137920,
574	37	82.2	207	5	US-10-425-115-305836	Sequence 305836,	647	37	82.2	310	4	US-10-437-963-124289	Sequence 124289,
575	37	82.2	207	5	US-10-320-335-539	Sequence 539, App	648	37	82.2	311	4	US-10-044-442-15	Sequence 15, Appl
576	37	82.2	208	4	US-10-425-115-198954	Sequence 198954,	649	37	82.2	318	4	US-10-437-963-127875	Sequence 127875,
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578	37	82.2	210	4	US-10-437-963-203491	Sequence 203491,	651	37	82.2	325	4	US-10-437-963-131905	Sequence 131905,
579	37	82.2	213	4	US-10-094-749-2061	Sequence 2061, App	652	37	82.2	325	5	US-10-450-763-52278	Sequence 52278, A
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581	37	82.2	214	4	US-10-296-115-1253	Sequence 1253, App	654	37	82.2	336	4	US-10-437-963-131484	Sequence 131484,
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583	37	82.2	215	4	US-10-425-115-315380	Sequence 315380,	656	37	82.2	340	5	US-10-872-932A-33	Sequence 32, Appl
584	37	82.2	216	4	US-10-767-701-40647	Sequence 40647, A	657	37	82.2	340	5	US-10-810-881A-32	Sequence 32, Appl
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586	37	82.2	221	4	US-10-437-963-107036	Sequence 107036,	659	37	82.2	341	4	US-10-437-963-159698	Sequence 158698,
587	37	82.2	222	4	US-10-437-963-200640	Sequence 200640,	660	37	82.2	341	5	US-10-220-335-688	Sequence 688, App
588	37	82.2	222	4	US-10-425-115-306497	Sequence 306497,	661	37	82.2	349	4	US-10-274-694-13	Sequence 13, Appl
589	37	82.2	222	6	US-11-063-325-29	Sequence 29, Appl	662	37	82.2	349	5	US-10-332-448-13	Sequence 13, Appl
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591	37	82.2	223	4	US-10-425-115-199000	Sequence 199000,	664	37	82.2	353	4	US-10-437-963-186466	Sequence 186466,
592	37	82.2	223	4	US-10-425-115-363118	Sequence 363118,	665	37	82.2	353	4	US-10-437-963-203523	Sequence 203523,
593	37	82.2	224	4	US-10-213-462-2	Sequence 2, Appli	666	37	82.2	356	4	US-10-437-963-116816	Sequence 116816,
594	37	82.2	224	4	US-10-425-114-65285	Sequence 65285, A	667	37	82.2	356	5	US-10-732-923-2942	Sequence 2942, App
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597	37	82.2	227	4	US-10-425-114-41509	Sequence 41509, A	670	37	82.2	361	5	US-10-739-930-9714	Sequence 9714, App
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600	37	82.2	232	4	US-10-425-115-262436	Sequence 262436,	673	37	82.2	369	4	US-10-437-963-162013	Sequence 162013,
601	37	82.2	234	4	US-10-425-114-42281	Sequence 42281, A	674	37	82.2	371	4	US-10-437-963-190340	Sequence 190340,
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603	37	82.2	236	5	US-10-450-763-38795	Sequence 38795, A	676	37	82.2	379	4	US-10-437-963-193373	Sequence 193373,
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605	37	82.2	239	4	US-10-425-115-199001	Sequence 199001,	678	37	82.2	382	4	US-10-425-115-275470	Sequence 275470,
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607	37	82.2	245	4	US-10-425-115-219886	Sequence 219886,	680	37	82.2	384	4	US-10-437-963-197276	Sequence 197276,
608	37	82.2	246	4	US-10-437-963-122595	Sequence 122595,	681	37	82.2	390	4	US-10-283-013-2	Sequence 2, Appli
609	37	82.2	249	3	US-09-764-868-965	Sequence 965, App	682	37	82.2	392	3	US-09-747-835A-55	Sequence 55, Appl
610	37	82.2	249	4	US-10-425-114-5426	Sequence 5426, A	683	37	82.2	392	4	US-10-312-312-55	Sequence 55, Appl
611	37	82.2	249	4	US-10-437-963-112100	Sequence 112100,	684	37	82.2	392	4	US-10-425-115-207742	Sequence 207742,

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686	37	82.2	400	4	US-10-425-115-322741	Sequence 322741,	759	37	82.2	467	3	US-09-905-075-195	Sequence 195, App
687	37	82.2	403	4	US-10-437-963-117453	Sequence 117453,	760	37	82.2	467	3	US-09-902-759-195	Sequence 195, App
688	37	82.2	404	5	US-10-450-763-35271	Sequence 35271, A	761	37	82.2	467	3	US-09-902-634-195	Sequence 195, App
689	37	82.2	404	5	US-10-450-763-58435	Sequence 58435, A	762	37	82.2	467	3	US-09-902-713-195	Sequence 195, App
690	37	82.2	404	5	US-10-450-763-59378	Sequence 59378, A	763	37	82.2	467	3	US-09-902-979-195	Sequence 195, App
691	37	82.2	404	5	US-10-450-763-56343	Sequence 56343, A	764	37	82.2	467	3	US-09-902-615-195	Sequence 195, App
692	37	82.2	405	4	US-10-437-963-146012	Sequence 146012,	765	37	82.2	467	3	US-09-903-925-195	Sequence 195, App
693	37	82.2	407	4	US-10-425-115-240814	Sequence 240814,	766	37	82.2	467	3	US-09-906-760A-195	Sequence 195, App
694	37	82.2	409	4	US-10-437-963-179750	Sequence 179750,	767	37	82.2	467	3	US-09-903-823-195	Sequence 195, App
695	37	82.2	414	4	US-10-437-963-158710	Sequence 158710,	768	37	82.2	467	3	US-09-907-652-195	Sequence 195, App
696	37	82.2	419	3	US-09-828-035-2	Sequence 2, Appli	769	37	82.2	467	3	US-09-902-572A-195	Sequence 195, App
697	37	82.2	419	4	US-10-345-680-44	Sequence 44, Appl	770	37	82.2	467	3	US-09-902-979-195	Sequence 195, App
698	37	82.2	419	4	US-10-146-733-29	Sequence 29, Appl	771	37	82.2	467	3	US-09-905-125-195	Sequence 195, App
699	37	82.2	419	4	US-10-352-684A-8	Sequence 8, Appli	772	37	82.2	467	3	US-09-906-815A-195	Sequence 195, App
700	37	82.2	419	4	US-10-391-399-19	Sequence 19, Appl	773	37	82.2	467	3	US-09-905-449-195	Sequence 195, App
701	37	82.2	419	4	US-10-768-158-12	Sequence 12, Appl	774	37	82.2	467	3	US-09-903-806-195	Sequence 195, App
702	37	82.2	420	5	US-10-989-826-57	Sequence 57, Appl	775	37	82.2	467	3	US-09-904-992-195	Sequence 195, App
703	37	82.2	420	4	US-10-437-963-1127880	Sequence 127880,	776	37	82.2	467	3	US-09-904-838-195	Sequence 195, App
704	37	82.2	421	4	US-10-437-963-197389	Sequence 197389,	777	37	82.2	467	3	US-09-906-777-195	Sequence 195, App
705	37	82.2	431	4	US-10-437-963-196423	Sequence 196423,	778	37	82.2	467	3	US-09-903-603A-195	Sequence 195, App
706	37	82.2	439	4	US-10-425-114-63388	Sequence 63388, A	779	37	82.2	467	3	US-09-904-532-195	Sequence 195, App
707	37	82.2	441	4	US-10-283-881-9	Sequence 9, Appli	780	37	82.2	467	3	US-09-904-766-195	Sequence 195, App
708	37	82.2	441	4	US-10-833-440-9	Sequence 9, Appli	781	37	82.2	467	3	US-09-904-920A-195	Sequence 195, App
709	37	82.2	448	4	US-10-425-115-282419	Sequence 282419,	782	37	82.2	467	3	US-09-904-877A-195	Sequence 195, App
710	37	82.2	449	5	US-10-450-763-38794	Sequence 38794, A	783	37	82.2	467	3	US-09-903-562-195	Sequence 195, App
711	37	82.2	450	4	US-10-437-963-120794	Sequence 120794,	784	37	82.2	467	3	US-09-905-618-195	Sequence 195, App
712	37	82.2	454	4	US-10-437-963-102727	Sequence 102727,	785	37	82.2	467	3	US-09-907-728-195	Sequence 195, App
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714	37	82.2	458	4	US-10-425-114-50377	Sequence 50377, A	787	37	82.2	467	3	US-09-904-938A-195	Sequence 195, App
715	37	82.2	465	3	US-09-942-146-1	Sequence 1, Appli	788	37	82.2	467	3	US-09-906-722A-195	Sequence 195, App
716	37	82.2	465	4	US-10-437-963-144224	Sequence 144224,	789	37	82.2	467	3	US-09-908-576-195	Sequence 195, App
717	37	82.2	465	4	US-10-437-963-147123	Sequence 147123,	790	37	82.2	467	4	US-10-052-586-16	Sequence 16, Appl
718	37	82.2	467	3	US-09-909-320-195	Sequence 195, App	791	37	82.2	467	4	US-10-174-590-16	Sequence 16, Appl
719	37	82.2	467	3	US-09-909-0888-195	Sequence 195, App	792	37	82.2	467	4	US-10-176-758-16	Sequence 16, Appl
720	37	82.2	467	3	US-09-905-291A-195	Sequence 195, App	793	37	82.2	467	4	US-10-175-737-16	Sequence 16, Appl
721	37	82.2	467	3	US-09-981-876-134	Sequence 134, App	794	37	82.2	467	4	US-10-174-581-16	Sequence 16, Appl
722	37	82.2	467	3	US-09-902-853-195	Sequence 195, App	795	37	82.2	467	4	US-10-176-483-16	Sequence 16, Appl
723	37	82.2	467	3	US-09-907-824-195	Sequence 195, App	796	37	82.2	467	4	US-10-176-749-16	Sequence 16, Appl
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725	37	82.2	467	3	US-09-904-011-195	Sequence 195, App	798	37	82.2	467	4	US-10-176-915-16	Sequence 16, Appl
726	37	82.2	467	3	US-09-903-640-195	Sequence 195, App	799	37	82.2	467	4	US-10-173-706-16	Sequence 16, Appl
727	37	82.2	467	3	US-09-908-093-195	Sequence 195, App	800	37	82.2	467	4	US-10-175-738-16	Sequence 16, Appl
728	37	82.2	467	3	US-09-906-742-195	Sequence 195, App	801	37	82.2	467	4	US-10-175-752-16	Sequence 16, Appl
729	37	82.2	467	3	US-09-148-545-134	Sequence 134, App	802	37	82.2	467	4	US-10-176-482-16	Sequence 16, Appl
730	37	82.2	467	3	US-09-906-838-195	Sequence 195, App	803	37	82.2	467	4	US-10-176-757-16	Sequence 16, Appl
731	37	82.2	467	3	US-09-907-613-195	Sequence 195, App	804	37	82.2	467	4	US-10-176-913-16	Sequence 16, Appl
732	37	82.2	467	3	US-09-907-942-195	Sequence 195, App	805	37	82.2	467	4	US-10-180-552-16	Sequence 16, Appl
733	37	82.2	467	3	US-09-904-859-195	Sequence 195, App	806	37	82.2	467	4	US-10-180-557-16	Sequence 16, Appl
734	37	82.2	467	3	US-09-909-204-195	Sequence 195, App	807	37	82.2	467	4	US-10-173-700-16	Sequence 16, Appl
735	37	82.2	467	3	US-09-904-820-195	Sequence 195, App	808	37	82.2	467	4	US-10-174-572-16	Sequence 16, Appl
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737	37	82.2	467	3	US-09-906-646-195	Sequence 195, App	810	37	82.2	467	4	US-10-174-582-16	Sequence 16, Appl
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739	37	82.2	467	3	US-09-903-786-195	Sequence 195, App	812	37	82.2	467	4	US-10-175-739-16	Sequence 16, Appl
740	37	82.2	467	3	US-09-902-903-195	Sequence 195, App	813	37	82.2	467	4	US-10-175-740-16	Sequence 16, Appl
741	37	82.2	467	3	US-09-903-749A-195	Sequence 195, App	814	37	82.2	467	4	US-10-175-743-16	Sequence 16, Appl
742	37	82.2	467	3	US-09-904-119-195	Sequence 195, App	815	37	82.2	467	4	US-10-176-488-16	Sequence 16, Appl
743	37	82.2	467	3	US-09-904-956-195	Sequence 195, App	816	37	82.2	467	4	US-10-176-492-16	Sequence 16, Appl
744	37	82.2	467	3	US-09-902-736-195	Sequence 195, App	817	37	82.2	467	4	US-10-176-747-16	Sequence 16, Appl
745	37	82.2	467	3	US-09-907-794-195	Sequence 195, App	818	37	82.2	467	4	US-10-176-750-16	Sequence 16, Appl
746	37	82.2	467	3	US-09-903-943-195	Sequence 195, App	819	37	82.2	467	4	US-10-176-985-16	Sequence 16, Appl
747	37	82.2	467	3	US-09-904-463-195	Sequence 195, App	820	37	82.2	467	4	US-10-176-987-16	Sequence 16, Appl
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751	37	82.2	467	3	US-09-905-056-195	Sequence 195, App	824	37	82.2	467	4	US-10-176-991-16	Sequence 16, Appl
752	37	82.2	467	3	US-09-909-064-195	Sequence 195, App	825	37	82.2	467	4	US-10-173-695-16	Sequence 16, Appl
753	37	82.2	467	3	US-09-904-553-195	Sequence 195, App	826	37	82.2	467	4	US-10-173-697-16	Sequence 16, Appl
754	37	82.2	467	3	US-09-905-381-195	Sequence 195, App	827	37	82.2	467	4	US-10-173-705-16	Sequence 16, Appl
755	37	82.2	467	3	US-09-904-485-195	Sequence 195, App	828	37	82.2	467	4	US-10-174-576-16	Sequence 16, Appl
756	37	82.2	467	3	US-09-905-348-195	Sequence 195, App	829	37	82.2	467	4	US-10-174-585-16	Sequence 16, Appl
757	37	82.2	467	3	US-09-905-088-195	Sequence 195, App	830	37	82.2	467	4	US-10-174-586-16	Sequence 16, Appl



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977 37 82.2 467 4 US-10-197-708-16 Sequence 16, Appl
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999 37 82.2 467 4 US-10-202-935-16 Sequence 16, Appl
1000 37 82.2 467 4 US-10-202-936-16 Sequence 16, Appl
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## ALIGNMENTS

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RESULT 1
US-10-192-257-6
; Sequence 6, Application US/10192257
; Publication No. US20030021786A1
; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Condition
; FILE REFERENCE: 1102865-0057
; CURRENT APPLICATION NUMBER: US/10/192,257
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/303,868
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical spacer peptide
US-10-192-257-6
Query Match 100.0%; Score 45; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSPPPC 7
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Db 1 SSSPPPC 7

RESULT 2
US-10-314-057-8
; Sequence 8, Application US/10314057
; Publication No. US20030068326A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip
; APPLICANT: Stephen, Grimes
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; TITLE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux Disease
; FILE REFERENCE: ACGUSA
; CURRENT APPLICATION NUMBER: US/10/314,057
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; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/700,378
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: PCT/US99/10734
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/085,610
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: human or synthetic peptide
US-10-314-057-8
Query Match 100.0%; Score 45; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSPPPC 7
   |||||
Db 1 SSSPPPC 7

RESULT 3
US-10-235-236-3
; Sequence 3, Application US/10235236
; Publication No. US20030086941A1
; GENERAL INFORMATION:
; APPLICANT: Michaeli, Dov
; Caplin, Martyn E.
; Watson, Susan A.
; Grimes, Stephen
; TITLE OF INVENTION: Immunogenic Compositions
; to the CCK-B/Gastrin Receptor and Methods for
; the Treatment of Tumors
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White & Case LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/235,236
; FILING DATE: 04-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,201
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8200
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-235-236-3
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Query Match 100.0%; Score 45; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
Db 1 SSPPPPC 7

## RESULT 4

US-10-104-607B-3  
; Sequence 3, Application US/10104607B  
; Publication No. US20030031574A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Combination Treatment of Pancreatic Cancer  
; FILE REFERENCE: 1102865-0052  
; CURRENT APPLICATION NUMBER: US/10/104,607B  
; CURRENT FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: 60/278,294  
; PRIOR FILING DATE: 2001-03-23  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Hypothetical synthetic peptide spacer  
US-10-104-607B-3

Query Match 100.0%; Score 45; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
Db 1 SSPPPPC 7

## RESULT 5

US-10-613-377A-10  
; Sequence 10, Application US/10613377A  
; Publication No. US20040208920A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059  
; CURRENT APPLICATION NUMBER: US/10/613,377A  
; CURRENT FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide spacer  
US-10-613-377A-10

Query Match 100.0%; Score 45; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
Db 1 SSPPPPC 7

## RESULT 6

US-10-759-832-10

; Sequence 10, Application US/10759832  
; Publication No. US20040247661A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059CIP  
; CURRENT APPLICATION NUMBER: US/10/759,832  
; CURRENT FILING DATE: 2004-01-15  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 10/613,377  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide spacer  
US-10-759-832-10

Query Match 100.0%; Score 45; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
Db 1 SSPPPPC 7

## RESULT 7

US-10-762-226-8  
; Sequence 8, Application US/10762226  
; Publication No. US20050025770A1  
; GENERAL INFORMATION:  
; APPLICANT: Gevas, Philip C.  
; APPLICANT: Karr, Stephen L.  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Watson, Susan A.  
; TITLE OF INVENTION: Immunological Methods for the Treatment of  
; FILE REFERENCE: 1102865-0031  
; CURRENT APPLICATION NUMBER: US/10/762,226  
; CURRENT FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: 60/011,411  
; PRIOR FILING DATE: 1996-02-08  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide spacer  
US-10-762-226-8

Query Match 100.0%; Score 45; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
Db 1 SSPPPPC 7

## RESULT 8

US-10-829-137-3  
; Sequence 3, Application US/10829137  
; Publication No. US20050187152A1  
; GENERAL INFORMATION:

; APPLICANT: Gevas, Philip  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Karr, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Watson, Susan  
; TITLE OF INVENTION: Prevention and Treatment of Hypergastrinemia  
; FILE REFERENCE: ACGUSA  
; CURRENT APPLICATION NUMBER: US/10/829,137  
; PRIOR FILING DATE: 2004-04-21  
; PRIOR APPLICATION NUMBER: US/09/700,329  
; PRIOR FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: PCT/US99/10751  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 60/085,714  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: human or synthetic peptide  
US-10-829-137-3

Query Match 100.0%; Score 45; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
Db 1 SSPPPPC 7

RESULT 9  
US-11-036-690-10  
; Sequence 10, Application US/11036690  
; Publication No. US20050169979A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059CIP  
; CURRENT APPLICATION NUMBER: US/11/036,690  
; CURRENT FILING DATE: 2005-01-14  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 10/613,377  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide spacer  
US-11-036-690-10

Query Match 100.0%; Score 45; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
Db 1 SSPPPPC 7

RESULT 10  
US-10-613-377A-13  
; Sequence 13, Application US/10613377A  
; Publication No. US20040208920A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059

; CURRENT APPLICATION NUMBER: US/10/613,377A  
; CURRENT FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 13  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide of amino acid sequence 1-6 of human gastrin 34  
; OTHER INFORMATION: linked to a spacer peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-613-377A-13

Query Match 100.0%; Score 45; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
Db 7 SSPPPPC 13

RESULT 11  
US-10-759-832-13  
; Sequence 13, Application US/10759832  
; Publication No. US20040247661A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059CIP  
; CURRENT APPLICATION NUMBER: US/10/759,832  
; CURRENT FILING DATE: 2004-01-15  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 10/613,377  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 13  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide of amino acid sequence 1-6 of human gastrin 34  
; OTHER INFORMATION: linked to a spacer peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-759-832-13

Query Match 100.0%; Score 45; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
Db 7 SSPPPPC 13

RESULT 12  
US-11-036-690-13  
; Sequence 13, Application US/11036690  
; Publication No. US20050169979A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine

FILE REFERENCE: 1102865-0059CIP  
CURRENT APPLICATION NUMBER: US/11/036,690  
CURRENT FILING DATE: 2005-01-14  
PRIOR APPLICATION NUMBER: 60/394,179  
PRIOR FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: 10/613,377  
PRIOR FILING DATE: 2003-07-03  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 13  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: synthetic peptide of amino acid sequence 1-6 of human gastrin 34  
OTHER INFORMATION: linked to a spacer peptide  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: (1)-(1)  
OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-11-036-690-13

Query Match 100.0%; Score 45; DB 6; Length 13;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
| | | | |  
Db 7 SSPPPPC 13

RESULT 13  
US-10-192-257-4  
Sequence 4, Application US/10192257  
Publication No. US20030021786A1  
GENERAL INFORMATION:  
APPLICANT: Apton Corporation  
TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Conditions  
FILE REFERENCE: 1102865-0057  
CURRENT APPLICATION NUMBER: US/10/192,257  
CURRENT FILING DATE: 2002-07-09  
PRIOR APPLICATION NUMBER: US 60/303,868  
PRIOR FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (1)-(1)  
OTHER INFORMATION: Xaa=pyroglutamic acid  
US-10-192-257-4

Query Match 100.0%; Score 45; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
| | | | |  
Db 10 SSPPPPC 16

RESULT 14  
US-10-762-226-6  
Sequence 6, Application US/10762226  
Publication No. US20050025770A1  
GENERAL INFORMATION:  
APPLICANT: Gevas, Philip C.  
APPLICANT: Karr, Stephen L.  
APPLICANT: Grimes, Stephen

APPLICANT: Michaeli, Dov  
APPLICANT: Watson, Susan A.  
TITLE OF INVENTION: Immunological Methods for the Treatment of  
FILE REFERENCE: 1102865-0031  
CURRENT APPLICATION NUMBER: US/10/762,226  
CURRENT FILING DATE: 2004-01-20  
PRIOR APPLICATION NUMBER: 60/011,411  
PRIOR FILING DATE: 1996-02-08  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: (1)-  
OTHER INFORMATION: Pyroglutamic acid residue  
US-10-762-226-6

Query Match 100.0%; Score 45; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
| | | | |  
Db 10 SSPPPPC 16

RESULT 15  
US-09-305-924-4  
Sequence 4, Application US/09305924A  
Publication No. US20030091579A1  
GENERAL INFORMATION:  
APPLICANT: Jack G. Manns  
APPLICANT: Stephen D. Acres  
APPLICANT: Richard Harland  
TITLE OF INVENTION: METHODS OF RAISING ANIMALS FOR MEAT PRODUCTION  
FILE REFERENCE: 9001-0048  
CURRENT APPLICATION NUMBER: US/09/305,924A  
CURRENT FILING DATE: 1999-05-05  
EARLIER APPLICATION NUMBER: US 60/084,217  
EARLIER FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 17  
TYPE: PRT  
ORGANISM: GnRH  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: (1)-  
OTHER INFORMATION: Xaa is pyroglutamic acid  
US-09-305-924-4

Query Match 100.0%; Score 45; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
| | | | |  
Db 11 SSPPPPC 17

RESULT 16  
US-10-613-377A-18  
Sequence 18, Application US/10613377A  
Publication No. US20040208920A1  
GENERAL INFORMATION:  
APPLICANT: Apton Corporation  
TITLE OF INVENTION: Liposomal Vaccine  
FILE REFERENCE: 1102865-0059

```
; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of GnRH amino acid sequence linked to a spacer
; OTHER INFORMATION: peptide
US-10-613-377A-18
```

```
Query Match          100.0%; Score 45; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SSPPPPC 7
        |||||
Db       11 SSPPPPC 17
```

```
RESULT 17
US-10-759-832-18
; Sequence 18, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of GnRH amino acid sequence linked to a spacer
US-10-759-832-18
```

```
Query Match          100.0%; Score 45; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SSPPPPC 7
        |||||
Db       11 SSPPPPC 17
```

```
RESULT 18
US-11-036-690-18
; Sequence 18, Application US/11036690
; Publication No. US20050169979A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/11/036,690
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of GnRH amino acid sequence linked to a spacer
; OTHER INFORMATION: peptide
US-11-036-690-18
```

```
Query Match          100.0%; Score 45; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SSPPPPC 7
        |||||
Db       11 SSPPPPC 17
```

```
RESULT 19
US-10-323-692-7
; Sequence 7, Application US/10323692
; Publication No. US20040001842A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Immunogenic Compositions to the CCK-B/Gastrin Receptor and
; FILE REFERENCE: 1102865-0032
; CURRENT APPLICATION NUMBER: US/10/323,692
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 09/076,372
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/046,201
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (16)..(22)
; OTHER INFORMATION: Synthetic peptide spacer
US-10-323-692-7
```

```
Query Match          100.0%; Score 45; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SSPPPPC 7
        |||||
Db       16 SSPPPPC 22
```

```
RESULT 20
US-10-323-692-4
; Sequence 4, Application US/10323692
; Publication No. US20040001842A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Immunogenic Compositions to the CCK-B/Gastrin Receptor and
; FILE REFERENCE: 1102865-0032
; CURRENT APPLICATION NUMBER: US/10/323,692
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 09/076,372
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/046,201
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
```

```
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(17)
; OTHER INFORMATION: Amino acid residue 5-21 of the CCK-B/Gastrin receptor
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(24)
; OTHER INFORMATION: Synthetic peptide spacer
US-10-323-692-4
Query Match 100.0%; Score 45; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 18 SSPPPPC 24

RESULT 21
US-10-323-692-12
; Sequence 12, Application US/10323692
; Publication No. US2004001842A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Immunogenic Compositions to the CCK-B/Gastrin Receptor and
; METHODS for the Treatment of Tumors
; FILE REFERENCE: 1102865-0032
; CURRENT APPLICATION NUMBER: US/10/323,692
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 09/076,372
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/046,201
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (22)..(28)
; OTHER INFORMATION: Synthetic spacer peptide
US-10-323-692-12
Query Match 100.0%; Score 45; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 22 SSPPPPC 28

RESULT 22
US-10-437-963-155896
; Sequence 155896, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; PLANTS and Uses Thereof for Plant Improvement
```

```
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 155896
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(118)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_55616C.1.pcp
US-10-437-963-155896
Query Match 100.0%; Score 45; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 62 SSPPPPC 68

RESULT 23
US-10-424-599-161477
; Sequence 161477, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; PLANTS and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 161477
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(149)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_116831C.1.pcp
US-10-424-599-161477
Query Match 100.0%; Score 45; DB 4; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 63 SSPPPPC 69

RESULT 24
US-10-437-963-133423
; Sequence 133423, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
```

```
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133423
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(149)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35295C.1.pap
US-10-437-963-133423

Query Match      100.0%; Score 45; DB 4; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSPPPPC 7
        |||||
DB      120 SSPPPPC 126

RESULT 25
US-10-437-963-184880
; Sequence 184880, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 184880
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(222)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_81830C.1.pap
US-10-437-963-184880

Query Match      100.0%; Score 45; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSPPPPC 7
        |||||
DB      83 SSPPPPC 89

RESULT 26
US-10-374-780A-1256
; Sequence 1256, Application US/10374780A
; Publication No. US2004001927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddle, James
; APPLICANT: Broun, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubeil III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1256
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Orthologous to G922
US-10-374-780A-1256

Query Match      100.0%; Score 45; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSPPPPC 7
        |||||
DB      194 SSPPPPC 200

RESULT 27
US-10-437-963-159281
; Sequence 159281, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
```

; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 159281  
; LENGTH: 259  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_58673C.1.pep  
US-10-437-963-159281

Query Match 100.0%; Score 45; DB 4; Length 259;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
| | | | |  
Db 18 SSPPPPC 24

RESULT 28  
US-10-425-115-252781  
; Sequence 252781, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/425.115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 252781  
; LENGTH: 279  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(279)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_162119C.1.pep  
US-10-425-115-252781

Query Match 100.0%; Score 45; DB 4; Length 279;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
| | | | |  
Db 76 SSPPPPC 82

RESULT 29  
US-10-437-963-103058  
; Sequence 103058, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 103058  
; LENGTH: 401  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_100525C.1.pep  
US-10-437-963-103058

Query Match 100.0%; Score 45; DB 4; Length 401;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
| | | | |  
Db 291 SSPPPPC 297

RESULT 30  
US-10-437-963-168762  
; Sequence 168762, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 168762  
; LENGTH: 437  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(437)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_67245C.1.pep  
US-10-437-963-168762

Query Match 100.0%; Score 45; DB 4; Length 437;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
| | | | |  
Db 301 SSPPPPC 307

RESULT 31  
US-10-437-963-162350  
; Sequence 162350, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

```
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162350
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1426)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-437-963-162350

Query Match      100.0%; Score 45; DB 4; Length 737;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 307 SSPPPPC 313

RESULT 32
US-10-425-115-353007
; Sequence 353007, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 353007
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(777)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION:
; OTHER INFORMATION: Clone ID: MRT4577_85111C.1.pep
US-10-425-115-353007

Query Match      100.0%; Score 45; DB 4; Length 777;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 13 SSPPPPC 19

RESULT 33
US-10-437-963-180227
; Sequence 180227, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/425,115

; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 180227
; LENGTH: 1426
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1426)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-437-963-180227

Query Match      100.0%; Score 45; DB 4; Length 1426;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 35 SSPPPPC 41

RESULT 34
US-10-425-115-241838
; Sequence 241838, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 241838
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(81)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION:
; OTHER INFORMATION: Clone ID: MRT4577_152134C.1.pep
US-10-425-115-241838

Query Match      93.3%; Score 42; DB 4; Length 81;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 60 STPPPPC 66

RESULT 35
US-10-425-115-229307
; Sequence 229307, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
```

; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 229307  
; LENGTH: 83  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_140721C.1.pep  
US-10-425-115-229307

Query Match 93.3%; Score 42; DB 4; Length 83;  
Best Local Similarity 85.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
|:|||||  
DB 4 SAPPSPC 10

## RESULT 36

US-10-425-115-284097  
; Sequence 284097, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 284097  
; LENGTH: 114  
; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(114)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577\_22196C.1.pep

US-10-425-115-284097

Query Match 93.3%; Score 42; DB 4; Length 114;  
Best Local Similarity 85.7%; Pred. No. 3.2e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
|:|||||  
DB 104 STPPPC 110

## RESULT 37

US-10-425-115-310052  
; Sequence 310052, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 310052  
; LENGTH: 133  
; TYPE: PRT

; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(133)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_45827C.1.pep  
US-10-425-115-310052

Query Match 93.3%; Score 42; DB 4; Length 133;  
Best Local Similarity 85.7%; Pred. No. 3.6e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
|:|||||  
DB 55 STPPPC 61

## RESULT 38

US-10-437-963-129535  
; Sequence 129535, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Barbazuk, Brad

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 129535

; LENGTH: 134

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_31784C.1.pep

US-10-437-963-129535

Query Match 93.3%; Score 42; DB 4; Length 134;  
Best Local Similarity 85.7%; Pred. No. 3.6e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
|:|||||  
DB 104 SAPPSPC 110

## RESULT 39

US-10-437-963-102751  
; Sequence 102751, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Barbazuk, Brad

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

```
; SEQ ID NO 102751
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(141)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_100244C.1.pep
US-10-437-963-102751

Query Match          93.3%; Score 42; DB 4; Length 141;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 33 ASPPPPC 39

RESULT 40
US-10-425-115-304261
; Sequence 304261, Application US/10425115
; Publication NO. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 304261
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(199)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_40558C.1.pep
US-10-425-115-304261

Query Match          93.3%; Score 42; DB 4; Length 199;
Best Local Similarity 85.7%; Pred. No. 5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 46 TSPPPPC 52

RESULT 41
US-10-437-963-127361
; Sequence 127361, Application US/10437963
; Publication NO. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
```

```
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 127361
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_29820C.1.pep
US-10-437-963-127361

Query Match          93.3%; Score 42; DB 4; Length 206;
Best Local Similarity 85.7%; Pred. No. 5.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 31 STPPPPC 37

RESULT 42
US-10-425-115-204474
; Sequence 204474, Application US/10425115
; Publication NO. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 204474
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(215)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_118071C.1.pep
US-10-425-115-204474

Query Match          93.3%; Score 42; DB 4; Length 215;
Best Local Similarity 85.7%; Pred. No. 5.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 195 TSPPPPC 201

RESULT 43
US-10-437-963-142834
; Sequence 142834, Application US/10437963
; Publication NO. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
```

; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 142834  
; LENGTH: 308  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_43801C.1.pep  
US-10-437-963-142834

Query Match 93.3%; Score 42; DB 4; Length 308;  
Best Local Similarity 85.7%; Pred. No. 7e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
|:|||||  
Db 81 SAPPPPC 87

## RESULT 44

US-10-437-963-124536  
; Sequence 124536, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 124536  
; LENGTH: 361

; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(361)

; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_27265C.1.pep  
US-10-437-963-124536

Query Match 93.3%; Score 42; DB 4; Length 361;  
Best Local Similarity 85.7%; Pred. No. 8e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
|:|||||  
Db 306 SAPPPPC 312

## RESULT 45

US-10-437-963-200332  
; Sequence 200332, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 200332  
; LENGTH: 528  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_95811C.1.pep  
US-10-437-963-200332

Query Match 93.3%; Score 42; DB 4; Length 528;  
Best Local Similarity 85.7%; Pred. No. 1.1e+03;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
|:|||||  
Db 37 SAPPPPC 43

## RESULT 46

US-10-425-114-72496  
; Sequence 72496, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 72496  
; LENGTH: 831

; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: UC-2MFLMOL7269A09\_FLI.pep  
US-10-425-114-72496

Query Match 93.3%; Score 42; DB 4; Length 831;  
Best Local Similarity 85.7%; Pred. No. 1.6e+03;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
|:|||||  
Db 15 STEPPEC 21

## RESULT 47

US-10-029-386-30577  
; Sequence 30577, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 30577  
; LENGTH: 58

```
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL137798.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.8
; OTHER INFORMATION: SWISSPROT HIT: O02626, EVALUATION 3.60e+00
US-10-029-386-30577

Query Match          91.1%; Score 41; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
Db 17 SPPPPC 22

RESULT 48
US-10-425-115-259087
; Sequence 259087, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 259087
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_167873C.1.pap
US-10-425-115-259087

Query Match          91.1%; Score 41; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
Db 32 SPPPPC 37

RESULT 49
US-10-437-963-142765
; Sequence 142765, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 142765
; LENGTH: 79
; TYPE: PRT
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; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_4373C.1.pap
US-10-437-963-142765

Query Match          91.1%; Score 41; DB 4; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
Db 47 SPPPPC 52

RESULT 50
US-10-437-963-165922
; Sequence 165922, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 165922
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_64681C.1.pap
US-10-437-963-165922

Query Match          91.1%; Score 41; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
Db 60 SPPPPC 65

Search completed: January 3, 2006, 09:55:47
Job time : 70.6667 secs
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:20:09 , Search time 5 Seconds  
(without alignments)  
10.484 Million cell updates/sec

Title: US-10-759-832-10

Perfect score: 45

Sequence: 1 SSPPPC 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 1000 summaries

Database : Published Applications AA New:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	37	82.2	240	6	US-10-467-657-3742
3	37	82.2	340	6	US-10-999-866-32
4	37	82.2	340	7	US-11-061-821-32
5	37	82.2	522	6	US-10-467-657-7238
6	37	82.2	616	7	US-11-155-492-3
7	37	82.2	670	6	US-10-995-561-528
8	37	82.2	4346	6	US-10-995-561-671
9	37	82.2	4347	6	US-10-995-561-670
10	37	82.2	4419	6	US-10-821-234-1155
11	36	80.0	197	7	US-11-013-247A-10
12	36	80.0	362	7	US-11-013-247A-7
13	36	80.0	364	7	US-11-013-247A-6
14	36	80.0	448	7	US-11-013-247A-5
15	36	80.0	501	7	US-11-013-247A-2
16	36	80.0	503	7	US-11-013-247A-4
17	36	80.0	529	7	US-11-013-247A-17
18	36	80.0	763	7	US-11-013-247A-35
19	36	80.0	868	6	US-10-995-561-792
20	36	80.0	2048	7	US-11-116-939-6
21	34.5	76.7	229	7	US-11-014-629-1
22	34	75.6	290	7	US-11-054-515-3231
23	34	75.6	309	7	US-11-065-669-2
24	34	75.6	309	7	US-11-054-515-3230
25	34	75.6	1311	6	US-10-509-422-5

33.5	74.4	420	6	US-10-131-826A-290	Sequence 290, App
33	73.3	146	6	US-10-821-234-1225	Sequence 1225, App
33	73.3	291	7	US-11-078-735-30	Sequence 30, Appl
33	73.3	314	7	US-11-179-977-17	Sequence 17, Appl
33	73.3	331	7	US-11-078-735-33	Sequence 33, Appl
33	73.3	332	7	US-11-078-735-51	Sequence 51, Appl
33	73.3	369	7	US-11-078-735-38	Sequence 38, Appl
33	73.3	380	7	US-11-116-939-2	Sequence 2, Appli
33	73.3	381	6	US-10-821-234-1342	Sequence 1342, Ap
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33	73.3	472	6	US-10-632-150-8	Sequence 8, Appli
33	73.3	472	7	US-11-073-457-8	Sequence 8, Appli
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33	73.3	484	7	US-11-078-735-43	Sequence 43, Appl
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33	73.3	723	6	US-10-131-826A-346	Sequence 346, App
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32	71.1	273	6	US-10-821-234-1203	Sequence 1203, Ap
32	71.1	275	6	US-10-821-234-1013	Sequence 1013, Ap
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32	71.1	456	6	US-10-477-507A-2	Sequence 4, Appli
32	71.1	478	7	US-11-037-829A-4	Sequence 933, App
32	71.1	484	6	US-10-821-234-933	Sequence 933, App
32	71.1	572	6	US-10-821-234-1290	Sequence 1290, Ap
32	71.1	591	6	US-10-770-726-71	Sequence 71, Appl
32	71.1	608	7	US-11-109-157A-11	Sequence 11, Appl
32	71.1	619	7	US-11-109-157A-42	Sequence 42, Appl
32	71.1	633	6	US-10-821-234-1146	Sequence 1146, Ap
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32	71.1	1686	7	US-11-109-157A-1	Sequence 1, Appli
32	71.1	2214	7	US-11-080-991-94	Sequence 94, Appl
32	71.1	2630	7	US-11-186-731-2	Sequence 2, Appli
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31	68.9	509	6	US-10-821-234-1093	Sequence 1093, Ap
31	68.9	827	6	US-10-821-234-1685	Sequence 1685, Ap
31	68.9	974	6	US-10-995-561-895	Sequence 895, App
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31	68.9	997	6	US-10-995-561-896	Sequence 896, App
31	68.9	1018	7	US-11-067-121-17	Sequence 17, Appl
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30	66.7	67	6	US-10-467-657-5340	Sequence 5340, Ap
30	66.7	168	7	US-11-010-874-7	Sequence 7, Appli
30	66.7	176	7	US-11-080-991-20	Sequence 20, Appl
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30	66.7	280	7	US-11-143-980-34	Sequence 34, Appl
30	66.7	287	7	US-11-174-150-30	Sequence 30, Appl
30	66.7	289	6	US-10-821-234-1289	Sequence 1289, Ap
30	66.7	292	6	US-10-821-234-966	Sequence 966, App
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30	66.7	371	6	US-10-995-561-572	Sequence 572, App
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30	66.7	377	7	US-11-102-821-113	Sequence 113, App

99	30	66.7	377	7	US-11-102-621-115	Sequence 115, App	172	29	64.4	320	6	US-10-995-561-947	Sequence 947, App
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101	30	66.7	411	6	US-10-524-919-4	Sequence 4, Appl1	174	29	64.4	366	7	US-11-000-463-897	Sequence 897, App
102	30	66.7	412	6	US-10-524-919-2	Sequence 2, Appl1	175	29	64.4	372	6	US-10-844-035-1	Sequence 1, Appl1
103	30	66.7	457	6	US-10-986-501-110	Sequence 110, App	176	29	64.4	373	6	US-10-995-561-948	Sequence 948, App
104	30	66.7	459	6	US-10-641-678-72	Sequence 72, Appl	177	29	64.4	375	6	US-10-995-561-946	Sequence 946, App
105	30	66.7	486	6	US-10-667-295-201	Sequence 201, App	178	29	64.4	385	6	US-10-995-561-945	Sequence 945, App
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109	30	66.7	540	6	US-10-821-234-1395	Sequence 1395, Ap	182	29	64.4	402	6	US-10-131-826A-468	Sequence 468, App
110	30	66.7	552	6	US-10-821-234-1022	Sequence 1022, Ap	183	29	64.4	405	6	US-10-821-234-1357	Sequence 1357, Ap
111	30	66.7	579	6	US-10-821-234-1352	Sequence 1352, Ap	184	29	64.4	408	7	US-11-140-417-6	Sequence 6, Appl1
112	30	66.7	609	7	US-11-058-555-2	Sequence 2, Appl1	185	29	64.4	413	6	US-10-967-648A-8	Sequence 8, Appl1
113	30	66.7	756	7	US-11-188-743-20	Sequence 20, Appl	186	29	64.4	417	6	US-10-971-560-4	Sequence 4, Appl1
114	30	66.7	812	7	US-11-010-874-1	Sequence 1, Appl1	187	29	64.4	429	7	US-11-071-062-9	Sequence 9, Appl1
115	30	66.7	816	7	US-11-057-058-10	Sequence 10, Appl	188	29	64.4	432	7	US-11-140-417-4	Sequence 4, Appl1
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117	30	66.7	921	7	US-11-183-624-2	Sequence 2, Appl1	190	29	64.4	437	6	US-10-967-648A-4	Sequence 4, Appl1
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121	30	66.7	997	7	US-11-057-058-33	Sequence 33, Appl	194	29	64.4	449	7	US-11-196-459-1	Sequence 1, Appl1
122	30	66.7	1011	7	US-11-057-058-31	Sequence 31, Appl	195	29	64.4	449	7	US-11-196-459-2	Sequence 2, Appl1
123	30	66.7	1028	7	US-11-067-121-7	Sequence 7, Appl1	196	29	64.4	461	6	US-10-623-155-343	Sequence 343, App
124	30	66.7	1036	6	US-10-131-826A-142	Sequence 142, App	197	29	64.4	463	6	US-10-641-678-71	Sequence 71, Appl
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132	29	64.4	39	6	US-10-986-501-278	Sequence 278, App	205	29	64.4	516	6	US-10-623-155-344	Sequence 344, App
133	29	64.4	39	6	US-10-986-501-364	Sequence 364, App	206	29	64.4	525	6	US-10-641-678-52	Sequence 52, Appl
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136	29	64.4	127	7	US-11-186-284-171	Sequence 171, App	209	29	64.4	548	7	US-11-119-769-3	Sequence 3, Appl1
137	29	64.4	134	7	US-11-195-459-8	Sequence 8, Appl1	210	29	64.4	560	7	US-11-080-991-62	Sequence 62, Appl
138	29	64.4	146	7	US-11-000-463-881	Sequence 881, App	211	29	64.4	564	7	US-11-186-284-159	Sequence 159, App
139	29	64.4	152	6	US-10-994-820A-13	Sequence 13, Appl	212	29	64.4	576	7	US-11-137-465-64	Sequence 64, Appl
140	29	64.4	157	6	US-10-994-820A-14	Sequence 14, Appl	213	29	64.4	580	6	US-10-821-234-1309	Sequence 1309, Ap
141	29	64.4	168	6	US-10-467-657-1878	Sequence 1878, Ap	214	29	64.4	586	6	US-10-623-155-152	Sequence 152, App
142	29	64.4	168	7	US-11-044-111-27	Sequence 27, Appl	215	29	64.4	586	6	US-10-623-155-338	Sequence 338, App
143	29	64.4	178	6	US-10-821-234-1052	Sequence 1052, Ap	216	29	64.4	597	6	US-10-884-730-381	Sequence 381, App
144	29	64.4	181	7	US-11-000-463-409	Sequence 409, App	217	29	64.4	600	6	US-10-606-302-3	Sequence 3, Appl1
145	29	64.4	184	6	US-10-821-234-1415	Sequence 1415, Ap	218	29	64.4	610	6	US-10-606-302-1	Sequence 1, Appl1
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149	29	64.4	206	7	US-10-467-657-4800	Sequence 4800, Ap	222	29	64.4	641	6	US-10-623-155-339	Sequence 339, App
150	29	64.4	212	7	US-11-015-546A-7	Sequence 7, Appl1	223	29	64.4	651	6	US-10-994-820A-34	Sequence 34, Appl
151	29	64.4	212	7	US-11-015-546A-5	Sequence 5, Appl1	224	29	64.4	654	7	US-11-110-011-3	Sequence 3, Appl1
152	29	64.4	218	6	US-10-667-295-151	Sequence 151, App	225	29	64.4	680	6	US-10-623-155-342	Sequence 342, App
153	29	64.4	219	7	US-11-015-546A-4	Sequence 4, Appl1	226	29	64.4	721	7	US-11-186-284-67	Sequence 67, Appl
154	29	64.4	224	6	US-10-994-820A-6	Sequence 6, Appl1	227	29	64.4	727	6	US-10-995-561-864	Sequence 864, App
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156	29	64.4	231	6	US-10-689-742-38	Sequence 38, Appl	229	29	64.4	782	6	US-10-995-561-861	Sequence 861, App
157	29	64.4	231	6	US-10-994-820A-8	Sequence 8, Appl1	230	29	64.4	847	6	US-10-995-561-863	Sequence 863, App
158	29	64.4	232	6	US-10-821-234-1199	Sequence 1199, Ap	231	29	64.4	847	6	US-10-995-561-865	Sequence 865, App
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161	29	64.4	261	6	US-10-821-234-930	Sequence 930, App	234	29	64.4	987	6	US-10-949-720-395	Sequence 395, App
162	29	64.4	262	6	US-10-689-742-65	Sequence 65, Appl	235	29	64.4	989	6	US-10-821-234-975	Sequence 975, App
163	29	64.4	269	7	US-11-015-546A-10	Sequence 10, Appl	236	29	64.4	990	6	US-10-821-234-1201	Sequence 1201, Ap
164	29	64.4	274	7	US-11-015-546A-12	Sequence 12, Appl	237	29	64.4	1178	6	US-10-995-561-851	Sequence 851, App
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251	29	64.4	2769	7	US-11-113-424-14	Sequence 14, Appl	324	28	62.2	160	7	US-11-157-049-18	Sequence 18, Appl
252	29	64.4	3063	7	US-11-186-284-26	Sequence 26, Appl	325	28	62.2	160	7	US-11-157-049-19	Sequence 19, Appl
253	29	64.4	5405	7	US-11-108-172-1116	Sequence 116, App	326	28	62.2	160	7	US-11-157-049-20	Sequence 20, Appl
254	28	62.2	10	7	US-11-120-543-47	Sequence 47, Appl	327	28	62.2	160	7	US-11-157-049-21	Sequence 21, Appl
255	28	62.2	18	7	US-11-085-775-9	Sequence 9, Appl	328	28	62.2	160	7	US-11-157-049-22	Sequence 22, Appl
256	28	62.2	18	7	US-11-174-089-9	Sequence 9, Appl	329	28	62.2	160	7	US-11-157-049-23	Sequence 23, Appl
257	28	62.2	18	7	US-11-174-089-10	Sequence 10, Appl	330	28	62.2	160	7	US-11-157-049-24	Sequence 24, Appl
258	28	62.2	18	7	US-11-174-089-11	Sequence 11, Appl	331	28	62.2	160	7	US-11-157-049-25	Sequence 25, Appl
259	28	62.2	18	7	US-11-174-089-12	Sequence 12, Appl	332	28	62.2	160	7	US-10-667-295-9	Sequence 9, Appl
260	28	62.2	18	7	US-11-174-089-13	Sequence 13, Appl	333	28	62.2	173	6	US-10-821-234-1074	Sequence 1074, App
261	28	62.2	18	7	US-11-174-089-14	Sequence 14, Appl	334	28	62.2	175	6	US-11-107-029-3	Sequence 3, Appl
262	28	62.2	18	7	US-11-174-089-15	Sequence 15, Appl	335	28	62.2	178	6	US-10-131-826A-446	Sequence 446, App
263	28	62.2	18	7	US-11-174-089-16	Sequence 16, Appl	336	28	62.2	180	6	US-10-131-826A-2	Sequence 2, Appl
264	28	62.2	19	6	US-10-503-575-185	Sequence 185, App	337	28	62.2	180	6	US-11-157-049-2	Sequence 2, Appl
265	28	62.2	19	6	US-10-503-575-186	Sequence 186, App	338	28	62.2	181	6	US-10-821-234-867	Sequence 867, App
266	28	62.2	19	6	US-11-157-049-31	Sequence 31, Appl	339	28	62.2	183	7	US-11-128-440-2	Sequence 2, Appl
267	28	62.2	20	6	US-10-485-788A-578	Sequence 578, App	340	28	62.2	188	6	US-10-131-826A-2	Sequence 2, Appl
268	28	62.2	21	7	US-11-198-847-291	Sequence 291, App	341	28	62.2	188	6	US-10-793-626-2718	Sequence 2718, App
269	28	62.2	22	7	US-11-198-847-328	Sequence 328, App	342	28	62.2	188	6	US-10-821-234-1316	Sequence 1316, App
270	28	62.2	25	7	US-11-198-847-252	Sequence 252, App	343	28	62.2	193	7	US-11-069-642-129	Sequence 129, App
271	28	62.2	29	7	US-11-198-847-304	Sequence 304, App	344	28	62.2	194	7	US-11-108-172-1126	Sequence 1126, App
272	28	62.2	29	7	US-11-198-847-305	Sequence 305, App	345	28	62.2	197	6	US-10-632-150-32	Sequence 32, Appl
273	28	62.2	30	6	US-10-821-234-887	Sequence 887, App	346	28	62.2	197	7	US-11-073-457-32	Sequence 32, Appl
274	28	62.2	31	6	US-10-467-657-1684	Sequence 1684, App	347	28	62.2	197	7	US-11-073-460-32	Sequence 123, App
275	28	62.2	34	7	US-11-198-847-253	Sequence 253, App	348	28	62.2	207	7	US-11-069-642-123	Sequence 7, Appl
276	28	62.2	48	6	US-10-467-657-738	Sequence 738, App	349	28	62.2	212	6	US-10-982-545-7	Sequence 282, App
277	28	62.2	48	6	US-10-467-657-746	Sequence 746, App	350	28	62.2	225	6	US-10-131-826A-282	Sequence 56, Appl
278	28	62.2	48	6	US-10-467-657-838	Sequence 838, App	351	28	62.2	231	6	US-10-821-234-943	Sequence 943, App
279	28	62.2	48	6	US-10-467-657-870	Sequence 870, App	352	28	62.2	233	6	US-10-821-234-1322	Sequence 1322, App
280	28	62.2	49	7	US-11-198-847-270	Sequence 270, App	353	28	62.2	250	6	US-10-986-501-120	Sequence 320, App
281	28	62.2	49	7	US-11-198-847-271	Sequence 271, App	354	28	62.2	255	7	US-10-131-826A-320	Sequence 36, Appl
282	28	62.2	49	7	US-11-198-847-272	Sequence 272, App	355	28	62.2	256	7	US-11-185-111-36	Sequence 133, App
283	28	62.2	55	6	US-10-467-657-7632	Sequence 7632, App	356	28	62.2	266	6	US-11-113-424-183	Sequence 5258, App
284	28	62.2	55	6	US-10-467-657-8394	Sequence 8394, App	357	28	62.2	268	6	US-10-467-657-5258	Sequence 56, Appl
285	28	62.2	57	6	US-10-467-657-7378	Sequence 7378, App	358	28	62.2	272	6	US-10-986-501-120	Sequence 120, App
286	28	62.2	61	7	US-11-157-049-34	Sequence 34, Appl	359	28	62.2	275	6	US-10-821-234-971	Sequence 971, App
287	28	62.2	66	6	US-10-821-234-1226	Sequence 1226, App	360	28	62.2	282	6	US-10-131-826A-312	Sequence 312, App
288	28	62.2	69	6	US-10-467-657-1680	Sequence 1680, App	361	28	62.2	282	6	US-10-572-587-28	Sequence 28, Appl
289	28	62.2	71	7	US-11-198-847-68	Sequence 68, Appl	362	28	62.2	282	7	US-11-080-591-34	Sequence 34, Appl
290	28	62.2	73	6	US-10-467-657-898	Sequence 898, App	363	28	62.2	283	7	US-11-186-284-99	Sequence 99, Appl
291	28	62.2	73	6	US-11-157-049-35	Sequence 35, Appl	364	28	62.2	285	6	US-10-972-587-26	Sequence 26, Appl
292	28	62.2	74	7	US-11-198-847-59	Sequence 59, Appl	365	28	62.2	293	6	US-10-821-234-1374	Sequence 1374, App
293	28	62.2	79	6	US-10-982-535A-21	Sequence 21, Appl	366	28	62.2	306	6	US-10-878-556A-56	Sequence 56, Appl
294	28	62.2	80	7	US-11-198-847-83	Sequence 83, Appl	367	28	62.2	306	6	US-10-878-556A-89	Sequence 89, Appl
295	28	62.2	80	7	US-11-198-847-86	Sequence 86, Appl	368	28	62.2	311	7	US-11-108-172-1061	Sequence 1061, App
296	28	62.2	80	7	US-11-198-847-152	Sequence 152, App	369	28	62.2	333	6	US-10-878-556A-174	Sequence 174, App
297	28	62.2	81	7	US-11-198-847-161	Sequence 161, App	370	28	62.2	334	6	US-10-995-561-822	Sequence 822, App
298	28	62.2	81	7	US-11-198-847-158	Sequence 158, App	371	28	62.2	343	6	US-10-821-234-953	Sequence 953, App
299	28	62.2	83	6	US-10-131-826A-42	Sequence 42, Appl	372	28	62.2	346	6	US-10-967-648A-10	Sequence 10, Appl
300	28	62.2	83	7	US-11-198-847-56	Sequence 56, Appl	373	28	62.2	349	7	US-11-147-047-47	Sequence 47, Appl
301	28	62.2	97	7	US-11-157-049-26	Sequence 26, Appl	374	28	62.2	350	7	US-11-095-624-2	Sequence 2, Appl
302	28	62.2	98	6	US-10-999-866-21	Sequence 21, Appl	375	28	62.2	350	7	US-11-095-624-3	Sequence 3, Appl
303	28	62.2	98	6	US-11-061-821-21	Sequence 21, Appl	376	28	62.2	350	7	US-11-095-624-4	Sequence 4, Appl
304	28	62.2	103	6	US-10-821-234-1005	Sequence 1005, App	377	28	62.2	354	6	US-10-821-234-1618	Sequence 1618, App
305	28	62.2	105	6	US-10-821-234-1149	Sequence 1149, App	378	28	62.2	358	7	US-11-085-775-3	Sequence 3, Appl
306	28	62.2	108	6	US-10-821-234-991	Sequence 991, App	379	28	62.2	376	6	US-10-878-556A-170	Sequence 170, App
307	28	62.2	111	6	US-10-821-234-1178	Sequence 1178, App	380	28	62.2	383	7	US-11-147-047-38	Sequence 38, Appl
308	28	62.2	114	6	US-10-821-234-938	Sequence 938, App	381	28	62.2	384	6	US-10-878-556A-91	Sequence 91, Appl
309	28	62.2	119	6	US-10-821-234-1044	Sequence 1044, App	382	28	62.2	389	7	US-11-000-463-316	Sequence 316, App
310	28	62.2	128	7	US-11-157-049-42	Sequence 42, Appl	383	28	62.2	391	6	US-10-878-556A-86	Sequence 86, Appl
311	28	62.2	133	6	US-10-821-234-1059	Sequence 1059, App	384	28	62.2	400	7	US-11-186-284-155	Sequence 155, App
312	28	62.2	135	6	US-10-667-295-157	Sequence 157, App	385	28	62.2	401	6	US-10-821-234-881	Sequence 881, App
313	28	62.2	141	7	US-11-000-463-435	Sequence 435, App	386	28	62.2	402	6	US-10-650-326B-21	Sequence 21, Appl
314	28	62.2	143	6	US-10-986-501-342	Sequence 342, App	387	28	62.2	405	6	US-11-051-568-29	Sequence 29, Appl
315	28	62.2	151	7	US-11-157-049-38	Sequence 38, Appl	388	28	62.2	406	6	US-10-821-234-931	Sequence 931, App
316	28	62.2	153	7	US-11-157-049-41	Sequence 41, Appl	389	28	62.2	406	6	US-10-131-826A-82	Sequence 82, Appl
317	28	62.2	154	7	US-11-157-049-37	Sequence 37, Appl	390	28	62.2	414	6	US-10-821-234-1170	Sequence 1170, App

391	28	62.2	424	6	US-10-878-556A-34	Sequence 34, Appl	464	28	62.2	853	6	US-10-821-234-1110	Sequence 1110, Ap
392	28	62.2	430	6	US-10-467-657-5700	Sequence 5700, Ap	465	28	62.2	853	6	US-10-420-192-6	Sequence 6, Appli
393	28	62.2	436	7	US-10-467-657-7448	Sequence 7448, Ap	466	28	62.2	863	7	US-11-114-906-32	Sequence 32, Appl
394	28	62.2	439	7	US-11-000-463-7488	Sequence 7488, Appl	467	28	62.2	876	7	US-11-114-906-30	Sequence 30, Appl
395	28	62.2	439	7	US-11-080-991-18	Sequence 18, Appl	468	28	62.2	881	6	US-10-623-155-430	Sequence 430, App
396	28	62.2	443	6	US-10-131-826A-318	Sequence 318, Appl	469	28	62.2	883	6	US-10-770-726-57	Sequence 57, Appli
397	28	62.2	445	7	US-11-000-463-461	Sequence 463, App	470	28	62.2	889	7	US-11-114-906-20	Sequence 20, Appl
398	28	62.2	461	6	US-10-509-464-7	Sequence 7, Appli	471	28	62.2	895	7	US-11-150-406-2	Sequence 2, Appli
399	28	62.2	470	6	US-10-878-556A-101	Sequence 101, App	472	28	62.2	895	7	US-11-114-906-18	Sequence 18, Appl
400	28	62.2	475	7	US-11-174-150-45	Sequence 45, Appl	473	28	62.2	903	7	US-11-057-058-65	Sequence 65, Appl
401	28	62.2	477	7	US-11-075-185-27	Sequence 27, Appl	474	28	62.2	920	6	US-10-821-234-1129	Sequence 1129, Ap
402	28	62.2	479	7	US-11-147-047-44	Sequence 44, Appl	475	28	62.2	920	6	US-10-623-155-357	Sequence 357, App
403	28	62.2	490	6	US-10-131-826A-310	Sequence 310, Appl	476	28	62.2	943	6	US-10-928-446A-190	Sequence 190, App
404	28	62.2	491	6	US-10-641-678-65	Sequence 65, Appl	477	28	62.2	943	6	US-10-821-234-1012	Sequence 1012, Ap
405	28	62.2	495	6	US-10-770-726-81	Sequence 81, Appl	478	28	62.2	943	6	US-10-623-155-161	Sequence 161, App
406	28	62.2	496	7	US-11-110-082-31	Sequence 31, Appl	479	28	62.2	947	6	US-10-928-446A-182	Sequence 182, App
407	28	62.2	496	7	US-11-186-284-103	Sequence 103, App	480	28	62.2	948	6	US-10-523-477-14	Sequence 14, Appl
408	28	62.2	505	7	US-11-063-343-38	Sequence 38, Appl	481	28	62.2	950	6	US-10-928-446A-184	Sequence 184, App
409	28	62.2	512	6	US-10-467-657-6780	Sequence 6780, Ap	482	28	62.2	955	6	US-10-928-446A-186	Sequence 186, App
410	28	62.2	512	6	US-11-099-691-10	Sequence 10, Appl	483	28	62.2	976	7	US-11-114-906-28	Sequence 28, Appl
411	28	62.2	522	7	US-10-995-561-1030	Sequence 1030, Ap	484	28	62.2	982	7	US-11-114-906-26	Sequence 26, Appl
412	28	62.2	527	7	US-11-120-543-18	Sequence 18, Appl	485	28	62.2	998	6	US-10-510-524-1	Sequence 1, Appli
413	28	62.2	537	7	US-11-109-156-28	Sequence 28, Appl	486	28	62.2	1012	6	US-10-995-561-908	Sequence 908, App
414	28	62.2	541	7	US-11-118-855-26	Sequence 26, Appl	487	28	62.2	1044	7	US-11-091-668-2	Sequence 2, Appli
415	28	62.2	543	7	US-11-113-224-6	Sequence 6, Appli	488	28	62.2	1056	7	US-11-044-111-22	Sequence 22, Appl
416	28	62.2	549	6	US-10-995-561-909	Sequence 909, App	489	28	62.2	1062	6	US-10-821-234-1079	Sequence 1079, Ap
417	28	62.2	555	6	US-10-821-234-1015	Sequence 1015, Ap	490	28	62.2	1072	7	US-11-109-157A-13	Sequence 13, Appl
418	28	62.2	559	6	US-10-821-234-947	Sequence 947, App	491	28	62.2	1073	6	US-10-467-657-5230	Sequence 5230, Ap
419	28	62.2	560	6	US-10-623-155-225	Sequence 225, App	492	28	62.2	1122	6	US-10-995-561-705	Sequence 705, App
420	28	62.2	563	6	US-10-821-234-1067	Sequence 1067, Ap	493	28	62.2	1129	6	US-10-995-561-706	Sequence 706, App
421	28	62.2	577	6	US-10-623-155-500	Sequence 500, App	494	28	62.2	1159	6	US-10-613-744-12	Sequence 12, Appl
422	28	62.2	587	6	US-10-623-155-501	Sequence 501, App	495	28	62.2	1163	7	US-11-044-899-2	Sequence 2, Appli
423	28	62.2	592	6	US-10-623-155-169	Sequence 169, App	496	28	62.2	1163	7	US-11-044-899-30	Sequence 30, Appl
424	28	62.2	592	6	US-10-995-561-994	Sequence 994, App	497	28	62.2	1170	7	US-11-080-026-2	Sequence 2, Appli
425	28	62.2	595	6	US-10-995-561-995	Sequence 995, App	498	28	62.2	1170	7	US-11-107-028-4	Sequence 4, Appli
426	28	62.2	601	6	US-10-995-561-993	Sequence 993, App	499	28	62.2	1174	6	US-10-995-561-697	Sequence 697, App
427	28	62.2	614	7	US-11-155-492-107	Sequence 107, App	500	28	62.2	1178	7	US-11-044-899-29	Sequence 29, Appl
428	28	62.2	615	6	US-10-982-545-14	Sequence 14, Appl	501	28	62.2	1187	6	US-10-821-234-955	Sequence 955, App
429	28	62.2	616	6	US-10-982-545-5	Sequence 5, Appli	502	28	62.2	1211	7	US-11-186-284-4	Sequence 4, Appli
430	28	62.2	628	7	US-11-147-047-45	Sequence 45, Appl	503	28	62.2	1271	6	US-10-770-726-46	Sequence 46, Appl
431	28	62.2	635	6	US-10-821-234-927	Sequence 927, App	504	28	62.2	1278	6	US-10-995-561-952	Sequence 952, App
432	28	62.2	635	6	US-10-995-561-996	Sequence 996, App	505	28	62.2	1308	7	US-11-113-202-16	Sequence 16, Appl
433	28	62.2	647	7	US-11-109-157A-15	Sequence 15, Appl	506	28	62.2	1410	6	US-10-821-234-1050	Sequence 1050, Ap
434	28	62.2	650	6	US-10-878-556A-110	Sequence 110, App	507	28	62.2	1627	6	US-10-821-234-1283	Sequence 1283, Ap
435	28	62.2	656	6	US-10-821-234-1121	Sequence 1121, Ap	508	28	62.2	2011	7	US-11-080-991-56	Sequence 56, Appl
436	28	62.2	658	7	US-11-109-157A-43	Sequence 43, Appl	509	28	62.2	2432	6	US-10-821-234-859	Sequence 899, App
437	28	62.2	668	6	US-10-995-561-992	Sequence 992, App	510	28	62.2	2725	7	US-11-113-424-52	Sequence 52, Appl
438	28	62.2	697	6	US-10-821-234-905	Sequence 905, App	511	28	62.2	3002	6	US-10-821-234-916	Sequence 916, App
439	28	62.2	708	7	US-11-078-189-10	Sequence 10, Appl	512	28	62.2	3011	6	US-10-985-205-3	Sequence 3, Appli
440	28	62.2	712	6	US-10-770-726-66	Sequence 66, Appl	513	28	62.2	3144	7	US-11-055-035-1	Sequence 23, Appl
441	28	62.2	718	6	US-10-918-857-2	Sequence 2, Appli	514	28	62.2	3375	6	US-11-044-111-23	Sequence 23, Appl
442	28	62.2	731	6	US-10-613-744-10	Sequence 10, Appl	515	28	62.2	3690	6	US-10-995-561-1016	Sequence 1016, Ap
443	28	62.2	735	7	US-11-184-380-24	Sequence 24, Appl	516	28	62.2	3714	6	US-10-995-561-1015	Sequence 1015, Ap
444	28	62.2	737	7	US-11-210-316-8	Sequence 8, Appli	517	28	62.2	4384	6	US-10-821-234-1076	Sequence 1076, Ap
445	28	62.2	748	6	US-10-821-234-888	Sequence 888, App	518	28	62.2	4384	6	US-10-821-234-1120	Sequence 1120, Ap
446	28	62.2	756	7	US-11-073-347-1	Sequence 1, Appli	519	27.5	61.1	255	7	US-11-115-086-11	Sequence 11, Appl
447	28	62.2	756	6	US-10-131-826A-392	Sequence 392, App	520	27	60.0	83	6	US-10-467-657-7924	Sequence 7924, Ap
448	28	62.2	776	7	US-11-114-906-24	Sequence 24, Appl	521	27	60.0	111	7	US-11-184-005-6	Sequence 6, Appli
449	28	62.2	789	7	US-11-114-906-22	Sequence 22, Appl	522	27	60.0	161	6	US-10-467-657-1338	Sequence 1338, Ap
450	28	62.2	790	6	US-10-918-857-6	Sequence 6, Appli	523	27	60.0	182	6	US-10-821-234-1114	Sequence 1114, Ap
451	28	62.2	791	6	US-10-623-155-170	Sequence 170, App	524	27	60.0	205	6	US-10-689-742-72	Sequence 72, Appl
452	28	62.2	795	6	US-10-821-234-1675	Sequence 1675, Ap	525	27	60.0	232	6	US-10-821-234-1023	Sequence 1023, Ap
453	28	62.2	815	7	US-11-073-113-3	Sequence 3, Appli	526	27	60.0	236	7	US-11-008-727-4	Sequence 4, Appli
454	28	62.2	834	6	US-10-928-446A-188	Sequence 188, App	527	27	60.0	353	7	US-11-182-592-4	Sequence 5, Appli
455	28	62.2	834	6	US-10-928-446A-192	Sequence 192, App	528	27	60.0	365	7	US-11-087-177-5	Sequence 5, Appli
456	28	62.2	834	6	US-10-928-446A-194	Sequence 194, App	529	27	60.0	388	6	US-10-995-561-838	Sequence 838, App
457	28	62.2	834	6	US-10-928-446A-196	Sequence 196, App	530	27	60.0	389	6	US-10-995-561-837	Sequence 837, App
458	28	62.2	834	6	US-10-928-446A-198	Sequence 198, App	531	27	60.0	428	6	US-10-131-826A-292	Sequence 292, App
459	28	62.2	834	6	US-10-928-446A-200	Sequence 200, App	532	27	60.0	470	7	US-11-008-727-20	Sequence 20, Appl
460	28	62.2	834	6	US-10-928-446A-202	Sequence 202, App	533	27	60.0	476	7	US-11-008-727-22	Sequence 22, Appl
461	28	62.2	837	6	US-10-995-561-698	Sequence 698, App	534	27	60.0	509	7	US-11-008-727-16	Sequence 16, Appl
462	28	62.2	837	7	US-11-094-519A-43	Sequence 43, Appl	535	27	60.0	510	6	US-10-641-678-43	Sequence 43, Appl
463	28	62.2	845	7	US-11-094-519A-42	Sequence 42, Appl	536	27	60.0	511	6	US-10-641-678-42	Sequence 42, Appl

537	27	60.0	540	6	US-10-641-678-44	Sequence 44, Appl	610	25.5	56.7	207	6	US-10-467-657-4678	Sequence 4678, Ap
538	27	60.0	548	7	US-11-137-465-47	Sequence 47, Appl	611	25.5	56.7	252	7	US-11-186-284-209	Sequence 209, App
539	27	60.0	548	6	US-10-858-730-21	Sequence 21, Appl	612	25.5	56.7	372	6	US-10-650-326B-13	Sequence 13, Appl
540	27	60.0	898	6	US-10-624-932-2	Sequence 2, Appl1	613	25	55.6	10	7	US-11-146-854-46	Sequence 46, Appl
541	27	60.0	902	7	US-11-144-987-8	Sequence 8, Appl1	614	25	55.6	10	7	US-11-146-854-49	Sequence 49, Appl
542	27	60.0	902	7	US-11-144-987-14	Sequence 14, Appl	615	25	55.6	11	7	US-11-054-515-3099	Sequence 3099, Ap
543	27	60.0	917	7	US-11-144-987-20	Sequence 20, Appl	616	25	55.6	17	7	US-11-062-186-46	Sequence 46, Appl
544	27	60.0	917	7	US-11-144-987-26	Sequence 26, Appl	617	25	55.6	39	6	US-10-467-657-3574	Sequence 3574, Ap
545	27	60.0	1463	6	US-10-971-982-3	Sequence 3, Appl1	618	25	55.6	77	6	US-10-467-657-1660	Sequence 1660, Ap
546	26.5	58.9	51	6	US-10-986-501-212	Sequence 212, App	619	25	55.6	78	6	US-10-467-657-1782	Sequence 1782, Ap
547	26	57.8	9	7	US-11-045-024-13956	Sequence 13956, A	620	25	55.6	81	6	US-10-952-535A-24	Sequence 24, Appl
548	26	57.8	11	7	US-11-045-024-12958	Sequence 12958, A	621	25	55.6	85	6	US-10-821-234-1091	Sequence 1091, Ap
549	26	57.8	15	7	US-11-045-024-12194	Sequence 12194, A	622	25	55.6	91	6	US-10-821-234-1091	Sequence 1474, Ap
550	26	57.8	15	7	US-11-045-024-13300	Sequence 13300, A	623	25	55.6	91	6	US-10-821-234-1703	Sequence 1703, Ap
551	26	57.8	32	6	US-10-467-657-2568	Sequence 2568, Ap	624	25	55.6	101	7	US-11-191-072-14	Sequence 14, Appl
552	26	57.8	15	7	US-10-467-657-1262	Sequence 1262, Ap	625	25	55.6	102	6	US-10-816-768-83	Sequence 83, Appl
553	26	57.8	55	6	US-10-467-657-1086	Sequence 1086, Ap	626	25	55.6	102	6	US-10-816-768-84	Sequence 84, Appl
554	26	57.8	55	6	US-10-467-657-842	Sequence 842, App	627	25	55.6	102	6	US-10-816-768-85	Sequence 85, Appl
555	26	57.8	98	6	US-10-485-788A-739	Sequence 739, App	628	25	55.6	102	6	US-10-816-768-86	Sequence 86, Appl
556	26	57.8	103	6	US-11-053-076-109	Sequence 109, App	629	25	55.6	103	6	US-10-467-657-3578	Sequence 3578, Ap
557	26	57.8	103	7	US-11-053-076-109	Sequence 109, App	630	25	55.6	109	7	US-11-123-896-248	Sequence 248, App
558	26	57.8	128	7	US-11-089-551A-51	Sequence 51, Appl	631	25	55.6	118	7	US-11-090-439-3	Sequence 3, Appl1
559	26	57.8	160	6	US-10-467-657-758	Sequence 758, App	632	25	55.6	119	7	US-11-191-072-12	Sequence 12, Appl
560	26	57.8	161	6	US-10-623-155-114	Sequence 114, App	633	25	55.6	119	7	US-11-191-072-13	Sequence 13, Appl
561	26	57.8	169	7	US-11-120-318-1	Sequence 1, Appl1	634	25	55.6	120	6	US-10-793-626-2214	Sequence 2214, Ap
562	26	57.8	185	6	US-10-967-527A-10	Sequence 10, Appl	635	25	55.6	146	6	US-10-485-788A-510	Sequence 510, App
563	26	57.8	195	6	US-10-995-561-563	Sequence 563, App	636	25	55.6	151	6	US-10-667-295-220	Sequence 220, App
564	26	57.8	201	6	US-10-467-657-458	Sequence 458, App	637	25	55.6	158	6	US-10-821-234-1294	Sequence 1294, Ap
565	26	57.8	209	6	US-10-467-657-24	Sequence 24, Appl	638	25	55.6	161	6	US-10-986-501-189	Sequence 189, App
566	26	57.8	209	6	US-10-467-657-7128	Sequence 7128, App	639	25	55.6	164	6	US-10-995-561-554	Sequence 554, App
567	26	57.8	228	6	US-10-848-889-1	Sequence 1, Appl1	640	25	55.6	168	6	US-10-821-234-1426	Sequence 1426, Ap
568	26	57.8	239	6	US-10-502-972-6	Sequence 6, Appl1	641	25	55.6	181	6	US-10-467-657-6708	Sequence 6708, Ap
569	26	57.8	240	6	US-10-689-742-210	Sequence 210, App	642	25	55.6	185	7	US-11-147-047-41	Sequence 41, Appl
570	26	57.8	250	7	US-11-191-374-11	Sequence 11, Appl	643	25	55.6	188	7	US-11-000-463-866	Sequence 866, App
571	26	57.8	250	7	US-11-191-375-11	Sequence 11, Appl	644	25	55.6	193	7	US-11-000-463-867	Sequence 867, App
572	26	57.8	250	7	US-11-191-388-11	Sequence 11, Appl	645	25	55.6	193	7	US-11-085-775-4	Sequence 4, Appl1
573	26	57.8	324	7	US-11-077-386-15	Sequence 15, Appl	646	25	55.6	202	6	US-10-821-234-1298	Sequence 1298, Ap
574	26	57.8	344	7	US-11-080-991-4	Sequence 4, Appl1	647	25	55.6	214	7	US-11-067-425A-73	Sequence 73, Appl
575	26	57.8	344	7	US-11-186-284-20	Sequence 20, Appl	648	25	55.6	218	7	US-11-143-980-33	Sequence 33, Appl
576	26	57.8	344	7	US-11-077-386-16	Sequence 16, Appl	649	25	55.6	224	7	US-11-114-922-88	Sequence 88, Appl
577	26	57.8	353	6	US-10-467-657-3964	Sequence 3964, Ap	650	25	55.6	243	7	US-11-054-515-1940	Sequence 1940, Ap
578	26	57.8	368	7	US-11-000-463-916	Sequence 916, App	651	25	55.6	243	7	US-11-147-047-40	Sequence 40, Appl
579	26	57.8	370	6	US-10-821-234-1105	Sequence 1105, App	652	25	55.6	251	6	US-10-485-788A-509	Sequence 509, App
580	26	57.8	379	7	US-11-060-029-17	Sequence 17, Appl	653	25	55.6	252	6	US-11-102-240-92	Sequence 92, Appl
581	26	57.8	386	7	US-11-060-029-13	Sequence 13, Appl	654	25	55.6	253	6	US-10-995-561-555	Sequence 555, App
582	26	57.8	388	7	US-11-000-463-444	Sequence 444, App	655	25	55.6	270	6	US-10-821-234-1348	Sequence 1348, Ap
583	26	57.8	393	7	US-11-077-712-4	Sequence 4, Appl1	656	25	55.6	271	6	US-10-667-295-98	Sequence 98, Appl
584	26	57.8	425	6	US-10-821-234-990	Sequence 990, App	657	25	55.6	275	7	US-11-063-343-27	Sequence 27, Appl
585	26	57.8	448	6	US-10-967-527A-16	Sequence 16, Appl	658	25	55.6	277	6	US-10-667-295-97	Sequence 97, Appl
586	26	57.8	492	6	US-10-821-234-1108	Sequence 1108, App	659	25	55.6	284	6	US-10-972-587-1	Sequence 1, Appl1
587	26	57.8	561	6	US-10-467-657-624	Sequence 624, App	660	25	55.6	284	6	US-10-793-626-1634	Sequence 1634, Ap
588	26	57.8	638	6	US-10-995-561-1025	Sequence 1025, App	661	25	55.6	296	6	US-10-667-295-96	Sequence 96, Appl
589	26	57.8	658	6	US-10-821-234-921	Sequence 921, App	662	25	55.6	297	6	US-10-878-556A-163	Sequence 163, App
590	26	57.8	669	6	US-10-878-556A-87	Sequence 87, Appl	663	25	55.6	298	6	US-10-821-234-1240	Sequence 1240, Ap
591	26	57.8	676	7	US-11-135-855-28	Sequence 28, Appl	664	25	55.6	308	6	US-10-995-561-944	Sequence 1332, Ap
592	26	57.8	717	7	US-11-135-855-29	Sequence 29, Appl	665	25	55.6	308	6	US-10-858-730-113	Sequence 944, App
593	26	57.8	728	7	US-11-103-957-81	Sequence 81, Appl	666	25	55.6	324	6	US-10-858-730-113	Sequence 113, App
594	26	57.8	736	6	US-10-467-657-4780	Sequence 4780, Ap	667	25	55.6	346	7	US-11-186-284-189	Sequence 189, App
595	26	57.8	768	6	US-10-995-561-956	Sequence 956, App	668	25	55.6	353	7	US-11-022-289-9	Sequence 9, Appl1
596	26	57.8	770	6	US-10-821-234-1269	Sequence 1269, App	669	25	55.6	354	6	US-10-999-866-31	Sequence 31, Appl
597	26	57.8	784	7	US-11-147-109-4	Sequence 4, Appl1	670	25	55.6	354	6	US-10-061-821-31	Sequence 31, Appl
598	26	57.8	790	6	US-10-995-561-955	Sequence 955, App	671	25	55.6	356	6	US-10-821-234-870	Sequence 870, App
599	26	57.8	830	6	US-10-995-561-957	Sequence 957, App	672	25	55.6	360	6	US-10-650-326B-8	Sequence 8, Appl1
600	26	57.8	830	6	US-10-995-561-958	Sequence 958, App	673	25	55.6	360	7	US-11-069-185-7	Sequence 7, Appl1
601	26	57.8	901	7	US-11-082-389-430	Sequence 430, App	674	25	55.6	366	6	US-10-215-455A-2	Sequence 2, Appl1
602	26	57.8	1023	6	US-10-131-826A-200	Sequence 200, App	675	25	55.6	373	7	US-11-044-051-71	Sequence 71, Appl
603	26	57.8	1207	6	US-10-821-234-1109	Sequence 1109, App	676	25	55.6	373	7	US-11-044-051-105	Sequence 105, App
604	26	57.8	1313	7	US-11-091-668-4	Sequence 4, Appl1	677	25	55.6	389	7	US-11-018-018-2	Sequence 2, Appl1
605	26	57.8	1981	6	US-10-374-954-23	Sequence 23, Appl	678	25	55.6	389	7	US-11-047-757-2	Sequence 2, Appl1
606	26	57.8	1998	6	US-10-374-954-21	Sequence 21, Appl	679	25	55.6	406	6	US-10-467-657-4288	Sequence 4288, Ap
607	26	57.8	2009	6	US-10-374-954-21	Sequence 21, Appl	680	25	55.6	406	6	US-10-957-569-15	Sequence 15, Appl
608	26	57.8	3588	6	US-10-995-561-672	Sequence 672, App	681	25	55.6	406	7	US-11-107-028-7	Sequence 7, Appl1
609	26	57.8	5179	7	US-11-108-172-1068	Sequence 1068, App	682	25	55.6	410	6	US-10-995-561-969	Sequence 969, App

683	25	55.6	420	7	US-11-183-914-4	Sequence 4, Appli	756	25	55.6	1250	7	US-11-137-465-62	Sequence 62, Appl
684	25	55.6	421	6	US-10-467-657-4102	Sequence 4102, Ap	757	25	55.6	1338	6	US-10-821-234-1622	Sequence 1622, Ap
685	25	55.6	423	6	US-10-878-556A-176	Sequence 176, App	758	25	55.6	1338	6	US-11-109-156-23	Sequence 23, Appl
686	25	55.6	425	7	US-11-096-276-2	Sequence 2, Appli	759	25	55.6	1402	6	US-10-971-982-2	Sequence 2, Appli
687	25	55.6	431	7	US-11-055-823-76	Sequence 76, Appl	760	25	55.6	1450	6	US-10-485-517-152	Sequence 152, App
688	25	55.6	437	6	US-10-967-648A-2	Sequence 2, Appli	761	25	55.6	1467	6	US-10-507-956-1	Sequence 1, Appli
689	25	55.6	445	7	US-11-115-564-3	Sequence 3, Appli	762	25	55.6	1501	6	US-10-793-626-2850	Sequence 2850, Ap
690	25	55.6	447	6	US-10-884-730-379	Sequence 379, App	763	25	55.6	1510	6	US-11-055-822-72	Sequence 72, Appl
691	25	55.6	458	7	US-11-183-914-11	Sequence 11, Appl	764	25	55.6	1616	6	US-10-821-234-1497	Sequence 1497, Ap
692	25	55.6	471	6	US-10-858-730-125	Sequence 125, App	765	25	55.6	1874	6	US-10-821-234-1182	Sequence 1182, Ap
693	25	55.6	482	6	US-10-878-556A-30	Sequence 30, Appl	766	25	55.6	1889	7	US-11-102-476-46	Sequence 46, Appl
694	25	55.6	483	6	US-10-632-150-48	Sequence 48, Appl	767	25	55.6	2314	7	US-11-097-728-2	Sequence 2, Appli
695	25	55.6	483	7	US-11-073-457-48	Sequence 48, Appl	768	25	55.6	2353	7	US-11-097-728-6	Sequence 6, Appli
696	25	55.6	483	7	US-11-113-424-24	Sequence 24, Appl	769	25	55.6	2764	6	US-10-995-561-691	Sequence 691, App
697	25	55.6	483	7	US-11-073-460-48	Sequence 48, Appl	770	25	55.6	2813	6	US-10-995-561-688	Sequence 688, App
698	25	55.6	487	7	US-11-113-424-56	Sequence 56, Appl	771	25	55.6	2919	6	US-10-821-234-1133	Sequence 1133, Ap
699	25	55.6	487	7	US-11-113-424-57	Sequence 57, Appl	772	24.5	54.4	148	6	US-10-526-716-4	Sequence 4, Appli
700	25	55.6	499	6	US-10-508-263-94	Sequence 94, Appl	773	24.5	54.4	339	6	US-10-878-556A-18	Sequence 18, Appl
701	25	55.6	501	7	US-11-191-072-2	Sequence 2, Appli	774	24.5	54.4	339	6	US-10-995-561-681	Sequence 681, App
702	25	55.6	511	6	US-10-524-647-106	Sequence 106, App	775	24.5	54.4	339	6	US-10-995-561-682	Sequence 682, App
703	25	55.6	511	6	US-11-152-747-4	Sequence 4, Appli	776	24.5	54.4	339	6	US-10-995-561-684	Sequence 684, App
704	25	55.6	512	7	US-11-108-172-1093	Sequence 1093, Ap	777	24.5	54.4	339	6	US-10-995-561-685	Sequence 685, App
705	25	55.6	513	7	US-11-000-463-458	Sequence 458, App	778	24.5	54.4	339	6	US-10-995-561-686	Sequence 686, App
706	25	55.6	522	7	US-11-080-991-104	Sequence 104, App	779	24.5	54.4	339	6	US-10-995-561-687	Sequence 687, App
707	25	55.6	533	7	US-11-147-047-33	Sequence 33, Appl	780	24.5	54.4	339	6	US-11-186-284-43	Sequence 43, Appl
708	25	55.6	534	7	US-11-075-185-17	Sequence 17, Appl	781	24.5	54.4	344	6	US-10-821-234-923	Sequence 923, App
709	25	55.6	534	7	US-11-057-732-2	Sequence 2, Appli	782	24.5	54.4	897	7	US-11-137-465-35	Sequence 35, Appl
710	25	55.6	536	6	US-10-641-678-70	Sequence 70, Appl	783	24.5	54.4	1122	6	US-10-821-234-1657	Sequence 1657, Ap
711	25	55.6	543	6	US-10-821-234-1158	Sequence 1158, Ap	784	24	53.3	30	7	US-11-008-727-10	Sequence 10, Appl
712	25	55.6	549	7	US-11-210-316-30	Sequence 30, Appl	785	24	53.3	32	7	US-11-112-277-14	Sequence 14, Appl
713	25	55.6	557	7	US-11-022-289-4	Sequence 4, Appli	786	24	53.3	38	6	US-10-986-501-355	Sequence 355, App
714	25	55.6	563	7	US-11-113-224-18	Sequence 18, Appl	787	24	53.3	38	7	US-11-174-089-49	Sequence 49, Appl
715	25	55.6	564	7	US-11-022-289-10	Sequence 10, Appl	788	24	53.3	38	7	US-11-174-089-50	Sequence 50, Appl
716	25	55.6	571	6	US-10-131-826A-542	Sequence 542, App	789	24	53.3	38	7	US-11-174-089-162	Sequence 162, App
717	25	55.6	580	6	US-10-995-561-987	Sequence 987, App	790	24	53.3	38	7	US-11-174-089-163	Sequence 163, App
718	25	55.6	586	7	US-11-073-112-18	Sequence 18, Appl	791	24	53.3	39	7	US-11-174-089-1	Sequence 1, Appli
719	25	55.6	595	7	US-11-182-946-9	Sequence 9, Appli	792	24	53.3	39	7	US-11-174-089-2	Sequence 2, Appli
720	25	55.6	601	7	US-11-103-957-3	Sequence 3, Appli	793	24	53.3	39	7	US-11-174-089-6	Sequence 6, Appli
721	25	55.6	604	6	US-10-995-561-839	Sequence 839, App	794	24	53.3	39	7	US-11-174-089-182	Sequence 182, App
722	25	55.6	618	6	US-10-821-234-1481	Sequence 1481, Ap	795	24	53.3	39	7	US-11-174-089-183	Sequence 183, App
723	25	55.6	627	7	US-11-037-829A-1	Sequence 1, Appli	796	24	53.3	39	7	US-11-174-089-211	Sequence 211, App
724	25	55.6	628	6	US-10-995-561-1002	Sequence 1002, Ap	797	24	53.3	39	7	US-11-174-089-212	Sequence 212, App
725	25	55.6	645	6	US-10-793-626-2984	Sequence 2984, Ap	798	24	53.3	39	7	US-11-174-089-213	Sequence 213, App
726	25	55.6	654	6	US-10-510-947-6	Sequence 6, Appli	799	24	53.3	39	7	US-11-174-089-214	Sequence 214, App
727	25	55.6	655	7	US-11-094-586-10	Sequence 10, Appl	800	24	53.3	39	7	US-11-174-089-215	Sequence 215, App
728	25	55.6	667	7	US-10-821-234-1477	Sequence 1477, Ap	801	24	53.3	39	7	US-11-174-089-216	Sequence 216, App
729	25	55.6	672	7	US-11-000-463-455	Sequence 455, App	802	24	53.3	39	7	US-11-174-089-217	Sequence 217, App
730	25	55.6	680	6	US-10-467-657-2008	Sequence 2008, Ap	803	24	53.3	39	7	US-11-174-089-218	Sequence 218, App
731	25	55.6	682	7	US-11-039-756-2	Sequence 2, Appli	804	24	53.3	39	7	US-11-174-089-219	Sequence 219, App
732	25	55.6	714	7	US-11-121-419-2	Sequence 2, Appli	805	24	53.3	39	7	US-11-174-089-220	Sequence 220, App
733	25	55.6	733	7	US-11-012-762-68	Sequence 68, Appl	806	24	53.3	39	7	US-11-174-089-221	Sequence 221, App
734	25	55.6	747	6	US-10-131-826A-212	Sequence 212, App	807	24	53.3	39	7	US-11-174-089-222	Sequence 222, App
735	25	55.6	747	6	US-10-995-561-840	Sequence 840, App	808	24	53.3	39	7	US-11-174-089-223	Sequence 223, App
736	25	55.6	771	7	US-11-147-047-34	Sequence 34, Appl	809	24	53.3	39	7	US-11-174-089-224	Sequence 224, App
737	25	55.6	773	6	US-10-821-234-1134	Sequence 1134, Ap	810	24	53.3	39	7	US-11-174-089-225	Sequence 225, App
738	25	55.6	879	6	US-10-770-726-78	Sequence 78, Appl	811	24	53.3	39	7	US-11-174-089-226	Sequence 226, App
739	25	55.6	884	6	US-10-995-561-786	Sequence 786, App	812	24	53.3	39	7	US-11-174-089-227	Sequence 227, App
740	25	55.6	888	6	US-10-131-826A-544	Sequence 544, App	813	24	53.3	39	7	US-11-174-089-228	Sequence 228, App
741	25	55.6	915	6	US-10-821-234-1514	Sequence 1514, Ap	814	24	53.3	39	7	US-11-174-089-229	Sequence 229, App
742	25	55.6	915	6	US-10-995-561-1003	Sequence 1003, Ap	815	24	53.3	39	7	US-11-174-089-230	Sequence 230, App
743	25	55.6	917	6	US-10-995-561-1000	Sequence 1000, Ap	816	24	53.3	39	7	US-11-174-089-231	Sequence 231, App
744	25	55.6	940	6	US-10-995-561-1004	Sequence 1004, Ap	817	24	53.3	39	7	US-11-174-089-232	Sequence 232, App
745	25	55.6	968	7	US-11-000-463-281	Sequence 281, App	818	24	53.3	39	7	US-11-174-089-233	Sequence 233, App
746	25	55.6	969	6	US-10-995-561-1001	Sequence 1001, Ap	819	24	53.3	39	7	US-11-174-089-234	Sequence 234, App
747	25	55.6	970	6	US-10-770-726-86	Sequence 86, Appl	820	24	53.3	39	7	US-11-174-089-235	Sequence 235, App
748	25	55.6	971	6	US-10-995-561-998	Sequence 998, App	821	24	53.3	39	7	US-11-174-089-236	Sequence 236, App
749	25	55.6	994	6	US-10-995-561-997	Sequence 997, App	822	24	53.3	39	7	US-11-174-089-237	Sequence 237, App
750	25	55.6	1016	7	US-11-103-957-41	Sequence 41, Appl	823	24	53.3	39	7	US-11-174-089-238	Sequence 238, App
751	25	55.6	1023	6	US-10-995-561-968	Sequence 968, App	824	24	53.3	39	7	US-11-174-089-239	Sequence 239, App
752	25	55.6	1029	6	US-10-821-234-908	Sequence 908, App	825	24	53.3	39	7	US-11-174-089-240	Sequence 240, App
753	25	55.6	1043	6	US-10-392-234A-34	Sequence 34, Appl	826	24	53.3	40	7	US-11-112-277-13	Sequence 13, Appl
754	25	55.6	1087	7	US-11-117-169-10	Sequence 10, Appl	827	24	53.3	40	7	US-11-112-277-25	Sequence 25, Appl
755	25	55.6	1119	6	US-10-131-826A-352	Sequence 352, App	828	24	53.3	48	6	US-10-467-657-3796	Sequence 3796, Ap

829	24	53.3	51	7	US-11-000-463-443	Sequence 443, App	902	24	53.3	466	7	US-11-110-082-33	Sequence 33, Appl
830	24	53.3	56	6	US-10-467-657-4714	Sequence 4714, App	903	24	53.3	482	6	US-10-821-234-972	Sequence 972, App
831	24	53.3	56	6	US-10-467-657-4718	Sequence 7218, App	904	24	53.3	497	7	US-10-793-628-1624	Sequence 1624, App
832	24	53.3	61	6	US-10-986-501-147	Sequence 147, App	905	24	53.3	531	7	US-11-008-727-18	Sequence 18, Appl
833	24	53.3	80	6	US-10-467-657-3504	Sequence 3504, App	906	24	53.3	574	7	US-11-102-240-164	Sequence 164, Appl
834	24	53.3	100	6	US-10-821-234-1135	Sequence 1135, App	907	24	53.3	581	7	US-11-067-231-153	Sequence 153, App
835	24	53.3	102	6	US-10-793-626-2616	Sequence 2616, App	908	24	53.3	592	6	US-10-467-962B-95	Sequence 95, Appl
836	24	53.3	114	6	US-10-467-657-8436	Sequence 8436, App	909	24	53.3	592	6	US-10-524-647-112	Sequence 112, App
837	24	53.3	126	7	US-11-113-424-184	Sequence 184, App	910	24	53.3	629	6	US-10-821-234-1528	Sequence 1528, App
838	24	53.3	140	6	US-10-967-093-6	Sequence 6, Appl	911	24	53.3	631	6	US-10-995-561-546	Sequence 546, App
839	24	53.3	142	7	US-11-186-284-105	Sequence 105, App	912	24	53.3	644	6	US-10-509-121-2	Sequence 2, Appl
840	24	53.3	145	6	US-11-058-542-2	Sequence 2, Appl	913	24	53.3	644	6	US-10-509-121-4	Sequence 4, Appl
841	24	53.3	148	6	US-10-467-657-5478	Sequence 5478, App	914	24	53.3	644	6	US-10-509-121-6	Sequence 6, Appl
842	24	53.3	152	7	US/11/020	Sequence 31, Appl	915	24	53.3	644	6	US-10-509-121-8	Sequence 8, Appl
843	24	53.3	165	6	US-10-821-234-1539	Sequence 1539, App	916	24	53.3	644	6	US-10-509-121-39	Sequence 39, Appl
844	24	53.3	168	7	US-11-000-463-824	Sequence 824, App	917	24	53.3	651	6	US-10-821-234-1666	Sequence 1666, App
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846	24	53.3	182	6	US-10-467-657-194	Sequence 194, App	919	24	53.3	654	6	US-10-770-726-82	Sequence 82, Appl
847	24	53.3	182	6	US-10-467-657-4708	Sequence 4708, App	920	24	53.3	660	6	US-10-131-826A-350	Sequence 350, App
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849	24	53.3	186	7	US-11-080-248-2	Sequence 2, Appl	922	24	53.3	715	6	US-10-131-826A-116	Sequence 116, App
850	24	53.3	187	6	US-10-821-234-1361	Sequence 1361, App	923	24	53.3	724	7	US-11-109-156-19	Sequence 19, Appl
851	24	53.3	189	6	US-10-878-556A-168	Sequence 168, App	924	24	53.3	732	7	US-11-078-189-14	Sequence 14, Appl
852	24	53.3	194	6	US-10-995-561-548	Sequence 548, App	925	24	53.3	736	7	US-11-078-189-11	Sequence 11, Appl
853	24	53.3	210	7	US-11-038-284-24	Sequence 24, Appl	926	24	53.3	751	7	US-11-114-906-8	Sequence 8, Appl
854	24	53.3	221	7	US-11-113-424-4	Sequence 4, Appl	927	24	53.3	764	7	US-11-114-906-6	Sequence 6, Appl
855	24	53.3	229	7	US-11-063-343-34	Sequence 34, Appl	928	24	53.3	777	6	US-10-821-234-1658	Sequence 1658, App
856	24	53.3	241	6	US-10-878-556A-35	Sequence 35, Appl	929	24	53.3	778	6	US-10-467-962B-18	Sequence 18, Appl
857	24	53.3	249	6	US-10-467-657-1580	Sequence 1580, App	930	24	53.3	795	6	US-10-821-234-1002	Sequence 1002, App
858	24	53.3	249	6	US-10-131-826A-110	Sequence 110, App	931	24	53.3	795	6	US-10-770-726-49	Sequence 49, Appl
859	24	53.3	288	6	US-10-878-556A-195	Sequence 195, App	932	24	53.3	814	6	US-10-878-556A-161	Sequence 161, App
860	24	53.3	258	7	US-11-038-284-23	Sequence 23, Appl	933	24	53.3	826	6	US-10-793-626-1066	Sequence 1066, App
861	24	53.3	262	7	US-11-183-914-2	Sequence 2, Appl	934	24	53.3	828	6	US-10-467-962B-99	Sequence 99, Appl
862	24	53.3	270	7	US-11-008-727-24	Sequence 24, Appl	935	24	53.3	838	7	US-11-114-906-40	Sequence 40, Appl
863	24	53.3	277	6	US-10-467-657-5130	Sequence 5130, App	936	24	53.3	839	7	US-11-076-431-2	Sequence 2, Appl
864	24	53.3	286	7	US-11-113-424-43	Sequence 43, Appl	937	24	53.3	839	7	US-11-076-431-4	Sequence 4, Appl
865	24	53.3	286	7	US-11-137-465-48	Sequence 48, Appl	938	24	53.3	839	7	US-11-076-431-6	Sequence 6, Appl
866	24	53.3	305	6	US-10-131-826A-264	Sequence 264, App	939	24	53.3	839	7	US-11-076-431-8	Sequence 8, Appl
867	24	53.3	305	6	US-10-821-234-1518	Sequence 1518, App	940	24	53.3	851	7	US-11-114-906-38	Sequence 38, Appl
868	24	53.3	308	6	US-10-967-527A-30	Sequence 30, Appl	941	24	53.3	858	6	US-10-878-556A-36	Sequence 36, Appl
869	24	53.3	312	6	US-10-723-207-2	Sequence 2, Appl	942	24	53.3	864	7	US-11-114-906-4	Sequence 4, Appl
870	24	53.3	318	6	US-10-821-234-1117	Sequence 1117, App	943	24	53.3	870	7	US-11-114-906-2	Sequence 2, Appl
871	24	53.3	318	7	US-11-109-156-15	Sequence 15, Appl	944	24	53.3	897	6	US-10-336-263A-58	Sequence 58, Appl
872	24	53.3	318	7	US-11-111-239-2	Sequence 2, Appl	945	24	53.3	951	6	US-11-114-906-36	Sequence 36, Appl
873	24	53.3	322	7	US-11-102-240-6	Sequence 6, Appl	946	24	53.3	954	6	US-10-467-962B-31	Sequence 31, Appl
874	24	53.3	323	6	US-10-821-234-981	Sequence 981, App	947	24	53.3	957	7	US-11-114-906-34	Sequence 34, Appl
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877	24	53.3	328	7	US-11-055-822-556	Sequence 556, App	950	24	53.3	1138	6	US-10-509-422-4	Sequence 4, Appl
878	24	53.3	337	6	US-10-821-234-1004	Sequence 1004, App	951	24	53.3	1161	7	US-11-075-646-8	Sequence 8, Appl
879	24	53.3	338	6	US-10-632-150-12	Sequence 12, App	952	24	53.3	1168	6	US-10-509-422-2	Sequence 2, Appl
880	24	53.3	338	7	US-11-073-457-12	Sequence 12, Appl	953	24	53.3	1189	6	US-10-821-234-1209	Sequence 1209, App
881	24	53.3	338	7	US-11-073-460-12	Sequence 12, Appl	954	24	53.3	1199	6	US-10-821-234-1126	Sequence 1126, App
882	24	53.3	358	6	US-10-821-234-878	Sequence 878, App	955	24	53.3	1302	7	US-11-004-057-6	Sequence 6, Appl
883	24	53.3	361	7	US-11-186-284-173	Sequence 173, App	956	24	53.3	1375	6	US-10-995-561-809	Sequence 809, App
884	24	53.3	383	6	US-10-392-234A-6	Sequence 6, Appl	957	24	53.3	1408	6	US-10-821-234-1045	Sequence 1045, App
885	24	53.3	389	7	US-11-108-528-70	Sequence 70, Appl	958	24	53.3	1458	7	US-11-096-274-2	Sequence 2, Appl
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887	24	53.3	390	7	US-11-105-864-2	Sequence 2, Appl	960	24	53.3	1538	6	US-10-995-561-772	Sequence 772, App
888	24	53.3	397	7	US-11-060-008-8	Sequence 8, Appl	961	24	53.3	1637	6	US-10-821-234-1204	Sequence 1204, App
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893	24	53.3	421	6	US-10-858-730-1	Sequence 1, Appl	966	24	53.3	2721	7	US-11-096-051-10	Sequence 10, Appl
894	24	53.3	422	6	US-10-821-234-1313	Sequence 1313, App	967	24	53.3	2725	7	US-11-096-051-8	Sequence 8, Appl
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897	24	53.3	449	6	US-10-131-826A-224	Sequence 224, App	970	24	53.3	5415	6	US-10-995-561-779	Sequence 779, App
898	24	53.3	452	6	US-10-995-561-817	Sequence 817, App	971	24	53.3	5464	6	US-10-995-561-775	Sequence 775, App
899	24	53.3	462	7	US-11-105-864-8	Sequence 8, Appl	972	24	53.3	5935	6	US-10-995-561-776	Sequence 776, App
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975 23.5 52.2 437 6 US-10-454-437-84 Sequence 84, Appl  
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993 23 51.1 9 7 US-11-045-024-13716 Sequence 13716, A  
994 23 51.1 9 7 US-11-045-024-13719 Sequence 13719, A  
995 23 51.1 10 7 US-11-045-024-1320 Sequence 1320, Ap  
996 23 51.1 10 7 US-11-045-024-3034 Sequence 3034, Ap  
997 23 51.1 10 7 US-11-045-024-5225 Sequence 5225, Ap  
998 23 51.1 10 7 US-11-045-024-6270 Sequence 6270, Ap  
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1000 23 51.1 10 7 US-11-045-024-7278 Sequence 7278, Ap

## ALIGNMENTS

RESULT 1  
US-11-022-289-12  
; Sequence 12, Application US/11022289  
; Publication No. US20050249723A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazar, Gregory Alan  
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES  
; FILE REFERENCE: 185831/US/2  
; CURRENT APPLICATION NUMBER: US/11/022,289  
; CURRENT FILING DATE: 2004-12-21  
; PRIOR APPLICATION NUMBER: US 60/531,752  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 12  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-022-289-12

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Best Local Similarity 100.0%; Pred. No. 24;  
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QY 3 PPPPC 7  
Db 1 PPPPC 5

RESULT 2  
US-10-467-657-3742  
; Sequence 3742, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 3742  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-3742

Query Match 82.2%; Score 37; DB 6; Length 240;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
Db 101 PPPPC 105

RESULT 3  
US-10-999-866-32  
; Sequence 32, Application US/10999866  
; Publication No. US20050266004A1  
; GENERAL INFORMATION:  
; APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann  
; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AND  
; FILE REFERENCE: CEN5042NP  
; CURRENT APPLICATION NUMBER: US/10/999,866  
; CURRENT FILING DATE: 2004-11-30  
; PRIOR APPLICATION NUMBER: 60/527,794  
; PRIOR FILING DATE: 2003-12-08  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 32  
; LENGTH: 340  
; TYPE: PRT  
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; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(102)  
; OTHER INFORMATION: CHI  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (103)..(108)  
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; LOCATION: (109)..(209)  
; OTHER INFORMATION: CH2  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (210)..(340)  
; OTHER INFORMATION: CH3  
US-10-999-866-32

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Best Local Similarity 100.0%; Pred. No. 31;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
Db 105 PPPPC 109

RESULT 4  
US-11-061-821-32  
; Sequence 32, Application US/11061821  
; Publication No. US20050266005A1

GENERAL INFORMATION:  
APPLICANT: Heavmet, George; Li, Li; O'Neill, Karyn  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING IL-13 RELATED PATHOLOGIES  
FILE REFERENCE: CEN5048 NP  
CURRENT APPLICATION NUMBER: US/11/061,821  
CURRENT FILING DATE: 2005-02-18  
PRIOR APPLICATION NUMBER: 60/548,648  
PRIOR FILING DATE: 2004-02-27  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver 3.3  
SEQ ID NO 32  
LENGTH: 340  
TYPE: PRT  
ORGANISM: Homo sapiens  
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NAME/KEY: MISC FEATURE  
LOCATION: (1)..(340)  
OTHER INFORMATION: IgA2 heavy chain constant region  
FEATURE:  
NAME/KEY: MISC FEATURE  
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NAME/KEY: MISC FEATURE  
LOCATION: (103)..(108)  
OTHER INFORMATION: hinge  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (109)..(209)  
OTHER INFORMATION: CH2  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (210)..(340)  
OTHER INFORMATION: CH3

US-11-061-821-32

Query Match 82.2%; Score 37; DB 7; Length 340;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
Db 105 PPPPC 109

## RESULT 5

US-10-467-657-7238  
Sequence 7238, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SpA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MORACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 7238  
LENGTH: 522  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-7238

Query Match 82.2%; Score 37; DB 6; Length 522;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
Db 473 PPPPC 477

## RESULT 6

US-11-155-492-3  
Sequence 3, Application US/11155492  
Publication No. US20050266479A1  
GENERAL INFORMATION:  
APPLICANT: Weissenbach, Jean  
APPLICANT: Hazan, Jamil  
TITLE OF INVENTION: CLONING, EXPRESSION AND CHARACTERIZATION OF THE SPG4  
TITLE OF INVENTION: GENE RESPONSIBLE FOR THE MOST COMMON FORM OF AUTOSOMAL  
TITLE OF INVENTION: DOMINANT SPASTIC PARAPLEGIA  
FILE REFERENCE: R-341894  
CURRENT APPLICATION NUMBER: US/11/155,492  
CURRENT FILING DATE: 2005-06-20  
PRIOR APPLICATION NUMBER: US/09/830,902  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: FR 99 11097  
PRIOR FILING DATE: 1999-09-03  
PRIOR APPLICATION NUMBER: PCT/FR00/02433  
PRIOR FILING DATE: 2000-09-04  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: PatentIn Vers. 2.0  
SEQ ID NO 3  
LENGTH: 616  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-155-492-3

Query Match 82.2%; Score 37; DB 7; Length 616;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
Db 24 PPPPC 28

## RESULT 7

US-10-995-561-528  
Sequence 528, Application US/10995561  
Publication No. US20050272054A1  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
TITLE OF INVENTION: DETECTION AND USES THEREOF  
FILE REFERENCE: CL001559  
CURRENT APPLICATION NUMBER: US/10/995,561  
CURRENT FILING DATE: 2004-11-24  
NUMBER OF SEQ ID NOS: 85702  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 528  
LENGTH: 670  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-995-561-528

Query Match 82.2%; Score 37; DB 6; Length 670;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
Db 463 PPPPC 467

## RESULT 8

US-10-995-561-671  
Sequence 671, Application US/10995561

```
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 671
; LENGTH: 4346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-671

Query Match      82.2%; Score 37; DB 6; Length 4346;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPPC 7
DB      276 PPPPC 280

RESULT 9
US-10-995-561-670
; Sequence 670, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 670
; LENGTH: 4347
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-670

Query Match      82.2%; Score 37; DB 6; Length 4347;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPPC 7
DB      276 PPPPC 280

RESULT 10
US-10-821-234-1155
; Sequence 1155, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821a
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1155
```

```
; LENGTH: 4419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1155

Query Match      82.2%; Score 37; DB 6; Length 4419;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPPC 7
DB      347 PPPPC 351

RESULT 11
US-11-013-247A-10
; Sequence 10, Application US/11013247A
; Publication No. US20050255496A1
; GENERAL INFORMATION:
; APPLICANT: GAO, ZEREN
; APPLICANT: SHEPPARD, PAUL O.
; APPLICANT: FOX, BRIAN A.
; APPLICANT: HOLLOWAY, JAMES L.
; APPLICANT: JASPERS, STEPHEN R.
; TITLE OF INVENTION: Zcnf12, A TUMOR NECROSIS FACTOR
; FILE REFERENCE: 03-23
; CURRENT APPLICATION NUMBER: US/11/013,247A
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 60/530,125
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-013-247A-10

Query Match      80.0%; Score 36; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSPPPP 6
DB      115 SSPPPP 120

RESULT 12
US-11-013-247A-7
; Sequence 7, Application US/11013247A
; Publication No. US20050255496A1
; GENERAL INFORMATION:
; APPLICANT: GAO, ZEREN
; APPLICANT: SHEPPARD, PAUL O.
; APPLICANT: FOX, BRIAN A.
; APPLICANT: HOLLOWAY, JAMES L.
; APPLICANT: JASPERS, STEPHEN R.
; TITLE OF INVENTION: Zcnf12, A TUMOR NECROSIS FACTOR
; FILE REFERENCE: 03-23
; CURRENT APPLICATION NUMBER: US/11/013,247A
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 60/530,125
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-013-247A-7

Query Match      80.0%; Score 36; DB 7; Length 362;
Best Local Similarity 100.0%; Pred. No. 45;
```

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPP 6  
 Db 139 SSPPPP 144

## RESULT 13

US-11-013-247A-6  
 ; Sequence 6, Application US/11013247A  
 ; Publication No. US20050255496A1

; GENERAL INFORMATION:  
 ; APPLICANT: GAO, ZEREN  
 ; APPLICANT: SHEPPARD, PAUL O.  
 ; APPLICANT: FOX, BRIAN A.  
 ; APPLICANT: HOLLOWAY, JAMES L.  
 ; APPLICANT: JASPERS, STEPHEN R.  
 ; TITLE OF INVENTION: Ztnf12, A TUMOR NECROSIS FACTOR

; FILE REFERENCE: 03-23  
 ; CURRENT APPLICATION NUMBER: US/11/013,247A  
 ; PRIOR FILING DATE: 2004-12-15

; PRIOR APPLICATION NUMBER: 60/530,125  
 ; PRIOR FILING DATE: 2003-12-16

; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6  
 ; LENGTH: 364

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-013-247A-6

Query Match 80.0%; Score 36; DB 7; Length 364;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPP 6  
 Db 141 SSPPPP 146

## RESULT 14

US-11-013-247A-5

; Sequence 5, Application US/11013247A  
 ; Publication No. US20050255496A1

; GENERAL INFORMATION:  
 ; APPLICANT: GAO, ZEREN

; APPLICANT: SHEPPARD, PAUL O.  
 ; APPLICANT: FOX, BRIAN A.

; APPLICANT: HOLLOWAY, JAMES L.  
 ; APPLICANT: JASPERS, STEPHEN R.

; TITLE OF INVENTION: Ztnf12, A TUMOR NECROSIS FACTOR

; FILE REFERENCE: 03-23

; CURRENT APPLICATION NUMBER: US/11/013,247A  
 ; PRIOR FILING DATE: 2004-12-15

; PRIOR APPLICATION NUMBER: 60/530,125  
 ; PRIOR FILING DATE: 2003-12-16

; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-013-247A-5

Query Match 80.0%; Score 36; DB 7; Length 448;

Best Local Similarity 100.0%; Pred. No. 52;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPP 6  
 Db 225 SSPPPP 230

## RESULT 17

US-11-013-247A-17

; Sequence 17, Application US/11013247A  
 ; Publication No. US20050255496A1

; GENERAL INFORMATION:  
 ; APPLICANT: GAO, ZEREN

; APPLICANT: SHEPPARD, PAUL O.

## RESULT 15

US-11-013-247A-2

; Sequence 2, Application US/11013247A  
 ; Publication No. US20050255496A1

; GENERAL INFORMATION:  
 ; APPLICANT: GAO, ZEREN

; APPLICANT: SHEPPARD, PAUL O.  
 ; APPLICANT: FOX, BRIAN A.

; APPLICANT: HOLLOWAY, JAMES L.  
 ; APPLICANT: JASPERS, STEPHEN R.

; TITLE OF INVENTION: Ztnf12, A TUMOR NECROSIS FACTOR

; FILE REFERENCE: 03-23

; CURRENT APPLICATION NUMBER: US/11/013,247A  
 ; PRIOR FILING DATE: 2004-12-15

; PRIOR APPLICATION NUMBER: 60/530,125  
 ; PRIOR FILING DATE: 2003-12-16

; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 501

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-013-247A-2

Query Match 80.0%; Score 36; DB 7; Length 501;

Best Local Similarity 100.0%; Pred. No. 57;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPP 6  
 Db 278 SSPPPP 283

## RESULT 16

US-11-013-247A-4

; Sequence 4, Application US/11013247A  
 ; Publication No. US20050255496A1

; GENERAL INFORMATION:  
 ; APPLICANT: GAO, ZEREN

; APPLICANT: SHEPPARD, PAUL O.  
 ; APPLICANT: FOX, BRIAN A.

; APPLICANT: HOLLOWAY, JAMES L.  
 ; APPLICANT: JASPERS, STEPHEN R.

; TITLE OF INVENTION: Ztnf12, A TUMOR NECROSIS FACTOR

; FILE REFERENCE: 03-23

; CURRENT APPLICATION NUMBER: US/11/013,247A  
 ; PRIOR FILING DATE: 2004-12-15

; PRIOR APPLICATION NUMBER: 60/530,125  
 ; PRIOR FILING DATE: 2003-12-16

; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 503

; TYPE: PRT

; ORGANISM: Mus musculus

US-11-013-247A-4

Query Match 80.0%; Score 36; DB 7; Length 503;

Best Local Similarity 100.0%; Pred. No. 57;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPP 6  
 Db 281 SSPPPP 286

```
; APPLICANT: FOX, BRIAN A.
; APPLICANT: HOLLOWAY, JAMES L.
; APPLICANT: JASPERS, STEPHEN R.
; TITLE OF INVENTION: Ztnf12, A TUMOR NECROSIS FACTOR
; FILE REFERENCE: 03-23
; CURRENT APPLICATION NUMBER: US/11/013,247A
; PRIOR FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 60/530,125
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-013-247A-17

Query Match      80.0%; Score 36; DB 7; Length 529;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPPPPP 6
Db      306 SPPPPP 311

RESULT 18
US-11-013-247A-35
; Sequence 35, Application US/11013247A
; Publication No. US20050255496A1
; GENERAL INFORMATION:
; APPLICANT: GAO, ZEREN
; APPLICANT: SHEPPARD, PAUL O.
; APPLICANT: FOX, BRIAN A.
; APPLICANT: HOLLOWAY, JAMES L.
; APPLICANT: JASPERS, STEPHEN R.
; TITLE OF INVENTION: Ztnf12, A TUMOR NECROSIS FACTOR
; FILE REFERENCE: 03-23
; CURRENT APPLICATION NUMBER: US/11/013,247A
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 60/530,125
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 763
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polypeptide sequence of the MBP-ztnf12 fusion
US-11-013-247A-35

Query Match      80.0%; Score 36; DB 7; Length 763;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPPPPP 6
Db      536 SPPPPP 541

RESULT 19
US-10-995-561-792
; Sequence 792, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
```

```
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 792
; LENGTH: 868
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-792

Query Match      80.0%; Score 36; DB 6; Length 868;
Best Local Similarity 85.7%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SPPPPP 7
Db      408 SPPPPRC 414

RESULT 20
US-11-116-939-6
; Sequence 6, Application US/11116939
; Publication No. US20050265995A1
; GENERAL INFORMATION:
; APPLICANT: Stephen Tomlinson
; APPLICANT: Richard J. Quigg
; TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
; FILE REFERENCE: 19113.0115U2
; CURRENT APPLICATION NUMBER: US/11/116,939
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 60/565,907
; PRIOR FILING DATE: 2004-04-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2048
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
; OTHER INFORMATION: construct
US-11-116-939-6

Query Match      80.0%; Score 36; DB 7; Length 2048;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SPPPPP 7
Db      1588 SPPPPRC 1594

RESULT 21
US-11-014-629-1
; Sequence 1, Application US/11014629
; Publication No. US20050244376A1
; GENERAL INFORMATION:
; APPLICANT: Hall, Frederick L.
; APPLICANT: Gordon, Erlinda M.
; TITLE OF INVENTION: TARGETED GENE DELIVERY TO EXTRACELLULAR MATRIX
; FILE REFERENCE: 30863-704.302
; CURRENT APPLICATION NUMBER: US/11/014,629
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: US 08/837,223
; PRIOR FILING DATE: 1997-04-10
; PRIOR APPLICATION NUMBER: US 09/904,923
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 229
; TYPE: PRT
; ORGANISM: moloney murine leukemia virus
US-11-014-629-1
```

```
Query Match          75.6%; Score 34.5; DB 7; Length 229;
Best Local Similarity 87.5%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 SSPPPPC 7
DB      65 SSPPGPPC 72

RESULT 22
US-11-054-515-3231
; Sequence 3231, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3231
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-054-515-3231

Query Match          75.6%; Score 34; DB 7; Length 290;
Best Local Similarity 71.4%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 SSPPPPC 7
DB      141 SAPPAPC 147

RESULT 23
US-11-065-669-2
; Sequence 2, Application US/11065669
; Publication No. US2005024411A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Kalled, Susan
; TITLE OF INVENTION: BAPF, INHIBITORS THEREOF AND THEIR USE IN THE
; TITLE OF INVENTION: MODULATION OF B-CELL RESPONSE
; FILE REFERENCE: 08201.0024-04000
; CURRENT APPLICATION NUMBER: US/11/065,669
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 10/045,574
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/911,777
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/143,228

Query Match          75.6%; Score 34.5; DB 7; Length 229;
Best Local Similarity 87.5%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 SSPPPPC 7
DB      65 SSPPGPPC 72

RESULT 22
US-11-054-515-3231
; Sequence 3231, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3231
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-054-515-3231

Query Match          75.6%; Score 34; DB 7; Length 309;
Best Local Similarity 71.4%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 SSPPPPC 7
DB      141 SAPPAPC 147

RESULT 24
US-11-054-515-3230
; Sequence 3230, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3230
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-054-515-3230

Query Match          75.6%; Score 34; DB 7; Length 309;
Best Local Similarity 71.4%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 SSPPPPC 7
DB      141 SAPPAPC 147

RESULT 25
US-10-509-422-5
; Sequence 5, Application US/10509422
; Publication No. US20050244825A1
```

; GENERAL INFORMATION:					
; APPLICANT: Liou, Simon					
; TITLE OF INVENTION: Human BMP2 Inducible Kinases					
; FILE REFERENCE: 004974.01015					
; CURRENT APPLICATION NUMBER: US/10/509,422					
; CURRENT FILING DATE: 2004-09-24					
; PRIOR APPLICATION NUMBER: PCT/EP03/080825					
; PRIOR FILING DATE: 2003-03-20					
; PRIOR APPLICATION NUMBER: US 60/367,512					
; PRIOR FILING DATE: 2002-03-27					
; PRIOR APPLICATION NUMBER: US 60/406,936					
; PRIOR FILING DATE: 2002-08-30					
; NUMBER OF SEQ ID NOS: 9					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 5					
; LENGTH: 1311					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-10-509-422-5					
Query Match            75.6%; Score 34; DB 6; Length 1311;					
Best Local Similarity   71.4%; Pred. No. 2.2e+02;					
Matches     5; Conservative   1; Mismatches   1; Indels     0; Gaps     0;					
Qy	1	SSPPPPC 7	:		
Db	1001	SAPPPSC 1007	:		
RESULT 26					
US-10-131-826A-290					
; Sequence 290, Application US/10131826A					
; Publication No. US20050245730A1					
; GENERAL INFORMATION:					
; APPLICANT: Baker, Kevin P.					
; APPLICANT: Beresini, Maureen					
; APPLICANT: DeForge, Laura					
; APPLICANT: Desnoyers, Luc					
; APPLICANT: Filvaroff, Ellen					
; APPLICANT: Gao, Wei-Qiang					
; APPLICANT: Gerritsen, Mary E.					
; APPLICANT: Goddard, Audrey					
; APPLICANT: Godowski, Paul J.					
; APPLICANT: Gurney, Austin L.					
; APPLICANT: Sherwood, Steven					
; APPLICANT: Smith, Victoria					
; APPLICANT: Stewart, Timothy A.					
; APPLICANT: Tumas, Daniel					
; APPLICANT: Watanabe, Colin X					
; APPLICANT: Wood, William					
; APPLICANT: Zhang, Zemin					
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC					
; FILE REFERENCE: F330R1C128					
; CURRENT APPLICATION NUMBER: US/10/131,826A					
; CURRENT FILING DATE: 2002-04-24					
; PRIOR APPLICATION NUMBER: 60/049911					
; PRIOR FILING DATE: 1997-06-18					
; PRIOR APPLICATION NUMBER: 60/056974					
; PRIOR FILING DATE: 1997-08-26					
; PRIOR APPLICATION NUMBER: 60/059113					
; PRIOR FILING DATE: 1997-09-17					
; PRIOR APPLICATION NUMBER: 60/059115					
; PRIOR FILING DATE: 1997-09-17					
; PRIOR APPLICATION NUMBER: 60/059117					
; PRIOR FILING DATE: 1997-09-17					
; PRIOR APPLICATION NUMBER: 60/059122					
; PRIOR FILING DATE: 1997-09-17					
; PRIOR APPLICATION NUMBER: 60/059184					
; PRIOR FILING DATE: 1997-09-17					
; PRIOR APPLICATION NUMBER: 60/059263					
; PRIOR FILING DATE: 1997-09-18					
; PRIOR APPLICATION NUMBER: 60/059352					

; PRIOR FILING DATE: 1997-09-19					
; PRIOR APPLICATION NUMBER: 60/059588					
; PRIOR FILING DATE: 1997-09-19					
; Remaining Prior Application data removed - See File Wrapper or PALM.					
; NUMBER OF SEQ ID NOS: 550					
; SEQ ID NO 290					
; LENGTH: 420					
; TYPE: PRT					
; ORGANISM: Homo Sapien					
US-10-131-826A-290					
Query Match            74.4%; Score 33.5; DB 6; Length 420;					
Best Local Similarity   70.0%; Pred. No. 1.1e+02;					
Matches     7; Conservative   0; Mismatches   0; Indels     3; Gaps     1;					
Qy	1	SSPPP---PC 7	:		
Db	37	SSPFPQPHPHC 46	:		
RESULT 27					
US-10-821-234-1225					
; Sequence 1225, Application US/10821234					
; Publication No. US20050255114A1					
; GENERAL INFORMATION:					
; APPLICANT: Labat, Ivan					
; APPLICANT: Stache-Crain, Birgit					
; APPLICANT: Andarmani, Susan					
; APPLICANT: Tang, Y. Tom					
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia					
; FILE REFERENCE: 821A					
; CURRENT APPLICATION NUMBER: US/10/821,234					
; CURRENT FILING DATE: 2004-04-07					
; PRIOR APPLICATION NUMBER: US 60/462,047					
; PRIOR FILING DATE: 2003-04-07					
; NUMBER OF SEQ ID NOS: 1704					
; SOFTWARE: pt_seq_genes version 1.0					
; SEQ ID NO 1225					
; LENGTH: 146					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-10-821-234-1225					
Query Match            73.3%; Score 33; DB 6; Length 146;					
Best Local Similarity   71.4%; Pred. No. 57;					
Matches     5; Conservative   0; Mismatches   2; Indels     0; Gaps     0;					
Qy	1	SSPPPPPC 7	:		
Db	37	SGPPEPEC 43	:		
RESULT 28					
US-11-078-735-30					
; Sequence 30, Application US/11078735					
; Publication No. US20050261477A1					
; GENERAL INFORMATION:					
; APPLICANT: CHAMPION, BRIAN ROBERT					
; APPLICANT: LENNARD, ANDREW CHRISTOPHER					
; APPLICANT: MCKENZIE, GRAHAM JAMES					
; APPLICANT: TUGAL, TAMARA					
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS					
; FILE REFERENCE: 674525-2019					
; CURRENT APPLICATION NUMBER: US/11/078,735					
; CURRENT FILING DATE: 2005-03-10					
; PRIOR APPLICATION NUMBER: PCT/GB03/03908					
; PRIOR FILING DATE: 2003-09-09					
; PRIOR APPLICATION NUMBER: PCT/GB03/03285					
; PRIOR FILING DATE: 2003-08-01					
; PRIOR APPLICATION NUMBER: PCT/GB03/01525					
; PRIOR FILING DATE: 2003-04-04					
; PRIOR APPLICATION NUMBER: GB 0300234.2					

; PRIOR FILING DATE: 2003-01-07  
; PRIOR APPLICATION NUMBER: PCT/GB02/05137  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: PCT/GB02/05133  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: GB 0220912.0  
; PRIOR FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: GB 0220913.8  
; PRIOR FILING DATE: 2002-09-10  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 30  
; LENGTH: 291  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: protein construct  
US-11-078-735-30

Query Match 73.3%; Score 33; DB 7; Length 291;  
Best Local Similarity 83.3%; Pred. No. 96;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SPPPPC 7  
Db 72 SPEPPC 77

## RESULT 29

US-11-179-977-17  
; Sequence 17, Application US/11179977  
; Publication No. US20050249789A1  
; GENERAL INFORMATION:  
; APPLICANT: Genencor International, Inc.  
; TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes  
; FILE REFERENCE: GC511-PCT  
; CURRENT APPLICATION NUMBER: US/11/179,977  
; CURRENT FILING DATE: 2005-07-12  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 314  
; TYPE: PRT  
; ORGANISM: Bacillus  
US-11-179-977-17

Query Match 73.3%; Score 33; DB 7; Length 314;  
Best Local Similarity 83.3%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPPPPC 6  
Db 69 STPEPP 74

## RESULT 30

US-11-078-735-33  
; Sequence 33, Application US/11078735  
; Publication No. US20050261477A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAMPION, BRIAN ROBERT  
; APPLICANT: LENNARD, ANDREW CHRISTOPHER  
; APPLICANT: MCKENZIE, GRAHAME JAMES  
; APPLICANT: TUGAL, TAMARA  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS  
; FILE REFERENCE: 674525-2019  
; CURRENT APPLICATION NUMBER: US/11/078,735  
; CURRENT FILING DATE: 2005-03-10  
; PRIOR APPLICATION NUMBER: PCT/GB03/03908  
; PRIOR FILING DATE: 2003-09-09  
; PRIOR APPLICATION NUMBER: PCT/GB03/03285

; PRIOR FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: PCT/GB03/01525  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: GB 0300234.2  
; PRIOR FILING DATE: 2003-01-07  
; PRIOR APPLICATION NUMBER: PCT/GB02/05137  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: PCT/GB02/05133  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: GB 0220912.0  
; PRIOR FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: GB 0220913.8  
; PRIOR FILING DATE: 2002-09-10  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 33  
; LENGTH: 331  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: protein construct  
US-11-078-735-33

Query Match 73.3%; Score 33; DB 7; Length 331;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SPPPPC 7  
Db 72 SPEPPC 77

## RESULT 31

US-11-078-735-51  
; Sequence 51, Application US/11078735  
; Publication No. US20050261477A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAMPION, BRIAN ROBERT  
; APPLICANT: LENNARD, ANDREW CHRISTOPHER  
; APPLICANT: MCKENZIE, GRAHAME JAMES  
; APPLICANT: TUGAL, TAMARA  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS  
; FILE REFERENCE: 674525-2019  
; CURRENT APPLICATION NUMBER: US/11/078,735  
; CURRENT FILING DATE: 2005-03-10  
; PRIOR APPLICATION NUMBER: PCT/GB03/03908  
; PRIOR FILING DATE: 2003-09-09  
; PRIOR APPLICATION NUMBER: PCT/GB03/03285  
; PRIOR FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: PCT/GB03/01525  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: GB 0300234.2  
; PRIOR FILING DATE: 2003-01-07  
; PRIOR APPLICATION NUMBER: PCT/GB02/05137  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: PCT/GB02/05133  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: GB 0220912.0  
; PRIOR FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: GB 0220913.8  
; PRIOR FILING DATE: 2002-09-10  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 51  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Di3Cys protein  
US-11-078-735-51

Query Match 73.3%; Score 33; DB 7; Length 332;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SPPPPC 7  
|||  
DB 72 SPEPPC 77

RESULT 32  
US-11-078-735-38  
; Sequence 38, Application US/11078735  
; Publication No. US20050261477A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAMPION, BRIAN ROBERT  
; APPLICANT: LENNARD, ANDREW CHRISTOPHER  
; APPLICANT: MCKENZIE, GRAHAME JAMES  
; APPLICANT: TUGAL, TAMARA  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS  
; FILE REFERENCE: 674525-2019  
; CURRENT APPLICATION NUMBER: US/11/078,735  
; CURRENT FILING DATE: 2005-03-10  
; PRIOR APPLICATION NUMBER: PCT/GB03/03908  
; PRIOR FILING DATE: 2003-09-09  
; PRIOR APPLICATION NUMBER: PCT/GB03/03285  
; PRIOR FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: PCT/GB03/01525  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: GB 030234.2  
; PRIOR FILING DATE: 2003-01-07  
; PRIOR APPLICATION NUMBER: PCT/GB02/05137  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: PCT/GB02/05133  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: GB 0220912.0  
; PRIOR FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: GB 0220913.8  
; PRIOR FILING DATE: 2002-09-10  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: Patent In Ver. 3.3  
; SEQ ID NO 38  
; LENGTH: 369  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: protein construct  
US-11-078-735-38

Query Match 73.3%; Score 33; DB 7; Length 369;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SPPPPC 7  
|||  
DB 72 SPEPPC 77

RESULT 33  
US-11-116-939-2  
; Sequence 2, Application US/11116939  
; Publication No. US20050265995A1  
; GENERAL INFORMATION:  
; APPLICANT: Stephen Tomlinson  
; APPLICANT: Richard J. Quijg  
; TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS  
; FILE REFERENCE: 19113.011502  
; CURRENT APPLICATION NUMBER: US/11/116,939  
; CURRENT FILING DATE: 2005-04-28  
; PRIOR APPLICATION NUMBER: 60/565,907  
; PRIOR FILING DATE: 2004-04-28

; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 380  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence; note=synthetic  
; OTHER INFORMATION: construct  
US-11-116-939-2

Query Match 73.3%; Score 33; DB 7; Length 380;  
Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
|||  
DB 276 SGPPPEC 282

RESULT 34  
US-10-821-234-1342  
; Sequence 1342, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pc\_seq\_genes Version 1.0  
; SEQ ID NO 1342  
; LENGTH: 381  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1342

Query Match 73.3%; Score 33; DB 6; Length 381;  
Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
|||  
DB 277 SGPPPEC 283

RESULT 35  
US-11-188-743-23  
; Sequence 23, Application US/11188743  
; Publication No. US20050272140A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicolaides, Nicholas  
; APPLICANT: Saes, Philip  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Grasso, Luigi  
; APPLICANT: Vogelstein, Bert  
; TITLE OF INVENTION: Methods for generating hypermutable  
; FILE REFERENCE: 01107,00097  
; CURRENT APPLICATION NUMBER: US/11/188,743  
; CURRENT FILING DATE: 2005-07-26  
; PRIOR APPLICATION NUMBER: US/10/641,068  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: US/09/788,657  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: 60/184,336  
; PRIOR FILING DATE: 2000-02-23

; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 23  
; LENGTH: 389,  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-188-743-23

Query Match 73.3%; Score 33; DB 7; Length 389;  
Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSPPPC 7  
|:|:|  
Db 362 STPPHC 368

RESULT 36  
US-11-116-939-9  
; Sequence 9, Application US/11116939  
; Publication No. US2005026595A1  
; GENERAL INFORMATION:  
; APPLICANT: Stephen Tomlinson  
; TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS  
; FILE REFERENCE: 19113.0115U2  
; CURRENT APPLICATION NUMBER: US/11/116,939  
; PRIOR FILING DATE: 2005-04-28  
; PRIOR APPLICATION NUMBER: 60/565,907  
; PRIOR FILING DATE: 2004-04-28  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 436,  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence; note=synthetic  
; OTHER INFORMATION: construct  
US-11-116-939-9

Query Match 73.3%; Score 33; DB 7; Length 436;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SSPPPC 7  
|:|:|  
Db 221 SGPPQC 227

RESULT 37  
US-10-632-150-8  
; Sequence 8, Application US/10632150  
; Publication No. US20050251871A1  
; GENERAL INFORMATION:  
; APPLICANT: Chisaur, D.  
; APPLICANT: Pagano, M.  
; APPLICANT: Latres, E.  
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS  
; FILE REFERENCE: 5914-081  
; CURRENT APPLICATION NUMBER: US/10/632,150  
; CURRENT FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: US/09/385,219  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: 60/098,355  
; PRIOR FILING DATE: 1998-08-28  
; PRIOR APPLICATION NUMBER: 60/118,568  
; PRIOR FILING DATE: 1999-02-03  
; PRIOR APPLICATION NUMBER: 60/124,449  
; PRIOR FILING DATE: 1999-03-15  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8

; LENGTH: 472  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-632-150-8

Query Match 73.3%; Score 33; DB 6; Length 472;  
Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPP 6  
:|:|:|  
Db 11 NSPPPP 16

RESULT 38  
US-11-073-457-8  
; Sequence 8, Application US/11073457  
; Publication No. US20050260556A1  
; GENERAL INFORMATION:  
; APPLICANT: Pagano, M.  
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF  
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS  
; FILE REFERENCE: 5914-090-999  
; CURRENT APPLICATION NUMBER: US/11/073,457  
; CURRENT FILING DATE: 2005-03-04  
; PRIOR APPLICATION NUMBER: 10/042,417  
; PRIOR FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 60/260,179  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 472  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-073-457-8

Query Match 73.3%; Score 33; DB 7; Length 472;  
Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPP 6  
:|:|:|  
Db 11 NSPPPP 16

RESULT 39  
US-11-073-460-8  
; Sequence 8, Application US/11073460  
; Publication No. US20050272066A1  
; GENERAL INFORMATION:  
; APPLICANT: Pagano, M.  
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF  
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS  
; FILE REFERENCE: 5914-090-999  
; CURRENT APPLICATION NUMBER: US/11/073,460  
; CURRENT FILING DATE: 2005-03-04  
; PRIOR APPLICATION NUMBER: 10/042,417  
; PRIOR FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 60/260,179  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 472  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-073-460-8

Query Match 73.3%; Score 33; DB 7; Length 472;  
Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Gap: 0;

```
Qy 2 SPPEPC 7
Db 72 SPPEPC 77

; OTHER INFORMATION: construct
US-11-116-939-11
Query Match 73.3%; Score 33; DB 7; Length 824;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SPPEPC 7
Db 490 SPPEPC 496

RESULT 45
US-10-821-234-1219
; Sequence 1219, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1219
; LENGTH: 1133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1219
Query Match 73.3%; Score 33; DB 6; Length 1133;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SPPEPC 7
Db 486 SPPEPC 491

RESULT 46
US-10-952-535A-23
; Sequence 23, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Lecerf, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952.535A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-952-535A-23
Query Match 71.1%; Score 32; DB 6; Length 64;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SPPEPC 7
Db 72 SPPEPC 77

; OTHER INFORMATION: construct
US-11-116-939-11
Query Match 73.3%; Score 33; DB 7; Length 723;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SPPEPC 7
Db 72 SPPEPC 77

RESULT 43
US-11-078-735-17
; Sequence 17, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAM JAMES
; APPLICANT: TUGAL, TAWARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078.735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 17
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-17
Query Match 73.3%; Score 33; DB 7; Length 723;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SPPEPC 7
Db 72 SPPEPC 77

RESULT 44
US-11-116-939-11
; Sequence 11, Application US/11116939
; Publication No. US20050265995A1
; GENERAL INFORMATION:
; APPLICANT: Stephen Tomlinson
; APPLICANT: Richard J. Quigg
; TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
; FILE REFERENCE: 19113.0115U2
; CURRENT APPLICATION NUMBER: US/11/116.939
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 60/565,907
; PRIOR FILING DATE: 2004-04-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
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QY 1 SSPPPP 6  
| | | | |  
Db 36 SGPPPP 41

RESULT 47  
US-11-123-896-269  
; Sequence 269, Application US/11123896  
; Publication No. US20050273881A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Navarro Acevedo, Pedro A.  
; APPLICANT: Harvell, Leslie  
; APPLICANT: Cahoon, Rebecca  
; APPLICANT: McCutchen, Billy Fred  
; APPLICANT: Lu, Albert  
; APPLICANT: Herrmann, Rafael  
; APPLICANT: Wong, James  
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of Use  
; FILE REFERENCE: 35718/246703  
; CURRENT APPLICATION NUMBER: US/11/123,896  
; CURRENT FILING DATE: 2005-05-06  
; PRIOR APPLICATION NUMBER: 60/300,152  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 60/300,241  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 469  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 269  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-11-123-896-269

Query Match 71.1%; Score 32; DB 7; Length 107;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPPPP 6  
| | | | |  
Db 84 SPPPPP 88

RESULT 48  
US-10-821-234-1369  
; Sequence 1369, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_SEQ\_genes Version 1.0  
; SEQ ID NO 1369  
; LENGTH: 147  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1369

Query Match 71.1%; Score 32; DB 6; Length 147;  
Best Local Similarity 83.3%; Pred. No. 77;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPP 6

Db 3 SSPPPP 8  
| | | | |

RESULT 49  
US-10-821-234-863  
; Sequence 863, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_SEQ\_genes Version 1.0  
; SEQ ID NO 863  
; LENGTH: 160  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-863

Query Match 71.1%; Score 32; DB 6; Length 160;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPPPP 6  
| | | | |  
Db 1 SPPPPP 5

RESULT 50  
US-10-821-234-1299  
; Sequence 1299, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_SEQ\_genes Version 1.0  
; SEQ ID NO 1299  
; LENGTH: 192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1299

Query Match 71.1%; Score 32; DB 6; Length 192;  
Best Local Similarity 83.3%; Pred. No. 95;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPP 6  
| | | | |  
Db 2 SEPpppp 7

Search completed: January 3, 2006, 09:55:47  
Job time : 6 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:05 ; Search time 7.33333 Seconds  
(without alignments)  
91.843 Million cell updates/sec

Title: US-10-759-832-10

Perfect score: 45

Sequence: 1 SSPPPPC 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR 80.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	91.1	343	2 T02071	glyceraldehyde-3-p
2	41	91.1	437	2 T14192	extensin homolog T
3	41	91.1	532	2 T04748	hypothetical prote
4	41	91.1	744	2 E86255	hypothetical prote
5	40	88.9	157	2 T02034	early light-induce
6	40	88.9	246	2 T46446	hypothetical prote
7	40	88.9	250	1 A31757	homeotic protein H
8	40	88.9	251	1 B60492	homeotic protein H
9	40	88.9	373	2 A47234	homeobox protein H
10	39	86.7	528	2 B42560	4-chlorobenzoate-C
11	39	86.7	1520	2 T00273	hypothetical prote
12	39	86.7	2098	2 T18397	protein CRP - mal
13	38	84.4	220	2 G86164	protein F15K9.8 [i
14	38	84.4	770	2 T00204	LDL receptor relat
15	38	84.4	990	2 T14756	hypothetical prote
16	38	84.4	1006	2 G86292	hypothetical prote
17	38	84.4	1487	2 S62048	probable membrane
18	37	82.2	31	2 S03295	Ig alpha chain C r
19	37	82.2	103	2 A86584	CT631 hypothetical
20	37	82.2	105	2 T22564	hypothetical prote
21	37	82.2	119	2 A86271	F21F23.19 protein
22	37	82.2	128	2 A72678	hypothetical prote
23	37	82.2	142	2 B41132	collagen-related p
24	37	82.2	147	2 S37485	gene megl protein
25	37	82.2	149	2 A41132	collagen-related p
26	37	82.2	160	2 D48232	cysteine-rich exte
27	37	82.2	161	2 E48232	cysteine-rich exte
28	37	82.2	163	2 T33130	hypothetical prote
29	37	82.2	165	2 C48232	cysteine-rich exte

30	37	82.2	172	1 RKR2S	ribulose-bisphosph
31	37	82.2	172	2 T27505	hypothetical prote
32	37	82.2	181	2 S22990	zein, 27K - maize
33	37	82.2	199	2 S14981	extensin class I (
34	37	82.2	211	2 T32976	hypothetical prote
35	37	82.2	215	2 T22572	hypothetical prote
36	37	82.2	223	1 ZMZM19	glutelin 2 precurs
37	37	82.2	223	1 S37108	cuticlin 2 - Caeno
38	37	82.2	236	1 S09256	homeotic protein H
39	37	82.2	240	2 T25814	hypothetical prote
40	37	82.2	263	2 S01360	salivary glue prot
41	37	82.2	271	2 S15750	transforming prote
42	37	82.2	324	2 T24102	hypothetical prote
43	37	82.2	340	1 A2HU	Ig alpha-2 chain C
44	37	82.2	340	2 I56230	Ig alpha-2 chain C
45	37	82.2	340	2 B23360	Ig alpha-2 chain C
46	37	82.2	348	2 AB3260	hypothetical membr
47	37	82.2	379	2 T05441	proline-rich prote
48	37	82.2	379	2 D85257	extensin-like prot
49	37	82.2	387	2 T21370	hypothetical prote
50	37	82.2	434	2 B84684	hypothetical prote
51	37	82.2	436	2 JN0591	serotonin receptor
52	37	82.2	447	2 A84718	hypothetical prote
53	37	82.2	450	2 T17234	hypothetical prote
54	37	82.2	457	2 T21063	hypothetical prote
55	37	82.2	469	2 A55484	p52(Sbc) protein -
56	37	82.2	473	2 S25776	transforming prote
57	37	82.2	494	2 B96534	hypothetical prote
58	37	82.2	635	1 WMBEW6	capsid protein - h
59	37	82.2	729	2 T35028	probable glycosyl
60	37	82.2	733	2 T47618	extensin-like prot
61	37	82.2	754	2 T50803	hypothetical prote
62	37	82.2	760	2 T06291	extensin homolog T
63	37	82.2	798	2 T21369	hypothetical prote
64	37	82.2	895	2 C86371	99.7K hypothetical
65	37	82.2	951	2 T47617	extensin-like prot
66	37	82.2	1001	2 T16419	hypothetical prote
67	37	82.2	1140	2 D88690	protein F41H0.3 (
68	37	82.2	1165	2 T16420	hypothetical prote
69	37	82.2	1736	2 T00391	hypothetical prote
70	37	82.2	2241	2 T02857	conserved hypothet
71	37	82.2	4391	2 A38096	parlecan precursor
72	36	80.0	30	2 S59482	hydroxyproline-ric
73	36	80.0	66	2 H84533	hypothetical prote
74	36	80.0	75	2 S14973	extensin class I (
75	36	80.0	80	2 S49761	structural cell wa
76	36	80.0	111	2 T19357	hypothetical prote
77	36	80.0	132	2 S14970	extensin class I (
78	36	80.0	139	2 S61885	extensin precursor
79	36	80.0	163	2 A29356	hydroxyproline-ric
80	36	80.0	181	2 S14974	extensin class I (
81	36	80.0	181	2 T48558	hypothetical prote
82	36	80.0	187	2 S38036	hypothetical prote
83	36	80.0	201	2 B84671	hypothetical prote
84	36	80.0	212	2 F84862	probable extensin
85	36	80.0	217	2 T09965	extensin CYC17 pre
86	36	80.0	224	2 T09328	extensin (clone Ex
87	36	80.0	224	2 T47477	hypothetical prote
88	36	80.0	225	2 T09964	extensin CYC15 pre
89	36	80.0	225	2 T52011	ethylene responsiv
90	36	80.0	229	2 F84685	hypothetical prote
91	36	80.0	242	2 S54156	extensin-like prot
92	36	80.0	254	2 B84901	hypothetical prote
93	36	80.0	258	2 S55036	tyrosine-rich hydr
94	36	80.0	263	2 T12698	extensin - common
95	36	80.0	264	2 T06789	hydroxyproline-ric
96	36	80.0	265	2 D96667	hypothetical prote
97	36	80.0	274	2 T02797	thymidylate kinase
98	36	80.0	278	2 S20790	extensin - almond
99	36	80.0	280	2 T03236	extensin precursor
100	36	80.0	283	2 S13383	hydroxyproline-ric
101	36	80.0	284	2 S71227	extensin I - Arabi
102	36	80.0	291	2 S33209	extensin-like prot

103	36	80.0	299	2	S12022	extensin - rape	176	36	80.0	1083	2	T05689	hypothetical prote
104	36	80.0	302	2	A96661	unknown protein, 8	177	36	80.0	1135	2	T30561	Scythe protein - A
105	36	80.0	304	2	A32993	transcription fac	178	36	80.0	1188	2	S49915	extensin-like prot
106	36	80.0	306	2	T06435	ribonuclease S5 ho	179	36	80.0	1286	2	A88396	protein M01E10.2 l
107	36	80.0	306	2	A24354	extensin precursor	180	36	80.0	1366	2	B84924	hypothetical prote
108	36	80.0	313	2	T48057	extensin-rich prote	181	36	80.0	1445	2	T50508	hypothetical prote
109	36	80.0	313	2	T52077	proline-rich prote	182	36	80.0	1494	2	T14355	protein-tyrosine-p
110	36	80.0	318	2	S33158	extensin - common	183	36	80.0	1508	2	T27828	hypothetical prote
111	36	80.0	319	2	A36600	growth factor-indu	184	36	80.0	1519	2	T27829	hypothetical prote
112	36	80.0	320	2	JC1255	TiS11 protein - ra	185	36	80.0	1616	2	J37183	gene APXL protein
113	36	80.0	322	2	S25299	extensin precursor	186	36	80.0	1748	1	JN0786	integrin beta-4 ch
114	36	80.0	326	2	S34427	tristetrapoline p	187	36	80.0	1801	2	T26774	hypothetical prote
115	36	80.0	350	2	T14191	extensin homolog T	188	36	80.0	2014	2	I36936	complement recepto
116	36	80.0	354	1	GNVSR	genome polyprotein	189	36	80.0	2489	2	I73012	complement C3b/C4b
117	36	80.0	358	2	E87309	hypothetical prote	190	36	80.0	2761	2	T29285	hypothetical prote
118	36	80.0	373	2	B96798	extensin (imported	191	36	80.0	3869	2	A48205	All-1 protein +GTE
119	36	80.0	388	2	S25298	extensin (clone to	192	36	80.0	3968	2	A44265	trithorax homolog
120	36	80.0	409	2	T47754	leucine zipper-con	193	35	77.8	620	2	E84481	probable protein k
121	36	80.0	409	2	T29517	hypothetical prote	194	35	77.8	941	2	S09851	hypothetical prote
122	36	80.0	414	2	S16322	light-induced prot	195	35	77.8	1737	2	T00209	MEG8 protein - hu
123	36	80.0	414	2	C86301	arginine/serine-ri	196	34.5	76.7	432	2	A25483	env polyprotein, r
124	36	80.0	416	2	JU0465	extensin precursor	197	34.5	76.7	445	1	VCFMLV	env polyprotein -
125	36	80.0	423	2	H84566	probable RING zinc	198	34.5	76.7	661	1	VCNVCB	env polyprotein -
126	36	80.0	429	2	T06296	extensin-like prot	199	34.5	76.7	665	1	VCWEM	env polyprotein -
127	36	80.0	431	2	B86346	F16F4.4 protein -	200	34.5	76.7	676	1	VCNVPV	env polyprotein pr
128	36	80.0	432	2	T06782	extensin - soybean	201	34.5	76.7	676	2	S70395	env polyprotein -
129	36	80.0	440	2	H86312	F2H15.2 protein -	202	34	75.6	119	2	C40513	hypothetical prote
130	36	80.0	443	1	I38239	transcription fact	203	34	75.6	221	2	S77396	hypothetical prote
131	36	80.0	443	2	G86388	unknown protein [i	204	34	75.6	258	2	S23106	p1A protein - shi
132	36	80.0	461	2	T10741	extensin-like prot	205	34	75.6	343	2	T23198	hypothetical prote
133	36	80.0	463	2	T47779	hypothetical prote	206	34	75.6	344	2	S42383	hypothetical prote
134	36	80.0	464	2	S22697	extensin - Volvox	207	34	75.6	345	2	T23202	hypothetical prote
135	36	80.0	467	2	S41318	hypothetical prote	208	34	75.6	456	2	S69070	hypothetical prote
136	36	80.0	478	2	P86388	hypothetical prote	209	34	75.6	570	2	S35069	transcription fact
137	36	80.0	498	1	VGBEGX	secreted glycoprot	210	34	75.6	591	2	A40684	early B-cell facto
138	36	80.0	499	2	T49630	phenylalanyl-CRNA	211	34	75.6	676	2	A45900	complement C3b rec
139	36	80.0	511	2	T04814	dihydrolipamide S	212	34	75.6	768	2	A42755	P-selectin precurs
140	36	80.0	513	2	T14194	extensin homolog T	213	34	75.6	768	2	I53821	P-selectin - rat
141	36	80.0	520	2	E97813	WASP, N-WASP, MENA	214	34	75.6	995	2	H59432	RhoGAP protein hom
142	36	80.0	522	2	E84833	hypothetical prote	215	34	75.6	1274	2	T37193	enamelin matrix pr
143	36	80.0	523	2	E96576	unknown protein, 4	216	34	75.6	1305	2	T31096	cyclin G-associate
144	36	80.0	541	2	A25896	yellow protein - f	217	34	75.6	1367	2	T33819	hypothetical prote
145	36	80.0	559	2	G84642	hypothetical prote	218	34	75.6	2207	1	GNNY1P	genome polyprotein
146	36	80.0	580	2	T10863	extensin precursor	219	34	75.6	2207	2	S09553	genome polyprotein
147	36	80.0	587	2	C70893	hypothetical prote	220	34	75.6	2209	1	GNNY3P	genome polyprotein
148	36	80.0	594	2	T15202	hypothetical prote	221	34	75.6	2209	1	GNNY2P	genome polyprotein
149	36	80.0	600	2	T14613	hypothetical prote	222	33	74.4	417	2	T08724	hypothetical prote
150	36	80.0	620	2	S06733	hydroxyproline-ric	223	33	73.3	42	2	T07030	extensin - tomato
151	36	80.0	633	2	S62057	proline-rich prote	224	33	73.3	72	2	C86188	hypothetical prote
152	36	80.0	641	2	T17278	hypothetical prote	225	33	73.3	78	2	T30471	hypothetical prote
153	36	80.0	658	2	T08153	cysteine proteinas	226	33	73.3	93	2	A25494	hydroxyproline-ric
154	36	80.0	682	2	AG2118	serine/threonine k	227	33	73.3	97	2	S36034	FL-160 protein - T
155	36	80.0	699	2	A96529	hypothetical prote	228	33	73.3	99	2	S33159	pAP8 protein - com
156	36	80.0	707	2	T14195	extensin homolog T	229	33	73.3	117	2	T46322	hypothetical prote
157	36	80.0	708	2	D96711	hypothetical prote	230	33	73.3	129	2	I61187	alpha-/A integrin
158	36	80.0	710	2	D96728	hypothetical prote	231	33	73.3	129	2	H75351	conserved hypothet
159	36	80.0	716	2	T26998	hypothetical prote	232	33	73.3	132	2	T08535	transfer origin pr
160	36	80.0	731	2	T19721	hypothetical prote	233	33	73.3	132	2	S22997	trak protein - Esc
161	36	80.0	733	2	G84668	hypothetical prote	234	33	73.3	152	2	T01505	hypothetical prote
162	36	80.0	733	2	JQ0532	OP protein - Kenne	235	33	73.3	154	2	A23162	extensin - carrot
163	36	80.0	753	2	S48059	metal-regulatory t	236	33	73.3	160	2	T25185	hypothetical prote
164	36	80.0	760	2	F86387	probable Pto kinas	237	33	73.3	162	2	D81747	conserved hypothet
165	36	80.0	786	2	T01456	extensin homolog F	238	33	73.3	166	2	T38982	hypothetical prote
166	36	80.0	816	2	B86285	hypothetical prote	239	33	73.3	169	2	T07623	extensin homolog H
167	36	80.0	819	2	T48307	hypothetical prote	240	33	73.3	175	2	S71560	early light-induce
168	36	80.0	847	2	T21700	hypothetical prote	241	33	73.3	175	2	T4775	hypothetical prote
169	36	80.0	847	2	F96531	hypothetical prote	242	33	73.3	181	2	T35751	hypothetical prote
170	36	80.0	912	2	B44450	ubiquitin-specific	243	33	73.3	182	2	B86462	hypothetical prote
171	36	80.0	953	2	T46227	hypothetical prote	244	33	73.3	186	2	T35736	hypothetical prote
172	36	80.0	971	2	T00268	hypothetical prote	245	33	73.3	188	2	B25317	gag polyprotein -
173	36	80.0	997	2	T28872	hypothetical prote	246	33	73.3	191	2	S57642	interferon precurs
174	36	80.0	1011	2	T17430	tol protein - Neur	247	33	73.3	191	2	F84522	probable proline-r
175	36	80.0	1057	2	T25396	hypothetical prote	248	33	73.3	197	2	T33453	hypothetical prote

249	33	73.3	198	2	E86261	F13K23.6 protein -	322	33	73.3	418	2	D71460	probable membrane
250	33	73.3	199	2	T52410	blue copper-bindin	323	33	73.3	418	2	T19800	hypothetical prote
251	33	73.3	200	2	T41745	RING-H2 finger pro	324	33	73.3	421	2	T04798	hypothetical prote
252	33	73.3	201	2	T52408	blue copper-bindin	325	33	73.3	422	2	T09742	drought-induced pr
253	33	73.3	202	2	T01605	phytoeyanin At2g44	326	33	73.3	426	1	T17336	hypothetical prote
254	33	73.3	208	2	A29851	gag polypeptide -	327	33	73.3	428	1	E38180	modulation protei
255	33	73.3	209	2	T20975	hypothetical prote	328	33	73.3	430	2	T28143	tapasin 1 homolog,
256	33	73.3	217	2	T15873	hypothetical prote	329	33	73.3	433	2	C88594	protein Y48A6B.10
257	33	73.3	218	2	S52286	hypothetical prote	330	33	73.3	437	2	S15704	transforming prote
258	33	73.3	225	2	C88633	NADH2 dehydrogenas	331	33	73.3	437	2	S55392	mem protein - fruit
259	33	73.3	228	2	A44982	protein F56B3.3 [i	332	33	73.3	438	2	E86181	hypothetical prote
260	33	73.3	229	2	S64049	collagen UCOL1 - p	333	33	73.3	440	2	A43519	complement recepto
261	33	73.3	232	2	A25317	hypothetical prote	334	33	73.3	440	2	A26359	decay-accelerating
262	33	73.3	240	2	A36791	gag polypeptide -	335	33	73.3	440	2	S51614	Algal-CAM - Volvox
263	33	73.3	245	1	S10092	hypothetical prote	336	33	73.3	440	2	JC7807	Wiskott-Aldrich sy
264	33	73.3	247	1	D24706	homeotic protein H	337	33	73.3	441	2	T22531	hypothetical prote
265	33	73.3	247	2	H95319	modulation protei	338	33	73.3	446	2	A34418	H-2 region II bind
266	33	73.3	252	2	JC2399	phosphoadenyl-l-su	339	33	73.3	446	2	T26988	hypothetical prote
267	33	73.3	253	2	T27166	PMS4 homolog misa	340	33	73.3	446	2	T07907	hydroxyproline-ric
268	33	73.3	254	2	S35743	hypothetical prote	341	33	73.3	447	2	E96008	probable glycoalyt
269	33	73.3	256	2	JC2398	p19 protein - avia	342	33	73.3	448	1	A56018	transcription fact
270	33	73.3	271	2	T26640	PMS3 homolog misa	343	33	73.3	448	2	D41727	retinoid X recepto
271	33	73.3	273	2	S23281	hypothetical prote	344	33	73.3	449	1	S30205	transcription fact
272	33	73.3	274	2	F86276	homeotic protein m	345	33	73.3	449	2	D87682	OmpA family protei
273	33	73.3	284	1	POFV09	P14L17.2 protein -	346	33	73.3	451	1	A40168	transcription fact
274	33	73.3	288	2	D84616	gag polypeptide -	347	33	73.3	451	2	A41651	retinoic acid rece
275	33	73.3	291	2	F75308	probable bHLH tran	348	33	73.3	452	2	A35068	complement factor
276	33	73.3	292	2	E90180	amino acid ABC tra	349	33	73.3	457	2	E96772	hypothetical prote
277	33	73.3	293	2	D96605	conserved hypothet	350	33	73.3	460	2	JL0145	interleukin-6 rece
278	33	73.3	298	2	S53761	unknown protein F1	351	33	73.3	462	2	S44490	RXR type hormone r
279	33	73.3	299	2	T17832	triose-phosphate i	352	33	73.3	468	2	F87359	leucine aminopepti
280	33	73.3	300	2	AD3356	hypothetical prote	353	33	73.3	474	2	E87650	peptidase, N20/M25
281	33	73.3	301	2	B83512	hypothetical prote	354	33	73.3	476	2	T45656	hypothetical prote
282	33	73.3	303	2	H35068	hypothetical prote	355	33	73.3	479	1	IXBE1F	alpha trans-induci
283	33	73.3	309	1	S09257	apolipoprotein H-r	356	33	73.3	480	2	A56694	keratin, type II,
284	33	73.3	309	1	POFV09	homeotic protein H	357	33	73.3	487	2	T49424	hypothetical prote
285	33	73.3	314	2	F70013	gag polypeptide -	358	33	73.3	489	2	T11622	extensin class 1 p
286	33	73.3	316	2	T20497	hypothetical prote	359	33	73.3	490	1	IXBE17	alpha trans-induci
287	33	73.3	321	2	AE2170	hypothetical prote	360	33	73.3	490	2	S67581	Slp4 protein - yea
288	33	73.3	325	2	T23426	hypothetical prote	361	33	73.3	490	2	T15097	hypothetical prote
289	33	73.3	330	2	T07911	hypothetical prote	362	33	73.3	497	2	JC2054	complement regulat
290	33	73.3	330	2	L55975	X/Y protein - mous	363	33	73.3	498	2	A87374	hypothetical prote
291	33	73.3	335	2	H86158	hypothetical prote	364	33	73.3	508	2	B96658	hypothetical prote
292	33	73.3	338	2	G96685	hypothetical prote	365	33	73.3	514	2	AD0826	transcription acti
293	33	73.3	338	2	B96529	hypothetical prote	366	33	73.3	519	1	FOLJG4	gag polypeptide -
294	33	73.3	340	2	L56234	decay-accelerating	367	33	73.3	520	2	I84718	RXR-beta1 isoform
295	33	73.3	349	2	T49791	hypothetical prote	368	33	73.3	523	2	T05994	protein kinase hom
296	33	73.3	358	1	WMBE38	infected cell prot	369	33	73.3	530	2	A45690	transactivator EBN
297	33	73.3	362	2	B64527	M-protein - Helico	370	33	73.3	531	2	T05644	hypothetical prote
298	33	73.3	362	2	A44083	meq protein - Mare	371	33	73.3	531	2	AG1812	hypothetical prote
299	33	73.3	363	2	T16755	hypothetical prote	372	33	73.3	536	2	T43349	nuclear receptor N
300	33	73.3	368	2	C29356	hydroxyproline-ric	373	33	73.3	542	2	B47022	chitinase (EC 3.2.
301	33	73.3	371	2	T00438	probable MYB fami	374	33	73.3	543	2	S25128	61K protein - Auto
302	33	73.3	371	2	T51636	myb-related transc	375	33	73.3	543	2	T05138	hypothetical prote
303	33	73.3	373	2	A70856	probable lpp2 prot	376	33	73.3	546	2	T02029	DNA-binding protei
304	33	73.3	379	2	S31719	proline-rich prote	377	33	73.3	548	2	S52735	transcription fact
305	33	73.3	380	2	T20269	hypothetical prote	378	33	73.3	552	2	S49338	probable acid-CoA
306	33	73.3	381	1	B26359	decay-accelerating	379	33	73.3	557	2	F69481	unknown protein F2
307	33	73.3	384	2	G96738	hypothetical prote	380	33	73.3	561	2	G96752	probable serine/th
308	33	73.3	389	2	G97332	hypothetical prote	381	33	73.3	566	2	H70985	hypothetical prote
309	33	73.3	390	2	T21367	hypothetical prote	382	33	73.3	570	2	T08778	Wiskott-Aldrich sy
310	33	73.3	392	2	T48360	farnesylated prote	383	33	73.3	574	2	T43556	Wiskott-Aldrich sy
311	33	73.3	393	2	JC5614	RNB6 protein - rat	384	33	73.3	574	2	T38819	Wiskott-Aldrich sy
312	33	73.3	393	2	T30048	hypothetical prote	385	33	73.3	583	1	A41129	radixin - mouse
313	33	73.3	396	2	T07021	extensin-like prot	386	33	73.3	583	1	A46127	radixin - human
314	33	73.3	396	2	T26987	hypothetical prote	387	33	73.3	583	1	S39805	probable calcium-d
315	33	73.3	397	2	S09813	hypothetical prote	388	33	73.3	583	2	H84810	hypothetical prote
316	33	73.3	398	2	A13231	conjugal transfer	389	33	73.3	584	2	S76424	hypothetical prote
317	33	73.3	398	2	S21883	bzip transcription	390	33	73.3	589	2	T29897	protein kinase DYR
318	33	73.3	402	2	A40678	T-cell adhesio re	391	33	73.3	589	2	JG0196	protein TiN15.25 l
319	33	73.3	402	2	S42367	lag-2 protein - Ca	392	33	73.3	594	2	G96525	protein TiN15.25 l
320	33	73.3	408	2	T21412	hypothetical prote	393	33	73.3	603	2	A82753	dihydrolipoamide d
321	33	73.3	411	2	A70509	hypothetical prote	394	33	73.3	604	2	T37994	probable splicing

395	33	73.3	614	2	T09902	hypothetical prote	468	33	73.3	1234	1	NEMSH	complement factor
396	33	73.3	623	2	B96681	F5114.14 protein (	469	33	73.3	1273	2	T42405	sax-3 protein - Ca
397	33	73.3	629	2	JG0195	protein kinase DYR	470	33	73.3	1298	1	EDBE75	immediate-early pr
398	33	73.3	632	2	S38042	probable purine nu	471	33	73.3	1331	2	T49813	related to gastric
399	33	73.3	633	2	B83478	probable two-compo	472	33	73.3	1495	2	S60255	transcription co-r
400	33	73.3	635	2	F70874	probable membrane	473	33	73.3	1522	2	T39371	transcription regu
401	33	73.3	638	2	I39196	amiloride sensitiv	474	33	73.3	1537	2	JC4172	DNA (cytosine-5-) -
402	33	73.3	643	2	S36017	finger protein tra	475	33	73.3	1557	2	T02859	probable serine/th
403	33	73.3	645	2	A71416	hypothetical prote	476	33	73.3	1603	2	A48613	gag/pol polyprotei
404	33	73.3	650	2	T04487	hypothetical prote	477	33	73.3	1706	2	I94499	zinc finger protei
405	33	73.3	656	2	B70803	hypothetical prote	478	33	73.3	1721	1	I38902	retinoblastoma bin
406	33	73.3	667	2	T17221	hypothetical prote	479	33	73.3	1794	2	T38459	hypothetical diver
407	33	73.3	673	2	T15551	hypothetical prote	480	33	73.3	1829	2	T41751	l-afadin - rat
408	33	73.3	676	2	T01381	env protein - muri	481	33	73.3	1872	2	T24683	hypothetical prote
409	33	73.3	688	2	T05941	transcription fact	482	33	73.3	1948	2	B69511	N conserved hypoth
410	33	73.3	699	2	T05225	extensin homolog F	483	33	73.3	1952	2	T48814	hypothetical prote
411	33	73.3	701	1	FOFVIR	gag polyprotein -	484	33	73.3	2124	2	T28658	polyketide synthas
412	33	73.3	701	2	S11454	gag polyprotein -	485	33	73.3	2195	2	S61103	SEC16 protein - ye
413	33	73.3	701	2	F48613	gag polyprotein -	486	33	73.3	2278	1	S56274	FAB1 protein - yea
414	33	73.3	701	2	D48613	gag polyprotein -	487	33	73.3	2357	2	A59249	class VII unconven
415	33	73.3	701	2	S35430	gag polyprotein -	488	33	73.3	2697	2	T25444	hypothetical prote
416	33	73.3	722	2	I48324	DELTA-like 1 - mou	489	33	73.3	2715	2	T13049	eyelid - fruit fly
417	33	73.3	726	2	S18208	rabphilin-3A-inter	490	33	73.3	3133	2	S52093	hemocytin - silkw
418	33	73.3	727	2	C84534	hypothetical prote	491	33	73.3	3848	2	T17414	tipc protein - sil
419	33	73.3	728	2	I50719	C-Delta-1 - chicke	492	33	73.3	4861	2	S71752	giant protein p619
420	33	73.3	731	2	T04455	hypothetical prote	493	33	73.3	4861	2	S71752	hydroxyproline-ric
421	33	73.3	732	2	B84902	hypothetical prote	494	33	73.3	57	2	F39690	neural cell adhesi
422	33	73.3	743	2	T39361	hypothetical prote	495	33	73.3	27	1	ZM2M5	glutelin 5 - maize
423	33	73.3	752	2	T20871	hypothetical prote	496	33	73.3	67	2	S14971	extensin class I (
424	33	73.3	753	2	G02173	semaphorin III fam	497	33	73.3	76	2	E97763	protein transport
425	33	73.3	755	1	S74695	hypothetical prote	498	33	73.3	80	2	T17576	hypothetical prote
426	33	73.3	759	2	T00875	hypothetical prote	499	33	73.3	83	2	JC2021	enhancer factor I
427	33	73.3	770	2	T00203	LbL receptor-relat	500	33	73.3	85	2	T02980	hypothetical prote
428	33	73.3	775	2	B83400	pyrrolquinoline q	501	33	73.3	90	2	S14972	extensin class I (
429	33	73.3	778	2	T30430	hypothetical prote	502	33	73.3	91	2	T30512	hypothetical prote
430	33	73.3	790	2	T25095	hypothetical prote	503	33	73.3	95	2	C84649	hypothetical prote
431	33	73.3	793	2	JC5539	Smoothed protein	504	33	73.3	103	2	T29597	hypothetical prote
432	33	73.3	805	2	T23237	hypothetical prote	505	33	73.3	105	2	T12554	hypothetical prote
433	33	73.3	808	2	D35069	complement factor	506	33	73.3	107	2	S09879	hypothetical prote
434	33	73.3	817	2	S51342	verprolin - yeast	507	33	73.3	108	1	RHHUS	somatoliberin prec
435	33	73.3	830	2	T04848	protein kinase hom	508	33	73.3	108	2	T05231	hypothetical prote
436	33	73.3	837	2	A57542	p96 protein - mous	509	33	73.3	111	2	S08438	vpx protein - huma
437	33	73.3	839	2	T04859	extensin homolog F	510	33	73.3	112	1	ASLJGH	vpu protein - huma
438	33	73.3	841	2	B82755	beta-hexosaminidas	511	33	73.3	112	1	ASLJSX	hypothetical prote
439	33	73.3	856	2	D86258	protein F5011.10 (	512	33	73.3	112	2	D72654	hypothetical prote
440	33	73.3	858	1	A42239	adenylate cyclase	513	33	73.3	118	2	B86393	hypothetical prote
441	33	73.3	858	2	JC2309	chitin synthase (E	514	33	73.3	121	2	T45832	hypothetical prote
442	33	73.3	858	2	JC2308	chitin synthase (E	515	33	73.3	122	2	PQ0452	extensin-like prot
443	33	73.3	874	2	T29548	hypothetical prote	516	33	73.3	134	2	A95995	hypothetical prote
444	33	73.3	875	1	FOFV29	gag-myc polyprotei	517	33	73.3	134	2	JC5572	proline-rich prote
445	33	73.3	875	1	FOFVHB	gag-myc polyprotei	518	33	73.3	138	2	C96734	hypothetical prote
446	33	73.3	903	2	T00074	hypothetical prote	519	33	73.3	139	2	A71099	hypothetical prote
447	33	73.3	905	1	RGBY85	regulatory protein	520	33	73.3	139	2	T46186	hypothetical prote
448	33	73.3	907	2	E96636	hypothetical prote	521	33	73.3	144	2	S10039	hypothetical prote
449	33	73.3	925	2	T02811	DNA excision/repai	522	33	73.3	144	2	B86364	hypothetical prote
450	33	73.3	926	2	T38198	COPII coated vesic	523	33	73.3	145	1	A35932	angiosgenin precurs
451	33	73.3	929	2	C96623	hypothetical prote	524	33	73.3	149	1	XKACP3	pepsin inhibitor 3
452	33	73.3	933	2	H84652	hypothetical prote	525	33	73.3	151	2	JQ1686	extensin-like prot
453	33	73.3	1011	1	JH0581	NAD ADP-ribosyltra	526	33	73.3	152	2	PQ0476	pistil extensin-li
454	33	73.3	1025	1	A43526	complement C3d/Eps	527	33	73.3	159	2	T49499	hypothetical prote
455	33	73.3	1048	2	T31425	C-terminal domain-	528	33	73.3	161	2	H85120	probable proline-r
456	33	73.3	1058	2	T13286	cappuccino gene pr	529	33	73.3	163	2	D84674	hypothetical prote
457	33	73.3	1063	2	T38732	probable helicase	530	33	73.3	164	2	G71427	hypothetical prote
458	33	73.3	1064	2	T13963	formin related pro	531	33	73.3	165	2	A31635	neural cell adhesi
459	33	73.3	1079	1	TVFVMI	gag-Rml-1-env polyp	532	33	73.3	166	2	T09593	CIC protein, cold-
460	33	73.3	1083	2	S76111	acriflavin resist	533	33	73.3	168	2	T20708	hypothetical prote
461	33	73.3	1087	2	T31100	probable potassium	534	33	73.3	172	2	A39458	carotene biosynthe
462	33	73.3	1110	2	T49091	gamma response I p	535	33	73.3	176	2	B85355	hypothetical prote
463	33	73.3	1162	2	T21557	hypothetical prote	536	33	73.3	176	2	F72651	hypothetical prote
464	33	73.3	1194	2	E96624	hypothetical prote	537	33	73.3	177	2	AB3269	outer membrane lip
465	33	73.3	1198	2	T28678	polyketide synthas	538	33	73.3	178	2	B87104	conserved hypothet
466	33	73.3	1201	2	G86441	unknown protein (l	539	33	73.3	182	2	T30760	hypothetical prote
467	33	73.3	1224	2	T40765	web1 protein homol	540	33	73.3	184	2	G85256	hypothetical prote

541	32	71.1	184	2	E72586	hypothetical prote	614	32	71.1	295	2	T22049	hypothetical prote
542	32	71.1	186	2	T52309	early light-induca	615	32	71.1	296	2	S74253	homeotic protein a
543	32	71.1	188	2	T45838	hypothetical prote	616	32	71.1	297	2	S63281	probable membrane
544	32	71.1	188	2	D29149	proline-rich prote	617	32	71.1	298	2	T18664	hypothetical prote
545	32	71.1	189	2	A83593	conserved hypotet	618	32	71.1	300	2	T08453	hypothetical prote
546	32	71.1	190	2	T43172	probable protein-t	619	32	71.1	301	2	T03914	hypothetical prote
547	32	71.1	190	2	T35570	hypothetical prote	620	32	71.1	302	2	T32711	hydroxyproline-ric
548	32	71.1	191	2	JQ1919	hypothetical prote	621	32	71.1	303	2	S28264	hypothetical prote
549	32	71.1	192	2	T30477	hypothetical prote	622	32	71.1	303	2	H70716	hypothetical prote
550	32	71.1	196	2	B84638	probable RS2p22 sp	623	32	71.1	304	2	T48281	tonB protein (impo
551	32	71.1	196	2	B48232	cysteine-rich exte	624	32	71.1	307	2	AE2596	hypothetical prote
552	32	71.1	196	2	A46605	female-specific ju	625	32	71.1	307	2	G97378	probable RNA bindi
553	32	71.1	198	2	A45067	laminin B1 chain v	626	32	71.1	309	2	T47685	hypothetical prote
554	32	71.1	198	2	D72538	probable [acyl-car	627	32	71.1	310	2	T45873	myb protein homolo
555	32	71.1	199	1	TVMSB1	transforming prote	628	32	71.1	311	2	T03827	hypothetical prote
556	32	71.1	199	2	T07622	extensin homolog -	629	32	71.1	312	2	T19360	hypothetical prote
557	32	71.1	200	2	T52627	splicing factor RS	630	32	71.1	314	2	E84518	probable spliceoso
558	32	71.1	200	2	T05112	splicing factor 9G	631	32	71.1	314	2	H70723	hypothetical prote
559	32	71.1	204	2	T35188	hypothetical prote	632	32	71.1	314	2	D71410	hypothetical prote
560	32	71.1	209	2	A48232	cysteine-rich exte	633	32	71.1	315	2	A56561	35K proline-rich p
561	32	71.1	209	2	C89005	protein T24A6.3 [1	634	32	71.1	317	2	A28996	proline-rich prote
562	32	71.1	211	2	S28304	hypothetical prote	635	32	71.1	318	2	F71409	probable light ind
563	32	71.1	218	2	F84748	probable AP2 domai	636	32	71.1	318	2	T29479	hypothetical prote
564	32	71.1	218	2	T21949	hypothetical prote	637	32	71.1	320	2	T18319	hypothetical prote
565	32	71.1	219	2	T10563	proline-rich prote	638	32	71.1	322	2	F86918	probable prephenat
566	32	71.1	221	2	T07176	extensin homolog -	639	32	71.1	322	2	T22403	hypothetical prote
567	32	71.1	221	2	H82857	tonB protein XF000	640	32	71.1	325	2	A55558	aluminum D-box bind
568	32	71.1	222	2	T43500	hypothetical prote	641	32	71.1	326	2	C90272	hypothetical prote
569	32	71.1	224	2	S44964	lmbO protein - Str	642	32	71.1	328	2	JQ0985	hydroxyproline-ric
570	32	71.1	224	2	T49923	hypothetical prote	643	32	71.1	330	2	T05717	probable extensin
571	32	71.1	226	2	D72769	hypothetical prote	644	32	71.1	334	2	H96629	hypothetical prote
572	32	71.1	233	2	T17218	hypothetical prote	645	32	71.1	334	2	T33836	dipeptide transpor
573	32	71.1	235	2	E75342	conserved hypotet	646	32	71.1	335	2	S16650	proline-rich prote
574	32	71.1	236	1	TVMSA1	transforming prote	647	32	71.1	335	2	B96591	proline-rich prote
575	32	71.1	236	2	T45835	hypothetical prote	648	32	71.1	335	2	T52078	recombination prot
576	32	71.1	242	2	A43904	homeotic protein G	649	32	71.1	336	2	S73678	protein F53C3.10 [
577	32	71.1	245	1	BLA958	virB1 protein prec	650	32	71.1	336	2	D88114	hypothetical prote
578	32	71.1	245	2	T26760	hypothetical prote	651	32	71.1	338	2	T36785	hypothetical prote
579	32	71.1	247	2	T33280	hypothetical prote	652	32	71.1	341	2	T37502	hypothetical prote
580	32	71.1	247	2	T17311	hypothetical prote	653	32	71.1	344	2	T29264	hypothetical prote
581	32	71.1	249	2	T41847	AcMNPV orf106 - Bo	654	32	71.1	345	2	D86362	hypothetical prote
582	32	71.1	252	2	AE3248	component of type	655	32	71.1	345	2	T01348	hypothetical prote
583	32	71.1	252	2	S48725	MDV specific prote	656	32	71.1	347	2	S41638	T-cell surface gly
584	32	71.1	254	2	T33280	hypothetical prote	657	32	71.1	347	2	T48323	hypothetical prote
585	32	71.1	257	2	T10586	small nuclear ribo	658	32	71.1	348	2	T47923	probable DNA-bandi
586	32	71.1	262	2	T06600	acetyl-CoA carboxy	659	32	71.1	348	2	T49166	hypothetical prote
587	32	71.1	262	2	T22489	hypothetical prote	660	32	71.1	350	2	G84807	methylenetetrahydr
588	32	71.1	264	2	P00478	plastil extensin-11	661	32	71.1	350	2	I55214	sialivary proline-r
589	32	71.1	264	2	T10572	hypothetical prote	662	32	71.1	350	2	S22456	hydroxyproline-ric
590	32	71.1	264	2	D34768	ORF4 protein - Orf	663	32	71.1	350	2	G75571	Mut7/nudix family
591	32	71.1	264	2	F72714	hypothetical prote	664	32	71.1	351	2	T00917	hypothetical prote
592	32	71.1	265	2	T04834	hypothetical prote	665	32	71.1	361	2	S19552	potassium channel
593	32	71.1	265	2	A87387	hypothetical prote	666	32	71.1	361	2	S19552	gene NKX6.1 protei
594	32	71.1	265	2	T46089	proline-rich prote	667	32	71.1	364	2	A48188	hepatic transcript
595	32	71.1	267	2	S08314	cell wall glycopro	668	32	71.1	365	2	A34894	cellular tumor ant
596	32	71.1	268	2	I50738	slug protein - chi	669	32	71.1	367	1	S02193	hypothetical prote
597	32	71.1	268	2	H84684	En/Spm-like transp	670	32	71.1	368	2	T51200	hypothetical prote
598	32	71.1	273	2	F87414	phage SPO1 DNA pol	671	32	71.1	371	2	T49786	hypothetical prote
599	32	71.1	275	1	TVRTFR	transforming prote	672	32	71.1	372	2	S74859	hypothetical prote
600	32	71.1	280	2	T11671	extensin-like prot	673	32	71.1	373	2	T52182	probable transcrip
601	32	71.1	281	2	S44052	structural protein	674	32	71.1	376	1	QOBEW2	UL53 protein - hum
602	32	71.1	282	2	T18608	hypothetical prote	675	32	71.1	376	2	S45763	hypothetical prote
603	32	71.1	285	2	T27458	hypothetical prote	676	32	71.1	376	2	T09578	nuclear protein JU
604	32	71.1	285	2	T18669	hypothetical prote	677	32	71.1	377	2	T52606	equimosa promoter
605	32	71.1	287	2	S41953	UDP-glucose glucos	678	32	71.1	378	2	T51647	myb-related transc
606	32	71.1	287	2	T34337	homeotic protein H	679	32	71.1	378	1	OKB01R	protein kinase (EC
607	32	71.1	288	2	J80659	hypothetical prote	680	32	71.1	379	2	S42529	opaque-2-related p
608	32	71.1	288	2	T21732	hypothetical prote	681	32	71.1	379	2	H96696	protein F1N21.16 [
609	32	71.1	289	2	A43562	homeotic protein H	682	32	71.1	380	1	OKPGIR	protein kinase (EC
610	32	71.1	289	2	S23402	sperm surface prot	683	32	71.1	381	1	OKT1R	protein kinase (EC
611	32	71.1	290	2	AC2030	hypothetical prote	684	32	71.1	381	2	T00674	hypothetical prote
612	32	71.1	291	2	T31592	hypothetical prote	685	32	71.1	383	2	AE2295	hypothetical prote
613	32	71.1	291	2	T27534	hypothetical prote	686	32	71.1	385	2	S78100	MAPK-activated pro

687	32	71.1	385	2	H95413	probable integrase	760	32	71.1	462	2	A13282	primosomal protein
688	32	71.1	385	2	H90436	oxidoreductase (F1	761	32	71.1	463	2	T45565	hypothetical prote
689	32	71.1	386	1	S51648	cellular tumor ant	762	32	71.1	465	2	G02738	FRAC-4 - human
690	32	71.1	388	2	G85147	hypothetical prote	763	32	71.1	467	2	T34874	hypothetical prote
691	32	71.1	389	2	S44643	hypothetical prote	764	32	71.1	468	2	F84686	hypothetical prote
692	32	71.1	390	1	TVMVCB	transforming prote	765	32	71.1	470	2	A30136	developmental cont
693	32	71.1	390	2	T45789	hypothetical prote	766	32	71.1	472	1	A49836	transcription fact
694	32	71.1	390	2	B84584	probable RING zinc	767	32	71.1	473	2	B85187	glycoprotein homol
695	32	71.1	390	2	G01936	Abl binding protei	768	32	71.1	473	2	S50755	hypothetical prote
696	32	71.1	391	2	S69192	serine O-acetyltra	769	32	71.1	474	2	A46584	adenyl cyclase-a
697	32	71.1	391	2	H95572	protein F12M16.13	770	32	71.1	474	2	I49572	adenyl cyclase-a
698	32	71.1	393	2	PQ0479	pistil extensin-li	771	32	71.1	475	2	A48120	adenyl cyclase-a
699	32	71.1	394	2	C84905	probable extensin	772	32	71.1	476	2	B41977	retinoic acid rece
700	32	71.1	404	1	Q0BE13	BMRF1 protein - hu	773	32	71.1	476	2	C64601	fucosyltransferase
701	32	71.1	404	2	S46269	synovial sarcoma t	774	32	71.1	476	2	C39481	serum response fac
702	32	71.1	405	2	T10630	ethylene-regulated	775	32	71.1	476	2	T37051	hypothetical prote
703	32	71.1	407	2	T48280	hypothetical prote	776	32	71.1	477	2	T04916	hypothetical prote
704	32	71.1	407	2	T24951	hypothetical prote	777	32	71.1	477	2	T46304	hypothetical prote
705	32	71.1	408	2	G96707	hypothetical prote	778	32	71.1	478	2	S75572	glucosyltransferas
706	32	71.1	412	2	B44418	surface antigen -	779	32	71.1	483	2	F71684	virB10 protein (vi
707	32	71.1	412	2	S30299	Krox-20 protein -	780	32	71.1	483	2	T25992	hypothetical prote
708	32	71.1	413	2	T15326	hypothetical prote	781	32	71.1	485	2	A33647	sulfated surface g
709	32	71.1	415	2	S55617	hypothetical prote	782	32	71.1	486	2	B39481	serum response fac
710	32	71.1	416	1	FOCH	transforming prote	783	32	71.1	487	2	S42442	nuclear protein BB
711	32	71.1	416	1	TVFVAC	transforming prote	784	32	71.1	488	2	A35156	cellulase (EC 3.2.
712	32	71.1	419	2	T10652	hypothetical prote	785	32	71.1	488	2	T32149	hypothetical prote
713	32	71.1	419	2	S56073	opaque-2 protein -	786	32	71.1	489	2	A45988	dentin matrix acid
714	32	71.1	419	2	T04886	DAG protein homol	787	32	71.1	489	2	B72518	hypothetical prote
715	32	71.1	420	2	T46910	hypothetical prote	788	32	71.1	490	1	IXBE33	alpha trans-induci
716	32	71.1	420	2	JC4716	zinc finger DNA-bi	789	32	71.1	490	2	J50689	virion protein 16
717	32	71.1	421	1	S11674	acrosin (EC 3.4.21	790	32	71.1	493	2	F84689	probable cytochrom
718	32	71.1	422	2	T32671	hypothetical prote	791	32	71.1	493	2	S34775	nicotinic acetylch
719	32	71.1	422	2	A83184	probable protein m	792	32	71.1	494	2	T02523	hypothetical prote
720	32	71.1	423	1	TVFV2E	transforming prote	793	32	71.1	495	2	T37936	hypothetical prote
721	32	71.1	423	2	T48121	hypothetical prote	794	32	71.1	499	2	I51257	retinoic acid rece
722	32	71.1	425	2	C64567	hypothetical prote	795	32	71.1	503	2	C84595	similar to pEARLI
723	32	71.1	426	2	JQ1696	fucosyltransferase	796	32	71.1	505	2	S72273	actin-depolymerizi
724	32	71.1	428	2	T47400	pistil extensin-li	797	32	71.1	506	2	B56201	transcription fact
725	32	71.1	430	2	JC2301	hypothetical prote	798	32	71.1	506	2	T19787	hypothetical prote
726	32	71.1	432	2	A82222	hypothetical 47.8K	799	32	71.1	507	2	S25831	myocyte-specific e
727	32	71.1	433	2	T09284	twitching motility	800	32	71.1	508	2	T09046	proline-rich prote
728	32	71.1	433	2	T07910	TEA domain-contain	801	32	71.1	510	2	F86649	hypothetical prote
729	32	71.1	434	2	T51450	hydroxyproline-ric	802	32	71.1	514	2	A56201	transcription fact
730	32	71.1	435	2	T51443	hypothetical prote	803	32	71.1	516	2	T00974	probable Srf6 prot
731	32	71.1	436	2	B55452	hypothetical prote	804	32	71.1	516	2	S28060	serum response fac
732	32	71.1	436	2	T07022	cartilage-derived	805	32	71.1	518	2	T45765	hypothetical prote
733	32	71.1	436	2	G71862	probable extensin	806	32	71.1	521	1	VCBEHB	glycoprotein gIII
734	32	71.1	438	1	XXWSN	alpha-(1,3)-fucosy	807	32	71.1	521	2	S54266	glycoprotein 9C -
735	32	71.1	438	2	T12494	phosphatidylcholin	808	32	71.1	526	2	A86274	F7A19.15 protein -
736	32	71.1	441	2	B86252	hypothetical prote	809	32	71.1	529	1	W7AD22	early E2A DNA-bind
737	32	71.1	441	2	T19306	hypothetical prote	810	32	71.1	529	1	W7AD25	early E2A DNA-bind
738	32	71.1	442	2	A38592	hypothetical prote	811	32	71.1	532	2	G84775	probable E2F5 fami
739	32	71.1	442	2	A38592	retinoic acid rece	812	32	71.1	532	2	S74453	hypothetical prote
740	32	71.1	443	1	C35991	Ca2+/H+ exchanger-	813	32	71.1	534	1	A48529	ubiquinol-cytochro
741	32	71.1	443	2	T17220	retinoic acid rece	814	32	71.1	538	2	C98308	aldehyde dehydroge
742	32	71.1	444	2	A48538	hypothetical prote	815	32	71.1	539	2	T28770	hypothetical prote
743	32	71.1	444	2	I51256	endothelin-3 recep	816	32	71.1	540	2	S44830	hypothetical prote
744	32	71.1	445	2	H96560	retinoic acid rece	817	32	71.1	541	2	T48811	F54P2.5 protein -
745	32	71.1	445	2	S00256	hypothetical prote	818	32	71.1	541	2	T48836	hypothetical prote
746	32	71.1	446	2	T49149	Krox-20 protein -	819	32	71.1	542	2	A44358	hypothetical prote
747	32	71.1	447	2	S37048	hypothetical prote	820	32	71.1	543	1	ERADDG	zyxin - chicken
748	32	71.1	447	2	B34714	cysteine proteinas	821	32	71.1	548	2	F96663	hypothetical prote
749	32	71.1	447	2	T49439	retinoic acid rece	822	32	71.1	553	2	T14354	probable somatic e
750	32	71.1	451	1	TVFV2C	hypothetical prote	823	32	71.1	557	2	S62522	nuclear protein SP
751	32	71.1	451	2	JC4199	gag-myc polyprotei	824	32	71.1	558	2	T50742	protoporphylin IX
752	32	71.1	451	2	A33903	heat-shock protein	825	32	71.1	559	1	C9HU	complement C9 prec
753	32	71.1	454	2	S06124	retinoic acid rece	826	32	71.1	563	2	JQ0623	nerve growth facto
754	32	71.1	456	2	S45137	retinoic acid rece	827	32	71.1	571	2	T08930	hypothetical prote
755	32	71.1	456	2	T33822	fushi tarazu segme	828	32	71.1	571	2	G84426	hypothetical prote
756	32	71.1	456	2	A40492	hypothetical prote	829	32	71.1	572	2	G02845	zyxin - human
757	32	71.1	458	2	A34714	early growth respo	830	32	71.1	575	2	H70906	probable ilvd prot
758	32	71.1	461	2	D96757	retinoic acid rece	831	32	71.1	577	2	T01945	hypothetical prote
759	32	71.1	462	1	QQBED4	hypothetical prote	832	32	71.1	581	2	E86408	F3H9.11 protein -

833	32	71.1	586	2	A41125	gamma-glutamyltran	906	32	71.1	811	2	C86326	hypothetical prote
834	32	71.1	590	2	G69095	glutamine-fructose	907	32	71.1	816	2	T17257	hypothetical prote
835	32	71.1	594	2	B48456	protein trihelix D	908	32	71.1	820	2	T00645	hypothetical prote
836	32	71.1	598	2	T48822	hypothetical prote	909	32	71.1	829	2	T33283	hypothetical prote
837	32	71.1	599	2	T01798	phosphorin-S - Vo	910	32	71.1	831	1	S76355	DNA helicase regc
838	32	71.1	601	1	QRM5N1	probable hormone x	911	32	71.1	852	2	G87304	hypothetical prote
839	32	71.1	601	2	H96740	hypothetical prote	912	32	71.1	852	2	T33824	hypothetical prote
840	32	71.1	602	2	T45760	hypothetical prote	913	32	71.1	878	2	H87315	hypothetical prote
841	32	71.1	615	2	A05269	collagen alpha 1(I	914	32	71.1	880	2	T48477	hypothetical prote
842	32	71.1	618	2	JC4366	transcription fact	915	32	71.1	884	2	D96730	unknown protein F5
843	32	71.1	622	2	T02244	probable DNA repai	916	32	71.1	886	2	A54442	3',5'-cyclic-nucle
844	32	71.1	628	2	D86466	69.4K hypothetical	917	32	71.1	888	2	JC5399	dual leucine zippe
845	32	71.1	631	2	T05016	hypothetical prote	918	32	71.1	888	2	A55318	serine/threonine p
846	32	71.1	633	2	F84564	probable protein k	919	32	71.1	896	2	B43817	transforming prote
847	32	71.1	639	2	H86362	hypothetical prote	920	32	71.1	898	2	T14764	hypothetical prote
848	32	71.1	641	2	JC7331	gamma-glutamyltran	921	32	71.1	905	2	A54654	centromere protein
849	32	71.1	642	2	T05683	hypothetical 70K p	922	32	71.1	923	2	I53280	progesterone recep
850	32	71.1	649	2	JQ0103	hypothetical 70K p	923	32	71.1	924	2	T06636	hypothetical prote
851	32	71.1	652	2	H86221	hypothetical prote	924	32	71.1	924	2	A44945	104K microne-mrho
852	32	71.1	656	1	Q08ET2	U25 protein - hum	925	32	71.1	952	2	T02751	DNA-directed RNA p
853	32	71.1	660	2	C82861	topoisomerase I XF	926	32	71.1	955	2	E84845	probable villin 2
854	32	71.1	662	1	A31349	arachidonate 15-11	927	32	71.1	962	2	T00262	hypothetical prote
855	32	71.1	662	2	T00497	polyadenylate-bind	928	32	71.1	963	2	T48707	related to regulat
856	32	71.1	663	2	S32825	arachidonate 12-11	929	32	71.1	970	2	D59435	Gem-interacting pr
857	32	71.1	664	2	C84747	probable protein k	930	32	71.1	972	2	T22488	hypothetical prote
858	32	71.1	664	2	T04013	hypothetical prote	931	32	71.1	974	2	T04910	hypothetical prote
859	32	71.1	664	2	T01368	hypothetical prote	932	32	71.1	976	2	T50669	villin 2 [imported
860	32	71.1	664	2	T33379	hypothetical prote	933	32	71.1	999	2	JC5278	oxygen-regulated p
861	32	71.1	669	2	S65551	factor H - bovine	934	32	71.1	999	2	S28897	glucose regulated
862	32	71.1	670	2	D86457	hypothetical prote	935	32	71.1	1001	2	T68689	hypothetical prote
863	32	71.1	671	2	T02504	hypothetical prote	936	32	71.1	1006	2	T42731	atrophin-1 related
864	32	71.1	679	2	A42073	potassium channel	937	32	71.1	1013	2	T46422	hypothetical prote
865	32	71.1	681	2	F85062	hypothetical prote	938	32	71.1	1014	2	T18759	hypothetical prote
866	32	71.1	693	2	T01122	probable serine/th	939	32	71.1	1018	2	S44758	CI4B9.6 protein -
867	32	71.1	694	2	T01005	hypothetical prote	940	32	71.1	1026	2	T20369	hypothetical prote
868	32	71.1	695	2	T24950	hypothetical prote	941	32	71.1	1027	2	T46296	hypothetical prote
869	32	71.1	700	2	S09899	bib protein - fru	942	32	71.1	1032	2	D83637	serine/threonine p
870	32	71.1	707	2	S60588	drebrin A - rat	943	32	71.1	1032	2	T18293	guanylate kinase-1
871	32	71.1	708	2	C86404	probable protein A	944	32	71.1	1039	2	T22117	hypothetical prote
872	32	71.1	711	2	S43464	ecdysteroid-induce	945	32	71.1	1047	2	A55617	masquerade precurs
873	32	71.1	713	1	S46838	hypothetical prote	946	32	71.1	1059	2	T20802	hypothetical prote
874	32	71.1	716	2	S45262	NP-AT component -	947	32	71.1	1075	2	T27623	hypothetical prote
875	32	71.1	728	2	T43632	serine/threonine p	948	32	71.1	1080	2	T27622	hypothetical prote
876	32	71.1	729	2	E70803	hypothetical prote	949	32	71.1	1091	1	IJCXNL	neural cell adhesi
877	32	71.1	730	2	A53064	folded gastrulatio	950	32	71.1	1092	2	T18305	replication factor
878	32	71.1	731	1	A55800	cucumislin (BC 3.4	951	32	71.1	1092	2	T18306	replication factor
879	32	71.1	731	2	B86369	hypothetical prote	952	32	71.1	1096	2	T48512	hypothetical prote
880	32	71.1	734	2	T04876	hypothetical prote	953	32	71.1	1097	2	T13033	cyclin T - fruit f
881	32	71.1	736	2	JH0681	gephyrin - rat	954	32	71.1	1100	2	T30967	transcription acti
882	32	71.1	737	2	S28030	DNA-binding protei	955	32	71.1	1108	2	A48508	cyclic-nucleotide
883	32	71.1	743	2	T09173	EH domain protein	956	32	71.1	1110	2	I59370	guanylate cyclase
884	32	71.1	745	2	T51370	hypothetical prote	957	32	71.1	1118	2	A48292	mucin, tracheobron
885	32	71.1	747	2	T23042	hypothetical prote	958	32	71.1	1120	2	JC7765	mitotic spindle as
886	32	71.1	747	2	S46608	hypothetical prote	959	32	71.1	1129	2	T19779	hypothetical prote
887	32	71.1	748	2	T49633	VTAl1 protein - ye	960	32	71.1	1139	2	A49370	BLA-associated cyc
888	32	71.1	749	2	T23045	hypothetical prote	961	32	71.1	1171	2	T13065	PIP82 protein - fr
889	32	71.1	755	2	T47731	hypothetical prote	962	32	71.1	1172	2	T00065	hypothetical prote
890	32	71.1	756	2	S74742	exopolysaccharide	963	32	71.1	1173	2	T31421	C-terminal domain-
891	32	71.1	760	2	B96724	hypothetical prote	964	32	71.1	1184	2	S50832	atrophin-1 - human
892	32	71.1	761	1	IJHUNG	neural cell adhesi	965	32	71.1	1184	2	G01763	atrophin-1 - human
893	32	71.1	762	2	C96853	hypothetical prote	966	32	71.1	1185	2	T19212	hypothetical prote
894	32	71.1	769	2	I56546	Shaw type potaasin	967	32	71.1	1193	2	T32016	hypothetical prote
895	32	71.1	769	2	S55554	male-specific leth	968	32	71.1	1201	2	T29329	hypothetical prote
896	32	71.1	772	2	T13078	KIAA0992 protein -	969	32	71.1	1206	2	S24407	formin isoform IV
897	32	71.1	773	2	A56720	mal-2 protein - fr	970	32	71.1	1213	2	S16356	ovo protein - fru
898	32	71.1	778	2	T38487	tastin - human	971	32	71.1	1213	2	A41724	limb deformity (ld
899	32	71.1	783	2	T01015	probable subtilisi	972	32	71.1	1216	2	T34101	hypothetical prote
900	32	71.1	786	1	A47547	serine proteinase	973	32	71.1	1226	2	T24045	hypothetical prote
901	32	71.1	791	2	C82940	hypothetical prote	974	32	71.1	1244	2	S76102	hypothetical prote
902	32	71.1	792	2	T43630	serine/threonine p	975	32	71.1	1252	2	T14272	cortactin-binding
903	32	71.1	801	2	T52605	squamosa promoter	976	32	71.1	1258	2	T29041	hypothetical prote
904	32	71.1	802	1	B44390	protein-tyrosine-p	977	32	71.1	1271	2	T49009	protein kinase lik
905	32	71.1	803	2	S76106	hypothetical prote	978	32	71.1	1275	2	T38397	probable GTPase ac

979 32 71.1 1276 2 E96776  
 980 32 71.1 1297 2 S25714  
 981 32 71.1 1313 2 F96673  
 982 32 71.1 1335 2 T18289  
 983 32 71.1 1339 1 S20052  
 984 32 71.1 1353 2 T00249  
 985 32 71.1 1388 2 A53317  
 986 32 71.1 1392 2 T51947  
 987 32 71.1 1400 2 T52359  
 988 32 71.1 1418 2 T37264  
 989 32 71.1 1434 2 T30172  
 990 32 71.1 1461 2 T41643  
 991 32 71.1 1468 2 S11515  
 992 32 71.1 1612 2 T30805  
 993 32 71.1 1621 2 T15264  
 994 32 71.1 1638 2 A42091  
 995 32 71.1 1651 2 T14160  
 996 32 71.1 1692 2 G01449  
 997 32 71.1 1733 1 B45344  
 998 32 71.1 1777 2 T34369  
 999 32 71.1 1802 2 H88444  
 1000 32 71.1 1819 2 T32008

## ALIGNMENTS

RESULT 1  
 T02071  
 C:Species: glyceraldehyde-3-phosphate dehydrogenase (NADP) (phosphorylating) (EC 1.2.1.13) A - rice  
 C:Species: Oryza sativa (rice)  
 C>Date: 26-Feb-1999 #sequence\_revision 26-Feb-1999 #text\_change 09-Jul-2004  
 C:Accession: T02071  
 R:Lee, M.C.; Kim, C.S.; Eun, M.Y.  
 submitted to the EMBL Data Library, September 1997  
 A:Description: Isolation and characterization of glyceraldehyde-3-phosphate dehydrogenase  
 A:Reference number: Z14541  
 A:Accession: T02071  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-343 <LEE>  
 A:Cross-references: UNIPROT:O22534; UNIPARC:UPI000009F325; EMBL:AF022730; NID:G2570494;  
 A:Experimental source: strain Milyang 2  
 C:Genetics:  
 A:Gene: GAPDH  
 C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase  
 C:Keywords: oxidoreductase

Query Match 91.1%; Score 41; DB 2; Length 343;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPDPCC 7  
 |||||  
 Db 6 SPDPCC 11

RESULT 2  
 T14192  
 extensin homolog T28D5.70 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
 C:Accession: T14192  
 R:Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro  
 submitted to the Protein Sequence Database, August 1999  
 A:Reference number: Z17931  
 A:Accession: T14192  
 A:Molecule type: DNA  
 A:Residues: 1-437 <BEV>  
 A:Cross-references: UNIPROT:O9STNO; UNIPARC:UPI000009D4CF; EMBL:AL109819  
 A:Experimental source: cultivar Columbia; BAC clone T28D5  
 C:Genetics:  
 A:Gene: ATSP:T28D5.70

A:Map position: 4  
 C:Superfamily: hydroxyproline-rich glycoprotein  
 Query Match 91.1%; Score 41; DB 2; Length 437;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPDPCC 7  
 |||||  
 Db 390 SPDPCC 395

## RESULT 3

T04748  
 hypothetical protein T16H5.30 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
 C:Accession: T04748  
 R:Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Bancroft, I.; Mewes, H.W.; Mayer,  
 submitted to the Protein Sequence Database, June 1998  
 A:Reference number: Z15383  
 A:Accession: T04748  
 A:Molecule type: DNA  
 A:Residues: 1-532 <BEV>  
 A:Cross-references: UNIPROT:O81849; UNIPARC:UPI000009CEE7; EMBL:AL024486  
 A:Experimental source: cultivar Columbia; BAC clone T16H5  
 C:Genetics:  
 A:Map position: 4  
 A:Introns: 141/3; 397/2  
 A>Note: T16H5.30

Query Match 91.1%; Score 41; DB 2; Length 532;  
 Best Local Similarity 100.0%; Pred. No. 90;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPDPCC 7  
 |||||  
 Db 490 SPDPCC 495

## RESULT 4

E86255  
 hypothetical protein [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C:Accession: E86255  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.,  
 ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: E86255  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-744 <STO>  
 A:Cross-references: UNIPROT:O65375; UNIPARC:UPI00000A65A5; GB:AE005172; NID:G3157926; P  
 C:Genetics:  
 A:Map position: 1

Query Match 91.1%; Score 41; DB 2; Length 744;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPDPCC 7  
 |||||  
 Db 528 SPDPCC 533

RESULT 5  
T02034  
early light-induced protein, low molecular weight - rice  
C;Species: Oryza sativa (rice)  
C;Date: 26-Feb-1999 #sequence\_revision 26-Feb-1999 #text\_change 09-Jul-2004  
C;Accession: T02034  
R;Lee, M.C.; Kim, C.S.; Eun, M.Y.  
submitted to the EMBL Data Library, August 1997  
A;Description: Isolation and characterization of low molecular early light-inducible protein  
A;Reference number: Z14505  
A;Accession: T02034  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-157 <LEE>  
A;Cross-references: UNIPROT:O22480; UNIPARC:UPI00000A4237; EMBL:AF017356; NID:G2407266;  
A;Experimental source: strain Milyang 23  
C;Superfamily: early light-induced protein

Query Match 88.9%; Score 40; DB 2; Length 157;  
Best Local Similarity 85.7%; Pred. No. 40;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
DB 130 SPPPPPC 136

RESULT 6  
T46446  
hypothetical protein DKFPz434G0128.1 - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, January 2000  
A;Reference number: Z23032  
A;Accession: T46446  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-246 <AAA>  
A;Cross-references: UNIPROT:P17483; UNIPARC:UPI000016ACB8; EMBL:AL137449  
A;Experimental source: adult testis; clone DKFPz434G0128  
C;Genetics:  
A;Note: DKFPz434G0128.1  
C;Superfamily: homeotic protein Hox D4; homeobox homology  
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 88.9%; Score 40; DB 2; Length 246;  
Best Local Similarity 85.7%; Pred. No. 61;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
DB 111 SPPPPPC 117

RESULT 7  
A31757  
homeotic protein Hox B4 - mouse  
N;Alternate names: Homeotic protein Hox 2.6  
C;Species: Mus musculus (house mouse)  
C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: A31757  
R;Graham, A.; Papalopulu, N.; Lorimer, J.; McVey, J.H.; Tuddenham, E.G.D.; Krumlauf, R.  
Genes Dev. 2, 1424-1438, 1988  
A;Title: Characterization of a murine homeo box gene, Hox-2.6, related to the Drosophila  
A;Reference number: A31757; MUID:89091992; PMID:2463210  
A;Accession: A31757  
A;Molecule type: DNA  
A;Residues: 1-250 <GRA>  
A;Cross-references: UNIPROT:P10284; UNIPARC:UPI0000026E78; EMBL:M36654; NID:g193943; PID:  
C;Genetics:

A;Gene: Hoxb-4  
A;Map position: 11  
A;Introns: 151/3  
C;Function:  
A;Description: control of embryonic development by tissue- and stage-specific regulation  
C;Superfamily: homeotic protein Hox D4; homeobox homology  
C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation  
F;162-219/Domain: homeobox homology <HOX>

Query Match 88.9%; Score 40; DB 1; Length 250;  
Best Local Similarity 85.7%; Pred. No. 61;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
DB 115 SPPPPPC 121

RESULT 8  
B60492  
homeotic protein Hox B4 - human  
N;Alternate names: homeotic protein Hox 2.6; homeotic protein Hox 2F  
C;Species: Homo sapiens (man)  
C;Date: 19-Mar-1993 #sequence\_revision 19-Mar-1993 #text\_change 09-Jul-2004  
C;Accession: B60492; C37042; S15543  
R;Reverali, F.A.; D'Esposito, M.; Acampora, D.; Bunone, G.; Negri, M.; Faiella, A.; Sto  
Differentiation 45, 61-69, 1990  
A;Title: Expression of HOX homeogenes in human neuroblastoma cell culture lines.  
A;Reference number: A60492; MUID:91153613; PMID:1981366  
A;Accession: B60492  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-231 <PEV>  
A;Cross-references: UNIPROT:P17483; UNIPARC:UPI0000062329  
R;Giampaolo, A.; Acampora, D.; Zappavigna, V.; Pannese, M.; D'Esposito, M.; Care, A.; F  
Differentiation 40, 191-197, 1989  
A;Title: Differential expression of human HOX-2 genes along the anterior-posterior axis  
A;Reference number: A37042; MUID:89378558; PMID:2570724  
A;Accession: C37042  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 160-227 <GTA>  
A;Cross-references: UNIPARC:UPI000016AA86; GB:X16174; NID:G32376; PIDN:CRA34296.1; PID:  
R;Boncinelli, E.; Acampora, D.; Zappavigna, V.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; St  
Genome 31, 745-756, 1989  
A;Title: Organization of human class I homeobox genes.  
A;Reference number: S15036; MUID:90215256; PMID:2576652  
A;Accession: S15543  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 162-227 <BON>  
A;Cross-references: UNIPARC:UPI00001745B5  
C;Genetics:  
A;Gene: GDB:HOXB4  
A;Cross-references: GDB:120663; OMIM:142965  
A;Map position: 17q21.3-17q21.3  
C;Function:  
A;Description: control of embryonic development by tissue- and stage-specific regulation  
C;Superfamily: homeotic protein Hox D4; homeobox homology  
C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation  
F;163-219/Domain: homeobox homology <HOX>

Query Match 88.9%; Score 40; DB 1; Length 251;  
Best Local Similarity 85.7%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
DB 116 SPPPPPC 122

RESULT 9  
A47234

homeobox protein H6 - human  
C:Species: Homo sapiens (man)  
C>Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 31-Dec-2004  
C:Accession: A47234  
R:Stadler, H.S.; Padanilam, B.J.; Buetow, K.; Murray, J.C.; Solursh, M.  
Proc. Natl. Acad. Sci. U.S.A. 89; 11579-11583, 1992  
A>Title: Identification and genetic mapping of a homeobox gene to the 4p16.1 region of h  
A:Reference number: A47234; MUID:93087572; PMID:1360670  
A:Accession: A47234  
A>Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-373 <STA>  
A:Cross-references: UNIPROT:Q9NP08; UNIPARC:UPI000006CCDF  
A:Experimental source: embryo craniofacial region  
A>Note: sequence extracted from NCBI backbone (NCBIN:119953, NCBIIP:119955)  
A:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F:201-257/Domain: homeobox homology <Hox>

Query Match 88.9%; Score 40; DB 2; Length 373;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
| | | | |  
Db 327 SRPPPPC 333

RESULT 10  
B42560  
4-chlorobenzoate-CoA ligase (EC 6.2.1.-) - Pseudomonas sp. (strain CBS-3)  
N:Alternate names: 4-chlorobenzoate dehalogenase 57K chain component  
C:Species: Pseudomonas sp.  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 26-May-2000  
R:Babbitt, P.C.; Kenyon, G.L.; Martin, B.M.; Charest, H.; Slyvestre, M.; Scholten, J.D.;  
Biochemistry 31; 5594-5604, 1992  
A>Title: Ancestry of the 4-chlorobenzoate dehalogenase: analysis of amino acid sequence  
A:Reference number: A42560; MUID:92304934; PMID:1351742  
A:Accession: B42560  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-528 <BAB>  
A:Cross-references: UNIPARC:UPI000017621E  
C:Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology  
C:Keywords: acid-thiol ligase; hydrolase  
F:49-496/Domain: acetate-CoA ligase homology <ACL>

Query Match 86.7%; Score 39; DB 2; Length 528;  
Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
| | | | |  
Db 144 SUPPPPC 150

RESULT 11  
T00273  
hypothetical protein KIAA0595 - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 09-Jul-2004  
C:Accession: T00273  
R:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.  
DNA Res. 5; 31-39, 1998  
A>Title: Prediction of the coding sequences of unidentified human genes. IX. The complet  
A:Reference number: Z14086; MUID:98290545; PMID:9628581  
A:Accession: T00273  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-1520 <NAG>  
A:Cross-references: UNIPROT:Q9B2E5; UNIPARC:UPI000017C1B8; EMBL:AB011167; NID:G3043713;  
A:Experimental source: brain  
C:Genetics:

A>Note: KIAA0595

Query Match 86.7%; Score 39; DB 2; Length 1520;  
Best Local Similarity 71.4%; Pred. No. 4.4e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
| | | | |  
Db 1196 AAPPPPC 1202

RESULT 12  
T18397  
protein CTRP - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T18397  
R:Trottein, F.; Triglia, T.; Cowman, A.F.  
Mol. Biochem. Parasitol. 74; 129-142, 1995  
A>Title: Molecular cloning of a gene from Plasmodium falciparum that codes for a protein  
A:Reference number: Z18926; MUID:96360471; PMID:8719155  
A:Accession: T18397  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-2098 <TRO>  
A:Cross-references: UNIPROT:Q25757; UNIPARC:UPI000008040C; EMBL:U34363; NID:G1098897; P1

Query Match 86.7%; Score 39; DB 2; Length 2098;  
Best Local Similarity 85.7%; Pred. No. 5.9e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
| | | | |  
Db 67 SVPPPPC 73

RESULT 13  
G86164  
protein F15K9.8 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: G86164  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408; 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: G86164  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-220 <STO>  
A:Cross-references: UNIPROT:Q9ZVT3; UNIPARC:UPI00000A8AE3; GB:AE005172; NID:G3850572; P1  
C:Genetics:  
A:Gene: F15K9.8  
A:Map position: 1

Query Match 84.4%; Score 38; DB 2; Length 220;  
Best Local Similarity 83.3%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7  
| | | | |  
Db 100 NPPPPC 105

RESULT 14  
T00204

LDL receptor related protein 105 - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 09-Jul-2004  
C/Accession: T00204  
R/Ighif, H.; Kim, D.H.; Fujita, T.; Endo, Y.; Saeki, S.; Yamamoto, T.T.  
Genomics 51, 132-135, 1998  
A/Title: CDNA cloning of a new low-density lipoprotein receptor-related protein and map  
A/Reference number: Z14121, MUID:98360101, PMID:9693042  
A/Accession: T00204  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-770 <ISH>  
A/Cross-references: UNIPROT:O75074; UNIPARC:UPI0000047A9D; EMBL:AB009462; NID:g3413957;  
C/Genetics:  
A/Gene: hLRp105  
F/166-200/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F/212-249/Domain: LDL receptor ligand-binding repeat homology <LDL>  
F/416-452/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
F/455-489/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
  
Query Match 84.4%; Score 38; DB 2; Length 770;  
Best Local Similarity 83.3%; Pred. No. 3.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 SPDPCC 7  
:|||||  
Db 750 NPPPPC 755  
  
RESULT 15  
T14756  
hypothetical protein DKPZp564F0923.1 - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: T14756  
R/Wambutt, R.; Heubner, D.; Meves, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, August 1999  
A/Reference number: Z18181  
A/Accession: T14756  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-990 <WAM>  
A/Cross-references: UNIPROT:Q9UG03; UNIPARC:UPI0000071BED; EMBL:AL110210  
A/Experimental source: fetal brain; clone DKPZp564F0923  
C/Genetics:  
A/Note: DKPZp564F0923.1  
  
Query Match 84.4%; Score 38; DB 2; Length 990;  
Best Local Similarity 83.3%; Pred. No. 4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 SPDPCC 7  
:|||||  
Db 258 APPPPC 263  
  
RESULT 16  
G86292  
hypothetical protein F7H2.17 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C/Accession: G86292  
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: G86292  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1006 <STO>  
A/Cross-references: UNIPROT:Q9LMQ1; UNIPARC:UPI000000A2407; GB:AB005172; NID:g8927662; P  
C/Genetics:  
A/Map position: 1  
  
Query Match 84.4%; Score 38; DB 2; Length 1006;  
Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 SPDPCC 7  
:|||||  
Db 371 APPPPC 376  
  
RESULT 17  
S62048  
probable membrane protein YGL197w - yeast (Saccharomyces cerevisiae)  
N/Alternate names: hypothetical protein G1307  
C/Species: Saccharomyces cerevisiae  
C/Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
C/Accession: S62048; S64214  
R/Klima, R.; Coglievina, M.; Bertani, I.; Zaccaria, P.; Bruschi, C.V.  
submitted to the EMBL Data Library, September 1995  
A/Reference number: S62045  
A/Accession: S62048  
A/Molecule type: DNA  
A/Residues: 1-1487 <KLI>  
A/Cross-references: UNIPROT:P53094; UNIPARC:UPI0000052E6A; EMBL:X91837; NID:g1177627; P  
R/Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.  
submitted to the Protein Sequence Database, May 1996  
A/Reference number: S64183  
A/Accession: S64214  
A/Molecule type: DNA  
A/Residues: 1-1487 <BRU>  
A/Cross-references: UNIPARC:UPI0000052E6A; EMBL:Z72719; NID:g1322824; PID:e243500; PID:  
A/Experimental source: strain S288C  
C/Genetics:  
A/Gene: SGD:MDS3  
A/Cross-references: SGD:S0003165; MIPS:YGL197w  
A/Map position: 7L  
C/Keywords: transmembrane protein  
F/1034-1050/Domain: transmembrane #status predicted <TM1>  
F/1052-1068/Domain: transmembrane #status predicted <TM2>  
  
Query Match 84.4%; Score 38; DB 2; Length 1487;  
Best Local Similarity 71.4%; Pred. No. 5.8e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 SPDPCC 7  
:|||||  
Db 873 NPPPPC 879  
  
RESULT 18  
S03295  
Ig alpha chain C region - chimpanzee (fragment)  
C/Species: Pan troglodytes (chimpanzee)  
C/Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 23-Jul-1999  
C/Accession: S03295  
R/Ueda, S.; Matsuda, F.; Honjo, T.  
J. Mol. Evol. 27, 77-83, 1988  
A/Title: Multiple recombinational events in primate immunoglobulin epsilon and alpha ge  
A/Reference number: S03295; MUID:88259241; PMID:3133489  
A/Accession: S03295  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-31 <UED>  
A/Cross-references: UNIPARC:UPI0000115DAD; EMBL:X08040; NID:g38233; PIDN:CAA30840.1; P  
C/Genetics:

A;Introns: 13/1  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 C;Keywords: immunoglobulin

Query Match 82.2%; Score 37; DB 2; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
 |||||  
 Db 15 PPPPC 19

## RESULT 19

A86584  
 C;Species: Chlamydomonas reinhardtii - Chlamydomonas reinhardtii (strain J138)  
 C;Species: Chlamydomonas reinhardtii, Chlamydomonas reinhardtii  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C;Accession: A86584  
 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, K.; Kishi, T.; Shiba, T.; Ise  
 Nucleic Acids Res. 28, 2311-2314, 2000  
 A;Title: Comparison of whole genome sequences of Chlamydomonas reinhardtii J138.  
 A;Reference number: A86491; MUID:20330349; PMID:10871362  
 A;Accession: A86584  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-103 <STO>  
 A;Cross-references: UNIPROT:Q5JSA8; UNIPARC:UPI00000CCD21; GB:BA000008; NID:g8979120; PI  
 A;Experimental source: strain J138  
 C;Genetics:  
 A;Gene: CPJ0747\_2

Query Match 82.2%; Score 37; DB 2; Length 103;  
 Best Local Similarity 100.0%; Pred. No. 70;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
 |||||  
 Db 47 PPPPC 51

## RESULT 20

T22564  
 C;Species: Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T22564  
 R;Burton, J.  
 submitted to the EMBL Data Library, October 1996  
 A;Reference number: Z19583  
 A;Accession: T22564  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-105 <WIL>  
 A;Cross-references: UNIPROT:Q9XVM6; UNIPARC:UPI0000061078; EMBL:Z81088; FIDN:CAB03125.1;  
 A;Experimental source: clone F53F1  
 C;Genetics:  
 A;Gene: CESP.F53F1.4  
 A;Map position: 5  
 A;Introns: 30/2

Query Match 82.2%; Score 37; DB 2; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 71;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
 |||||  
 Db 34 PPPPC 38

## RESULT 21

A86271  
 F21F23.19 protein - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C;Accession: A86271  
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: A86271  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-119 <STO>  
 A;Cross-references: UNIPROT:Q9LMX3; UNIPARC:UPI00000A4143; GB:AE005172; NID:g8920579; PI  
 C;Genetics:  
 A;Map position: 1

Query Match 82.2%; Score 37; DB 2; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 80;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
 |||||  
 Db 58 PPPPC 62

## RESULT 22

A72678  
 C;Species: Aeropyrum pernix  
 C;Species: Aeropyrum pernix  
 C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
 C;Accession: A72678  
 R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah  
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K  
 DNA Res. 6, 83-101, 1999  
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum  
 A;Reference number: A72450; MUID:99310339; PMID:10382966  
 A;Accession: A72678  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-128 <KAW>  
 A;Cross-references: UNIPROT:Q9YDS2; UNIPARC:UPI000005DCSE; DBJ:AP000060; NID:g5104188;  
 A;Experimental source: strain K1  
 C;Genetics:  
 A;Gene: APE0845

Query Match 82.2%; Score 37; DB 2; Length 128;  
 Best Local Similarity 85.7%; Pred. No. 85;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPPC 7  
 |||||  
 Db 42 SSPPPPPC 48

## RESULT 23

B41132  
 C;Species: Hydra magnipapillata  
 C;Species: Hydra magnipapillata (fragment)  
 C;Date: 05-Jun-1992 #sequence\_revision 05-Jun-1992 #text\_change 15-Sep-2003  
 C;Accession: B41132; S21930  
 R;Kurz, E.M.; Holstein, T.W.; Petri, B.M.; Engel, J.; David, C.N.  
 J. Cell Biol. 115, 1159-1169, 1991  
 A;Title: Mini-collagens in hydra nematocytes.  
 A;Reference number: A41132; MUID:92064646; PMID:1955459  
 A;Accession: B41132  
 A;Status: preliminary  
 A;Molecule type: mRNA

A;Residues: 1-142 <KUR>  
A;Cross-references: UNIPARC:UPI000007BD62; EMBL:X61046; NID:G9448; PIDN:CAA43380.1; PID:  
A;Note: submitted to the EMBL Data Library, July 1991

Query Match 82.2%; Score 37; DB 2; Length 142;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 117 PPPPC 121

#### RESULT 24

S37485  
gene mag1 protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Oct-2004

C;Accession: I48669; S37485

R;Ironak-Le Roux, D.; Senorale-Pose, M.; Rougeon, F.

Gene 142, 175-182, 1994

A;Title: Three novel SMR1-related cDNAs characterized in the submaxillary gland of mice

A;Reference number: I48669; MUID:94252564; PMID:8194749

A;Accession: I48669

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-147 <RES>

A;Cross-references: UNIPROT:Q61900; UNIPARC:UPI0000023168; EMBL:X71629; NID:G406256; PID:

C;Genetics:

A;Gene: mag1

C;Superfamily: Proline-rich peptide P-B

Query Match 82.2%; Score 37; DB 2; Length 147;

Best Local Similarity 100.0%; Pred. No. 97;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 75 PPPPC 79

#### RESULT 25

A41132

collagen-related protein 1 precursor - Hydra magnipapillata

C;Species: Hydra magnipapillata

C;Date: 05-Jun-1992 #sequence\_revision 05-Jun-1992 #text\_change 15-Sep-2003

C;Accession: A41132; S21929

R;Kurz, E.M.; Holstein, T.W.; Petri, B.M.; Engel, J.; David, C.N.

J. Cell Biol. 115, 1159-1169, 1991

A;Title: Mini-collagens in hydra nematocytes.

A;Reference number: A41132; MUID:92064646; PMID:1955459

A;Accession: A41132

A;Molecule type: mRNA

A;Status: preliminary

A;Residues: 1-149 <KUR>

A;Cross-references: UNIPARC:UPI000007667C; EMBL:X61045; NID:G9446; PIDN:CAA43379.1; PID:  
A;Note: submitted to the EMBL Data Library, July 1991

Query Match 82.2%; Score 37; DB 2; Length 149;

Best Local Similarity 100.0%; Pred. No. 98;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 123 PPPPC 127

#### RESULT 26

D48232

cysteine-rich extensin-like protein 4 precursor - common tobacco (fragment)

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004

C;Accession: D48232

R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.  
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993  
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain  
A;Reference number: A48232; MUID:93342083; PMID:8341705

A;Accession: D48232

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-160 <WUA>

A;Cross-references: UNIPROT:Q08197; UNIPARC:UPI000017766F; GB:L13442

A;Note: authors failed to translate the codon GCT for residue 11 as Ala, and GTA for residue 117

A;Note: authors translated the codon TCT for residue 60 as Pro, and CCA for residue 117

C;Genetics:

A;Gene: CELP-4

C;Superfamily: glutelin

C;Keywords: cell wall; extracellular matrix; fertilization; glycoprotein

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-159/Product: cysteine-rich extensin-like protein 4 #status experimental <MAT>

Query Match 82.2%; Score 37; DB 2; Length 160;

Best Local Similarity 100.0%; Pred. No. 18+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 73 PPPPC 77

#### RESULT 27

E48232

cysteine-rich extensin-like protein 5 precursor - common tobacco

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004

C;Accession: E48232

R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.

Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993

A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain

A;Reference number: A48232; MUID:93342083; PMID:8341705

A;Accession: E48232

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-161 <WUA>

A;Cross-references: UNIPROT:Q08198; UNIPARC:UPI00000A99C3; GB:L13443; NID:G310930; PIDN:

C;Genetics:

A;Gene: CELP-5

C;Superfamily: glutelin

C;Keywords: cell wall; extracellular matrix; fertilization; glycoprotein

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-160/Product: cysteine-rich extensin-like protein 5 #status experimental <MAT>

Query Match 82.2%; Score 37; DB 2; Length 161;

Best Local Similarity 100.0%; Pred. No. 18+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 74 PPPPC 78

#### RESULT 28

T33130

hypothetical protein C23H5.9 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T33130

R;Lamar, E.; Kramer, J.

submitted to the EMBL Data Library, May 1998

A;Description: The sequence of C. elegans cosmid C23H5.

A;Reference number: Z21286

A;Accession: T33130

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-163 <LAM>

A;Cross-references: UNIPROT:O61832; UNIPARC:UPI0000080484; EMBL:AF067609; PIDN:AAC17537

A:Experimental source: strain Bristol N2; clone C23H5

C:Genetics:

A:Gene: CESP:C23H5.9

A:Map position: 4

A:Introns: 1/3; 101/3; 126/2

Query Match 82.2%; Score 37; DB 2; Length 163;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7

Db 66 PPPPC 70

RESULT 29

C48232

Cysteine-rich extensin-like protein 3 precursor - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004

C:Accession: C48232

R:Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.

Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993

A:Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain

A:Reference number: A48232; MUID:93342083; PMID:8341705

A:Accession: C48232

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-165 <WUA>

A:Cross-references: UNIPROT:Q08186; UNIPARC:UPI00000AA5D7; GB:L13441; NID:g310926; PIDN:

A:Note: authors translated the codon GAT for residue 35 as Glu

C:Genetics:

A:Gene: CELP-3

C:Superfamily: glutelin

C:Keywords: cell wall; extracellular matrix; fertilization; glycoprotein

F:1-15/Domain: signal sequence #status predicted <SIG>

F:20-165/Product: cysteine-rich extensin-like protein 3 #status experimental <MAT>

Query Match 82.2%; Score 37; DB 2; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7

Db 71 PPPPC 75

RESULT 30

RKZS

Ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - rice

C:Species: Oryza sativa (rice)

C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004

C:Accession: S01235

R:Xie, Y.; Wu, R.

Nucleic Acids Res. 16, 7749, 1988

A:Title: Nucleotide sequence of a ribulose-1,5-bisphosphate carboxylase/oxygenase small

A:Reference number: S01235; MUID:88319987; PMID:3412915

A:Accession: S01235

A:Molecule type: DNA

A:Residues: 1-172 <XIE>

A:Cross-references: UNIPROT:P05347; UNIPARC:UPI000013339F; EMBL:X07515; NID:g20340; PIDN

C:Comment: Ribulose-bisphosphate carboxylase, a major component of leaf protein, is also

helic carbon dioxide fixation) as well as the oxidative fragmentation of the pentose sub

ive site.

C:Comment: Each active molecule contains eight large chains, synthesized on the chloropl

n cytoplasmic ribosomes and converted to mature small chains during or immediately after

C:Comment: This protein is coded by one member of a small multigene family.

C:Genetics:

A:Gene: rbcS

A:Introns: 47/3

C:Superfamily: ribulose-bisphosphate carboxylase small chain

C:Keywords: Calvin cycle; carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase; c

F:1-45/Domain: transit peptide (chloroplast) #status predicted <TNP>

F:46-172/Product: ribulose-bisphosphate carboxylase small chain #status predicted <MAT>

Query Match 82.2%; Score 37; DB 1; Length 172;

Best Local Similarity 85.7%; Pred. No. 1.1e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7

Db 19 SSPPPPC 25

RESULT 31

T27505

hypothetical protein ZC168.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T27505

R:Berkas, W.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z20378

A:Accession: T27505

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-172 <WIL>

A:Cross-references: UNIPROT:Q23248; UNIPARC:UPI00000813B6; EMBL:Z70312; PIDN:CAA94385.1;

A:Experimental source: clone ZC168

C:Genetics:

A:Gene: CESP:ZC168.5

A:Map position: 4

A:Introns: 112/3

Query Match 82.2%; Score 37; DB 2; Length 172;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7

Db 43 PPPPC 47

RESULT 32

S22990

zein, 27K - maize (fragment)

C:Species: Zea mays (maize)

C:Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C:Accession: S22990; S14852

R:Das, O.P.; Poliak, E.; Ward, K.; Messing, J.

Nucleic Acids Res. 19, 3325-3330, 1991

A:Title: A new allele of the duplicated 27kD zein locus of maize generated by homologous

A:Reference number: S22990; MUID:91288213; PMID:2062649

A:Accession: S22990

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-181 <DAS>

A:Cross-references: UNIPROT:Q41886; UNIPARC:UPI00000A87CB; EMBL:X58197; NID:g22549; PIDN

A:Experimental source: allele 27K

C:Superfamily: glutelin

Query Match 82.2%; Score 37; DB 2; Length 181;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7

Db 79 PPPPC 83

RESULT 33

S14981

extensin class I (clone w1-8 L) - tomato (fragment)

C:Species: Lycopersicon esculentum (tomato)

C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 11-Jan-2000

C:Accession: S14981

R;Showalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.

Plant Mol. Biol. 16, 547-565, 1991

A;Title: Tomato extensin and extensin-like cDNAs: structure and expression in response to wounding

A;Reference number: S14970; MUID:91329690; PMID:1714316

A;Accession: S14981

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-199 <SHO>

A;Cross-references: UNIPARC:UPI0000178840; EMBL:X55692

A;Experimental source: cv. UC828

C;Superfamily: hydroxyproline-rich glycoprotein

C;Keywords: cell wall; glycoprotein; hydroxyproline

Query Match 82.2%; Score 37; DB 2; Length 199;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 129 PPPPC 133

RESULT 34

T32976

hypothetical protein F57H12.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T32976

R;Bentley, D.; Le, T.T.

submitted to the EMBL Data Library, February 1998

A;Description: The sequence of C. elegans cosmid F57H12.

A;Reference number: 221258

A;Accession: T32976

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-211 <BEN>

A;Cross-references: UNIPROT:O45098; UNIPARC:UPI0000007884A; EMBL:AF045644; PIDN:AAC02599.

A;Experimental source: strain Bristol N2; clone F57H12

C;Genetics:

A;Gene: CESP:F57H12.3

A;Map position: 4

A;Introns: 30/3; 159/3

Query Match 82.2%; Score 37; DB 2; Length 211;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 32 PPPPC 36

RESULT 35

T22572

hypothetical protein F53F1.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 05-Oct-2004

C;Accession: T22572

R;Burton, J.

submitted to the EMBL Data Library, October 1996

A;Reference number: 219583

A;Accession: T22572

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-215 <WIL>

A;Cross-references: UNIPARC:UPI0000006107B; EMBL:Z81088; PIDN:CA803133.1; GSPDB:GN00023;

A;Experimental source: clone F53F1

C;Genetics:

A;Gene: CESP:F53F1.5

A;Map position: 5

A;Introns: 30/2

Query Match 82.2%; Score 37; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 34 PPPPC 38

RESULT 36

ZMZM19

glutelin 2 precursor (clone pME119) - maize

N;Alternate names: 27K zein; alcohol-soluble reduced glutelin; Zc2 protein

C;Species: Zea mays (maize)

C;Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 09-Jul-2004

C;Accession: A93557; A29017; S12144; A23014

R;Prat, S.; Cortadas, J.; Puigdomenech, J.; Palau, J.

Nucleic Acids Res. 13, 1493-1504, 1985

A;Title: Nucleic acid (cDNA) and amino acid sequences of the maize endosperm protein gl

A;Reference number: A93557; MUID:85215560; PMID:3839076

A;Accession: A93557

A;Molecule type: mRNA

A;Residues: 1-223 <PR1>

A;Cross-references: UNIPROT:P04706; UNIPARC:UPI0000000D13; GB:X02230; NID:G22288; PIDN:

A;Experimental source: inbred line E-10

R;Prat, S.; Perez-Grau, L.; Puigdomenech, P.

Gene 52, 41-49, 1987

A;Title: Multiple variability in the sequence of a family of maize endosperm proteins.

A;Reference number: A29017; MUID:87248094; PMID:3596247

A;Accession: A29017

A;Molecule type: mRNA

A;Residues: 1-223 <PR2>

A;Cross-references: UNIPARC:UPI0000000D13

A;Experimental source: inbred lines W64 and W64O2

A;Note: the authors called this clone pME125

R;Reina, M.; Ponte, I.; Guillen, P.; Boronat, A.; Palau, J.

Nucleic Acids Res. 18, 6426, 1990

A;Title: Sequence analysis of a genomic clone encoding a Zc2 protein from Zea mays W64

A;Reference number: S12144; MUID:91057132; PMID:2243788

A;Accession: S12144

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-223 <REI>

A;Cross-references: UNIPARC:UPI0000000D13; EMBL:X53514; NID:G22516; PIDN:CAA37594.1; PI

A;Experimental source: strain W64A, clone p268C

C;Comment: Glutelin 2 accounts for about 15% of the total endosperm protein and is loca

C;Superfamily: Glutelin

C;Keywords: duplication; seed; storage protein

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-223/Product: Glutelin 2 #status predicted <MAT>

F;31-36,37-42,43-48,49-54,55-60,61-66,73-78/Region: duplication

Query Match 82.2%; Score 37; DB 1; Length 223;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 79 PPPPC 83

RESULT 37

S37108

Cuticlin 2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Oct-2004

C;Accession: S37108

R;Sebastiano, M.; Zai, F.; Lassandro, F.; Nola, M.; Ristatore, F.; Bazzicalupo, P.

submitted to the EMBL Data Library, September 1993

A;Description: A second Cuticlin gene from C. elegans.

A;Reference number: S37108

A;Accession: S37108

A;Status: preliminary

A;Molecule type: DNA

A:Residues: 1-231 <SEB>  
A:Cross-references: UNIPROT:P34682; UNIPARC:UPI0000128706; EMBL:X74838; NID:G398752; PID:  
C:Genetics:  
A:Introns: 30/2

Query Match 82.2%; Score 37; DB 2; Length 231;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
DB 34 PPPPC 38

RESULT 38  
S09256  
homeotic protein Hox D4 - chicken  
N:Alternate names: homeotic protein Chox-4.2; homeotic protein Chox-a  
C:Species: Gallus gallus (chicken)  
C:Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 24-Jul-1997  
C:Accession: S09256  
R:Sasaki, H.; Yokoyama, E.; Kuroiwa, A.  
Nucleic Acids Res. 18, 1749-1747, 1990  
A:Title: Specific DNA binding of the two chicken deformed family homeodomain proteins, C  
A:Reference number: S09256; MUID:90245562; PMID:1970866  
A:Accession: S09256  
A:Molecule type: mRNA  
A:Residues: 1-236 <SAS>  
A:Cross-references: UNIPARC:UPI00001745B3; EMBL:X52671; EMBL:X52672  
C:Genetics:  
A:Gene: hoxd-4  
C:Function:  
A:Description: control of embryonic development by tissue- and stage-specific regulation  
C:Superfamily: homeotic protein Hox D4; homeobox homology  
C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation  
F:146-202/Domain: homeobox homology <Hox>

Query Match 82.2%; Score 37; DB 1; Length 236;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
DB 95 PPPPC 99

RESULT 39  
T25814  
hypothetical protein K10C2.5 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T25814  
R:Minx, P.  
submitted to the EMBL Data Library, November 1995  
A:Description: The sequence of C. elegans cosmid K10C2.  
A:Reference number: Z20092  
A:Accession: T25814  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-240 <MIN>  
A:Cross-references: UNIPROT:Q94273; UNIPARC:UPI0000077436; EMBL:U39852; PIDN:AAB06901.1;  
C:Genetics:  
A:Gene: CESP:K10C2.5  
A:Introns: 10/3; 63/2; 139/3; 180/3  
C:Superfamily: glutelin

Query Match 82.2%; Score 37; DB 2; Length 240;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
DB 56 PPPPC 60

RESULT 40  
S01360  
salivary glue protein sgs-3 precursor - fruit fly (Drosophila yakuba)  
C:Species: Drosophila yakuba  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-Jul-2004  
C:Accession: S01360; C29988  
R:Martin, C.H.; Mayeda, C.A.; Meyerowitz, E.M.  
J. Mol. Biol. 201, 273-287, 1988  
A:Title: Evolution and expression of the Sgs-3 glue gene of Drosophila.  
A:Reference number: S01358; MUID:88332966; PMID:3138416  
A:Accession: S01360  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-263 <MAR>  
A:Cross-references: UNIPROT:P13728; UNIPARC:UPI00000135928  
C:Genetics:  
A:Gene: Sgs-3  
A:Cross-references: FlyBase:FBgn0013172  
C:Superfamily: salivary glue protein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-263/Product: salivary glue protein sgs-3 #status predicted <MAT>

Query Match 82.2%; Score 37; DB 2; Length 263;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
DB 62 PPPPC 66

RESULT 41  
S15750  
transforming protein (fra-1) - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S15750; I56863; S08010  
R:Matsumi, M.; Tokuhara, M.; Konuma, Y.; Nomura, N.; Ishizaki, R.  
Oncogene 5, 249-255, 1990  
A:Title: Isolation of human fos-related genes and their expression during monocyte-macro  
A:Reference number: S15749; MUID:90191709; PMID:2107490  
A:Accession: S15750  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-271 <MAT>  
A:Cross-references: UNIPROT:P15407; UNIPARC:UPI0000049C8A; EMBL:X16707; NID:G31462; PIDN:  
R:Tsuchiya, H.; Fujii, M.; Niki, T.; Tokuhara, M.; Matsui, M.; Seiki, M.  
J. Virol. 67, 7001-7007, 1993  
A:Title: Human T-cell leukemia virus type 1 Tax activates transcription of the human fra  
A:Reference number: I56863; MUID:94047311; PMID:8230424  
A:Accession: I56863  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-5 <RES>  
A:Cross-references: UNIPARC:UPI000011E87B; GB:D16365; NID:G537351; PIDN:BAA03867.1; PID:  
C:Genetics:  
A:Gene: fra-1  
C:Superfamily: fos transforming protein; fos/jun DNA-binding domain homology  
C:Keywords: DNA binding; nucleus  
F:100-140/Domain: fos/jun DNA-binding domain homology <FJD>

Query Match 82.2%; Score 37; DB 2; Length 271;  
Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSSPPPC 7  
DB 190 SSSPPPC 196

RESULT 42

## T24102

hypothetical protein R102.6 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T24102  
R;Berke, M.  
submitted to the EMBL Data Library, March 1996  
A;Reference number: Z19841  
A;Accession: T24102  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-324 <WIL>  
A;Cross-references: UNIPROT:Q21892; UNIPARC:UPI000007F577; EMBL:Z70309; PIDN:CAA94360.1;  
A;Experimental source: clone R102  
C;Genetics:  
A;Gene: CESP:R102.6  
A;Map position: 4  
A;Introns: 42/3, 91/1, 114/2, 161/3, 198/2, 221/1, 281/3

Query Match 82.2%; Score 37; DB 2; Length 324;  
Best Local Similarity 100.0%; Pred. No. 26+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
|||||  
DB 254 PPPPC 258

## RESULT 43

A2HU  
Ig alpha-2 chain C region - human  
C;Species: Homo sapiens (man)  
C;Date: 17-Dec-1982 #sequence\_revision 17-Dec-1982 #text\_change 16-Jul-1999  
C;Accession: A93828; A93829; A02172  
R;Torano, A.; Putnam, F.W.  
Proc. Natl. Acad. Sci. U.S.A. 75, 966-969, 1978  
A;Title: Complete amino acid sequence of the alpha2 heavy chain of a human IgA2 immunoglobulin  
A;Reference number: A93828; MUID:78137069; PMID:416441  
A;Contents: But  
A;Accession: A93828  
A;Molecule type: protein  
A;Residues: 1-340 <TOR>  
A;Cross-references: UNIPARC:UPI00001737C3  
A;Note: the disulfide bond formed by Cys-77 is unaccounted for  
R;Tazukida, Y.; Wang, C.C.; Putnam, F.W.  
Proc. Natl. Acad. Sci. U.S.A. 76, 1104-1108, 1979  
A;Title: Structure of the A2m (1) allotype of human IgA-a recombinant molecule.  
A;Reference number: A93829; MUID:79180140; PMID:286295  
A;Contents: myeloma protein Lan  
A;Accession: A93829  
A;Molecule type: protein  
A;Residues: 1-92, 'P', 94-101, 'P', 103-278, 'P', 280-295, 'D', 297-325, 'V', 327-334, 'V', 336-340  
A;Cross-references: UNIPARC:UPI00001737C4  
A;Note: this chain does not form a disulfide bond with the light chain  
A;Note: the A2m(1) allotype appears to be a recombinant chain, being identical (except for Bur alpha-1 chain from positions 279 to 340  
C;Comment: The A2m(2) allotype sequence of the myeloma protein But is shown.  
C;Genetics:

A;Gene: GDB:IGHA2  
A;Cross-references: GDB:119333; OMIM:147000  
A;Map position: 14q32.33-14q32.33  
C;Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin  
F;127-193/Domain: immunoglobulin homology <IM1>  
F;230-302/Domain: immunoglobulin homology <IM2>  
F;26-85, 110-167, 134-191, 237-300/Disulfide bonds: #status predicted  
F;47, 92, 131, 205, 327/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;101/disulfide bonds: interchain (to light chain) #status predicted  
F;109, 169/disulfide bonds: interchain (to alpha chain) #status predicted  
F;179/disulfide bonds: interchain (to alpha chain in another subunit) #status predicted  
F;339/disulfide bonds: interchain (to J chain) #status predicted

Query Match 82.2%; Score 37; DB 1; Length 340;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
|||||  
DB 105 PPPPC 109

## RESULT 44

I56230  
Ig alpha-2 chain - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000  
C;Accession: I56230  
R;Chintalacharuvu, K.R.; Raines, M.; Morrison, S.L.  
J. Immunol. 152, 5299-5304, 1994  
A;Title: Divergence of human alpha-chain constant region gene sequences. A novel recombinant  
A;Reference number: I56230; MUID:94246170; PMID:8189047  
A;Accession: I56230  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-340 <RES>  
A;Cross-references: UNIPARC:UPI0000113F66; GB:S71043; NID:G546798; PIDN:AAB30803.1; PID  
C;Genetics:  
A;Gene: IGA2  
A;Introns: 103/1; 210/1  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;230-302/Domain: immunoglobulin homology <IM>

Query Match 82.2%; Score 37; DB 2; Length 340;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
|||||  
DB 105 PPPPC 109

## RESULT 45

I9 alpha-2 chain C region (allotype A2m(1)) - human  
C;Species: Homo sapiens (man)  
C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004  
C;Accession: B22360  
R;Planagan, J.G.; Lefranc, M.P.; Rabbitts, T.H.  
Cell 36, 681-686, 1984  
A;Title: Mechanisms of divergence and convergence of the human immunoglobulin alpha-1 chain  
A;Reference number: A94653; MUID:84130179; PMID:6421489  
A;Accession: B22360  
A;Molecule type: DNA  
A;Residues: 1-340 <PLA>  
A;Cross-references: UNIPROT:P01877; UNIPARC:UPI000004718E  
C;Genetics:  
A;Gene: GDB:IGHA2  
A;Cross-references: GDB:119333; OMIM:147000  
A;Map position: 14q32.33-14q32.33  
A;Introns: 1/1 103/1; 210/1  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;230-302/Domain: immunoglobulin homology <IM>

Query Match 82.2%; Score 37; DB 2; Length 340;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
|||||  
DB 105 PPPPC 109

## RESULT 46

AB3260  
 hypothetical membrane spanning protein BMEI0063 [imported] - Brucella melitensis (strain  
 C:Species: Brucella melitensis  
 C>Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
 C:Accession: AB3260  
 R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,  
 .; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess  
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A>Title: The genome sequence of the facultative intracellular pathogen Brucella melitens  
 A:Reference number: AD3252; PMID:11756688  
 A:Accession: AB3260  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-348 <XNU>  
 A:Cross-references: UNIPROT:Q8YJL9; UNIPARC:UPI0000057B2C; GB:AE008917; PIDN:AA151245.1;  
 A:Experimental source: strain 16M  
 C:Genetics:  
 A:Gene: BMEI0063  
 A:Map position: 1

Query Match 82.2%; Score 37; DB 2; Length 348;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
 |||||  
 DB 215 PPPPC 219

RESULT 47  
 T05441  
 proline-rich protein F7K2.50 - Arabidopsis thaliana (fragment)  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
 C:Accession: T05441  
 R:Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuelle  
 submitted to the Protein Sequence Database, November 1998  
 A:Reference number: Z15416  
 A:Accession: T05441  
 A:Molecule type: DNA  
 A:Residues: 1-379 <BEV>  
 A:Cross-references: UNIPROT:Q9SUX2; UNIPARC:UPI00000AB780; EMBL:AL033545  
 A:Experimental source: cultivar Columbia; BAC clone F7K2  
 C:Genetics:  
 A:Map position: 4  
 A:Note: F7K2.50  
 C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 82.2%; Score 37; DB 2; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
 |||||  
 DB 36 PPPPC 40

RESULT 48  
 D85257  
 extensin-like protein [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
 C:Accession: D85257  
 R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin  
 Nature 402, 769-777, 1999  
 A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
 A:Reference number: A85001; MUID:20083488; PMID:10617198  
 A:Accession: D85257  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-379 <STO>  
 A:Cross-references: UNIPROT:Q9SUX2; UNIPARC:UPI00000AB780; GB:NC\_001268; NID:g7269093; F  
 C:Genetics:

A:Gene: AT4G22470  
 A:Map position: 4  
 C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 82.2%; Score 37; DB 2; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
 |||||  
 DB 36 PPPPC 40

RESULT 49  
 T21370  
 hypothetical protein F25H8.5b - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T21370  
 R:Gajadaty, S.  
 submitted to the EMBL Data Library, February 1996  
 A:Reference number: Z19413  
 A:Accession: T21370  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-387 <WIL>  
 A:Cross-references: UNIPROT:Q19790; UNIPARC:UPI000002A229; EMBL:Z69360; PIDN:CAA93286.1;  
 A:Experimental source: clone F25H8  
 C:Genetics:  
 A:Gene: CESP:F25H8.5b  
 A:Map position: 4  
 A:Introns: 23/3; 43/1; 303/1; 321/1; 343/1; 380/1

Query Match 82.2%; Score 37; DB 2; Length 387;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
 |||||  
 DB 107 PPPPC 111

RESULT 50  
 B84684  
 hypothetical protein At2g28380 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
 C:Accession: B84684  
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402, 761-768, 1999  
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; MUID:20083487; PMID:10617197  
 A:Accession: B84684  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-434 <STO>  
 A:Cross-references: UNIPROT:Q9SKN2; UNIPARC:UPI000009F29E; GB:AE002093; NID:g4432839; P  
 C:Genetics:  
 A:Gene: At2g28380  
 A:Map position: 2

Query Match 82.2%; Score 37; DB 2; Length 434;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
 |||||  
 DB 307 PPPPC 311

Search completed: January 3, 2006, 09:11:39

Job time : 18.3333 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:06 ; Search time 71.6667 Seconds  
(without alignments)  
68.912 Million cell updates/sec

Title: US-10-759-832-10  
Perfect score: 45  
Sequence: 1 SSPPPPC 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Uniprot 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	205	Q5TQW7	ANOCA
2	45	100.0	759	Q5ZDR5	ORYSA
3	45	100.0	1641	Q5NCY0	MOUSE
4	45	100.0	1641	Q4VC26	MOUSE
5	42	93.3	194	Q7QW27	GIADIA lam
6	42	93.3	708	Q4RM61	TETNG
7	42	93.3	1617	Q8AXW5	TELE
8	41	91.1	124	Q6YX71	ORYSA
9	41	91.1	215	Q657J3	ORYSA
10	41	91.1	234	Q52KH0	MOUSE
11	41	91.1	300	Q6YV83	ORYSA
12	41	91.1	343	Q22534	ORYSA
13	41	91.1	366	Q3LH09	ORYSA
14	41	91.1	426	Q9DCD9	MOUSE
15	41	91.1	437	Q9STN0	ARATH
16	41	91.1	485	Q58B61	MOUSE
17	41	91.1	485	Q91207	MOUSE
18	41	91.1	487	Q99KX4	MOUSE
19	41	91.1	494	Q874V7	FODAN
20	41	91.1	519	Q4SHL4	TETNG
21	41	91.1	532	Q81849	ARATH
22	41	91.1	612	Q4S8D5	TETNG
23	41	91.1	643	Q55W78	CRYLE
24	41	91.1	643	Q55W78	CRYLE
25	41	91.1	744	Q65375	ARATH
26	41	91.1	752	Q5W617	ORYSA
27	41	91.1	849	Q5ZD97	ORYSA
28	41	91.1	855	Q4RQ54	TETNG
29	40	88.9	60	Q6H8G9	ORYSA
30	40	88.9	71	Q87616	SIVCZ
31	40	88.9	136	Q4TUD0	TETNG

Q9XG80	oryza sativ
Q6K970	oryza sativ
Q22480	oryza sativ
Q92WT0	adiantum ca
P10284	mus musculus
Q4VBG0	mus musculus
P17483	homo sapien
Q51ZV5	magnaporthe
Q48113	tetradodon n
Q5B116	brachydanio
Q9NP08	homo sapien
Q6C595	yarrowia li
Q7ZX99	xenopus lae
Q69TY6	oryza sativ
Q15054	homo sapien
Q880N7	oryza sativ
Q8C663	mus musculus
Q69Q83	oryza sativ
Q8VFN4	micrococcu
Q7X161	oryza sativ
Q66993	feline leuk
Q84NP3	oryza sativ
Q5VV66	homo sapien
Q9BUJ3	homo sapien
Q52KY5	gallus gall
Q4Q4G6	leishmania
Q5WML3	oryza sativ
Q6P3W1	homo sapien
Q9BZE5	homo sapien
Q6P3U5	homo sapien
Q5VV67	homo sapien
Q76N31	homo sapien
Q25757	plasmodium
Q97267	plasmodium
Q511E7	gecko japon
Q00397	homo sapien
Q70555	mus musculus
Q8CF45	mus musculus
Q5NBP7	oryza sativ
Q6AVC8	oryza sativ
Q4IKZ8	gibberella
Q4UJH3	ricettaia
Q6K1Q2	oryza sativ
Q65XW7	oryza sativ
Q5ZB22	oryza sativ
Q26822	trypanosoma
Q84M78	oryza sativ
Q9ZV73	arabidopsia
Q9W3V7	drosophila
Q657B8	oryza sativ
Q94HJ8	oryza sativ
Q61824	caenorhabdi
Q966K7	caenorhabdi
Q7F8S8	oryza sativ
Q81GF4	drosophila
Q9VAN8	drosophila
Q4SCC2	tetradodon n
Q6Z242	oryza sativ
Q4V078	xanthomonas
Q8PDY6	xanthomonas
Q7X174	oryza sativ
Q6ZC69	oryza sativ
Q94DE7	oryza sativ
Q5VFN3	oryza sativ
Q5QLQ4	oryza sativ
Q6H6Z9	oryza sativ
Q00324	homo sapien
Q69UB7	oryza sativ
Q4TEE6	tetradodon n
Q4RWU6	tetradodon n
Q8QS05	pongine her
Q4JNM0	aspergillus
Q4X1P5	aspergillus

105	38	84.4	591	2	Q6ZJ44	ORYSA	Q6ZJ44	oryza sativ	178	37	82.2	161	2	Q08198	TOBAC	Q08198	nicotiana t
106	38	84.4	662	2	Q7XN77	ORYSA	Q7XN77	oryza sativ	179	37	82.2	163	2	Q61832	CABEL	Q61832	caenorhabdi
107	38	84.4	740	2	Q84TY4	ORYSA	Q84TY4	oryza sativ	180	37	82.2	163	2	Q9CU08	MOUSE	Q9CU08	mus musculus
108	38	84.4	770	1	LRP3	HUMAN	Q75074	homo sapien	181	37	82.2	165	2	Q726V1	HUMAN	Q726V1	homo sapien
109	38	84.4	904	2	Q91WU4	HV1	Q91WU4	human herpe	182	37	82.2	165	2	Q08196	TOBAC	Q08196	nicotiana t
110	38	84.4	1006	2	Q9LWQ1	ARATH	Q9LWQ1	arabidopsi	183	37	82.2	166	2	Q58GP5	9H1V1	Q58GP5	human immun
111	38	84.4	1037	2	Q4T8U2	TETNG	Q4T8U2	tetraodon n	184	37	82.2	172	1	RES1	ORYSA	RES1	oryza sativ
112	38	84.4	1329	1	GP124	MOUSE	Q91ZV8	mus musculus	185	37	82.2	172	2	Q23248	CABEL	Q23248	caenorhabdi
113	38	84.4	1444	2	Q5KL30	CRVNE	Q5KL30	cryptococu	186	37	82.2	172	2	Q19521	CABEL	Q19521	caenorhabdi
114	38	84.4	1444	2	Q5SV52	CRVNE	Q5SV52	cryptococu	187	37	82.2	172	2	Q16990	ACRDO	Q16990	acropora do
115	38	84.4	1469	2	Q6PD04	MOUSE	Q6PD04	mus musculus	188	37	82.2	176	2	Q60ZU9	CAEBR	Q60ZU9	caenorhabdi
116	38	84.4	1487	1	MDS3	YEAST	P53004	saccharomyc	189	37	82.2	178	2	Q69TQ6	ORYSA	Q69TQ6	oryza sativ
117	38	84.4	1517	2	Q6KAS1	MOUSE	Q6KAS1	mus musculus	190	37	82.2	178	2	Q8C2V0	MOUSE	Q8C2V0	mus musculus
118	38	84.4	1636	1	PTN23	HUMAN	Q9H3S7	homo sapien	191	37	82.2	179	2	Q5SZ16	HUMAN	Q5SZ16	homo sapien
119	38	84.4	1744	2	Q7M732	MOUSE	Q7M732	mus musculus	192	37	82.2	181	2	Q6ESW7	ORYSA	Q6ESW7	oryza sativ
120	37	82.2	42	2	Q4YA85	PLABDE	Q4YA85	plasmodium	193	37	82.2	181	2	Q41866	MAIZE	Q41866	zea mays
121	37	82.2	52	2	Q5DQ93	ECOLI	Q5DQ93	escherichia	194	37	82.2	186	2	Q91Y41	9HEPC	Q91Y41	hepatitis c
122	37	82.2	56	2	Q8MM17	ACRPR	Q8MM17	acropora pr	195	37	82.2	186	2	Q91Y42	9HEPC	Q91Y42	hepatitis c
123	37	82.2	56	2	Q8MM18	ACRPR	Q8MM18	acropora pa	196	37	82.2	186	2	Q91Y84	9HEPC	Q91Y84	hepatitis c
124	37	82.2	56	2	Q8MM19	ACRCE	Q8MM19	acropora ce	197	37	82.2	186	2	Q91YK1	9HEPC	Q91YK1	hepatitis c
125	37	82.2	56	2	Q8MU23	ACRPL	Q8MU23	acropora pa	198	37	82.2	186	2	Q91YK2	9HEPC	Q91YK2	hepatitis c
126	37	82.2	56	2	Q8MU24	ACRPL	Q8MU24	acropora pa	199	37	82.2	186	2	Q91YK3	9HEPC	Q91YK3	hepatitis c
127	37	82.2	56	2	Q8MUZ4	9CNID	Q8MUZ4	acropora na	200	37	82.2	188	2	Q6K9R2	ORYSA	Q6K9R2	oryza sativ
128	37	82.2	57	2	Q5VPE7	ORYSA	Q5VPE7	oryza sativ	201	37	82.2	188	2	Q7F932	ORYSA	Q7F932	oryza sativ
129	37	82.2	67	2	Q61LK4	CAEBR	Q61LK4	caenorhabdi	202	37	82.2	188	2	Q7X7P6	ORYSA	Q7X7P6	oryza sativ
130	37	82.2	70	2	Q87620	SIVCZ	Q87620	chimpanzee	203	37	82.2	190	2	Q7YR89	BOVIN	Q7YR89	bos taurus
131	37	82.2	73	1	SPR2E	HUMAN	Q9BYE4	homo sapien	204	37	82.2	192	2	Q4RA45	TETNG	Q4RA45	tetraodon n
132	37	82.2	76	1	SPR2E	MOUSE	Q70556	mus musculus	205	37	82.2	200	2	Q5T188	HUMAN	Q5T188	homo sapien
133	37	82.2	76	1	SPR2F	MOUSE	Q70557	mus musculus	206	37	82.2	202	2	Q7XLD8	ORYSA	Q7XLD8	oryza sativ
134	37	82.2	76	1	SPR2I	MOUSE	Q70560	mus musculus	207	37	82.2	207	2	Q6F348	ORYSA	Q6F348	oryza sativ
135	37	82.2	76	1	Q552K8	DICDI	Q552K8	dictyosteli	208	37	82.2	208	2	Q61TA7	CAEBR	Q61TA7	caenorhabdi
136	37	82.2	77	2	Q54U52	DICDI	Q54U52	dictyosteli	209	37	82.2	209	2	Q61R60	CAEBR	Q61R60	caenorhabdi
137	37	82.2	77	2	Q28593	SHEEP	Q28593	ovis aries	210	37	82.2	211	2	Q45098	CAEBR	Q45098	caenorhabdi
138	37	82.2	78	2	Q8XSB6	RALSO	Q8XSB6	raletonia s	211	37	82.2	212	2	Q6AUB6	ORYSA	Q6AUB6	oryza sativ
139	37	82.2	97	2	Q41986	ARATH	Q41986	arabidopsi	212	37	82.2	213	2	Q7Q5C0	ANOCA	Q7Q5C0	anopheles g
140	37	82.2	103	2	Q9JSA8	CHLUP	Q9JSA8	chlamydia p	213	37	82.2	213	2	Q6K7Q2	ORYSA	Q6K7Q2	oryza sativ
141	37	82.2	104	2	Q61R59	CAEBR	Q61R59	caenorhabdi	214	37	82.2	213	2	Q7XL77	ORYSA	Q7XL77	oryza sativ
142	37	82.2	105	2	Q9XVM6	CAEBR	Q9XVM6	caenorhabdi	215	37	82.2	213	2	Q8LNV3	ORYSA	Q8LNV3	oryza sativ
143	37	82.2	106	2	Q62L03	BURMA	Q62L03	burkholderi	216	37	82.2	215	2	Q9N5B2	CAEBL	Q9N5B2	caenorhabdi
144	37	82.2	110	2	Q6EPT0	ORYSA	Q6EPT0	oryza sativ	217	37	82.2	217	2	Q9NBJ4	ORYSA	Q9NBJ4	oryza sativ
145	37	82.2	119	2	Q9LWX3	ARATH	Q9LWX3	arabidopsi	218	37	82.2	218	2	Q9CUH6	MOUSE	Q9CUH6	mus musculus
146	37	82.2	124	2	Q75G67	ORYSA	Q75G67	oryza sativ	219	37	82.2	222	2	Q95S23	DROME	Q95S23	drosoophila
147	37	82.2	124	2	Q484Y0	TETNG	Q484Y0	tetraodon n	220	37	82.2	223	1	GLU2	MAIZE	GLU2	zea mays
148	37	82.2	127	2	Q9BZ82	HUMAN	Q9BZ82	homo sapien	221	37	82.2	223	2	Q548E9	MAIZE	Q548E9	zea mays
149	37	82.2	127	2	Q6BPN4	ORYSA	Q6BPN4	oryza sativ	222	37	82.2	225	2	Q5N9Q2	ORYSA	Q5N9Q2	oryza sativ
150	37	82.2	127	2	Q9CV08	MOUSE	Q9CV08	mus musculus	223	37	82.2	225	2	Q7XL76	ORYSA	Q7XL76	oryza sativ
151	37	82.2	128	2	Q9YDS3	AERPE	Q9YDS3	aeropyrum p	224	37	82.2	227	2	Q5N7Q1	ORYSA	Q5N7Q1	oryza sativ
152	37	82.2	128	2	Q94163	ORYSA	Q94163	oryza sativ	225	37	82.2	231	1	CUT2	CABEL	CUT2	caenorhabdi
153	37	82.2	131	2	Q7XJV2	ORYSA	Q7XJV2	oryza sativ	226	37	82.2	231	2	Q60ZN0	CAEBR	Q60ZN0	caenorhabdi
154	37	82.2	133	2	Q5QNM2	ORYSA	Q5QNM2	oryza sativ	227	37	82.2	234	2	Q61V01	CAEBR	Q61V01	caenorhabdi
155	37	82.2	134	2	Q624C0	CAEBR	Q624C0	caenorhabdi	228	37	82.2	235	1	HXD4	CHICK	HXD4	gallus gall
156	37	82.2	134	2	Q9DIH9	9VIRU	Q9DIH9	torque teno	229	37	82.2	238	2	Q81922	CAPAN	Q81922	capicum an
157	37	82.2	136	2	Q62268	ORYSA	Q62268	oryza sativ	230	37	82.2	240	2	Q94273	CABEL	Q94273	caenorhabdi
158	37	82.2	137	2	Q527S6	ORYSA	Q527S6	oryza sativ	231	37	82.2	241	2	Q624B8	CAEBR	Q624B8	caenorhabdi
159	37	82.2	138	2	Q84TS2	ORYSA	Q84TS2	oryza sativ	232	37	82.2	241	2	Q9GP48	9TURB	Q9GP48	discocelis
160	37	82.2	138	2	Q9LWN5	ORYSA	Q9LWN5	oryza sativ	233	37	82.2	243	2	P97309	MOUSE	P97309	mus musculus
161	37	82.2	139	2	Q6ZTT3	HUMAN	Q6ZTT3	homo sapien	234	37	82.2	247	2	Q4S4M6	TETNG	Q4S4M6	tetraodon n
162	37	82.2	140	2	Q9N5B1	CABEL	Q9N5B1	caenorhabdi	235	37	82.2	249	2	Q7XL78	ORYSA	Q7XL78	oryza sativ
163	37	82.2	141	2	Q9N2L6	CABEL	Q9N2L6	caenorhabdi	236	37	82.2	260	2	Q8BTA3	MOUSE	Q8BTA3	mus musculus
164	37	82.2	142	2	Q00485	9CNID	Q00485	hydra sp. m	237	37	82.2	262	2	Q5VNE1	ORYSA	Q5VNE1	oryza sativ
165	37	82.2	143	2	Q6YTX2	ORYSA	Q6YTX2	oryza sativ	238	37	82.2	263	1	SGS3	DROVA	SGS3	drosoophila
166	37	82.2	143	2	Q94LL9	ORYSA	Q94LL9	oryza sativ	239	37	82.2	263	2	Q5T0R9	HUMAN	Q5T0R9	homo sapien
167	37	82.2	145	2	Q5T0S3	HUMAN	Q5T0S3	homo sapien	240	37	82.2	266	2	Q7XL73	ORYSA	Q7XL73	oryza sativ
168	37	82.2	146	2	Q61LS5	CAEBR	Q61LS5	caenorhabdi	241	37	82.2	269	2	Q6ZBG7	ORYSA	Q6ZBG7	oryza sativ
169	37	82.2	146	2	Q04300	9RHIZ	Q04300	agrobacteri	242	37	82.2	269	2	Q803H2	BRARE	Q803H2	brachydanio
170	37	82.2	146	2	Q9AEB9	MYCAB	Q9AEB9	mycobacteri	243	37	82.2	271	1	FOSL1	HUMAN	FOSL1	homo sapien
171	37	82.2	147	1	SMR1	MOUSE	SMR1	mus musculus	244	37	82.2	271	2	Q53GM9	HUMAN	Q53GM9	homo sapien
172	37	82.2	147	2	Q6AT10	ORYSA	Q6AT10	oryza sativ	245	37	82.2	271	2	Q6FG51	HUMAN	Q6FG51	homo sapien
173	37	82.2	149	2	Q00484	9CNID	Q00484	hydra sp. m	246	37	82.2	274	2	Q6GT81	CAEBR	Q6GT81	caenorhabdi
174	37	82.2	154	2	Q5F0G9	NEUCR	Q5F0G9	neurospora	247	37	82.2	279	2	Q6ZQX5	HUMAN	Q6ZQX5	homo sapien
175	37	82.2	156	2	Q9YXS7	CABEL	Q9YXS7	caenorhabdi	248	37	82.2	280	2	Q8ZNEC	PYRAE	Q8ZNEC	pyrobaculum
176	37	82.2	157	2	Q08197	TOBAC	Q08197	nicotiana t	249	37	82.2	283	2	Q4HQ56	CAMUP	Q4HQ56	campylobact
177	37	82.2	161	2	Q61HS7	CAEBR	Q61HS7	caenorhabdi	250	37	82.2	289	2	Q81XZ1	HUMAN	Q81XZ1	homo sapien

251	37	82.2	289	2	Q5BL00_HUMAN	Q5BL00_homo sapien	324	37	82.2	449	2	Q8GRV1_ORYSA	Q8GRV1_oryza sativ
252	37	82.2	290	1	HADB_HUMAN	F13378_homo sapien	325	37	82.2	450	2	Q9UFV9_HUMAN	Q9UFV9_homo sapien
253	37	82.2	291	2	Q570M7_9TRYP	Q570M7_trypanosoma	326	37	82.2	452	2	Q6IQ33_CAEBR	Q6IQ33_caenorhabdi
254	37	82.2	292	2	Q58J62_SHEEP	Q58J62_ovis aries	327	37	82.2	454	2	Q4RJKE_TETNG	Q4RJKE_tetraodon n
255	37	82.2	293	2	Q57189_HUMAN	Q57189_homo sapien	328	37	82.2	458	2	Q7XBZ0_ORYSA	Q7XBZ0_oryza sativ
256	37	82.2	296	2	Q59BL3_HUMAN	Q59BL3_homo sapien	329	37	82.2	458	2	Q84TK1_ARATH	Q84TK1_arabidopsis
257	37	82.2	301	2	Q94CR5_ORYSA	Q94CR5_oryza sativ	330	37	82.2	458	2	Q9AYL9_ORYSA	Q9AYL9_oryza sativ
258	37	82.2	303	2	Q9AN43_ORYSA	Q9AN43_oryza sativ	331	37	82.2	461	2	Q8H634_ORYSA	Q8H634_oryza sativ
259	37	82.2	306	2	Q9AN43_BRAJA	Q9AN43_bradyrhizob	332	37	82.2	461	2	Q7X7W8_PEA	Q7X7W8_pisum sativ
260	37	82.2	311	2	Q7SSM6_NEUCR	Q7SSM6_neurospora	333	37	82.2	461	2	FUCO2_PONPY	FUCO2_pongo pygma
261	37	82.2	311	2	Q9N3U2_CABEL	Q9N3U2_caenorhabdi	334	37	82.2	465	1	Q8XOD6_NEUCR	Q8XOD6_neurospora
262	37	82.2	311	2	Q69NG0_ORYSA	Q69NG0_oryza sativ	335	37	82.2	465	1	FUCO2_HUMAN	Q9BTY2_homo sapien
263	37	82.2	315	2	Q8FLW0_COREF	Q8FLW0_corenebacte	336	37	82.2	468	2	Q5ZDL9_ORYSA	Q5ZDL9_oryza sativ
264	37	82.2	316	2	Q5JND8_ORYSA	Q5JND8_oryza sativ	337	37	82.2	468	2	Q5EDN9_DICDI	Q5EDN9_dicyosteli
265	37	82.2	317	2	Q4G016_RAT	Q4G016_rattus norv	338	37	82.2	469	2	Q5MB24_RAT	Q5MB24_rattus norv
266	37	82.2	318	2	Q5PQY8_BRARE	Q5PQY8_brachydanio	339	37	82.2	469	2	Q7PKK5_ANOGA	Q7PKK5_anopheles g
267	37	82.2	321	2	Q654E7_ORYSA	Q654E7_oryza sativ	340	37	82.2	471	2	Q5T185_HUMAN	Q5T185_homo sapien
268	37	82.2	323	2	Q652K6_ORYSA	Q652K6_oryza sativ	341	37	82.2	473	2	Q6H5V2_ORYSA	Q6H5V2_oryza sativ
269	37	82.2	324	2	Q21892_CABEL	Q21892_caenorhabdi	342	37	82.2	473	2	Q5TOS2_HUMAN	Q5TOS2_homo sapien
270	37	82.2	324	2	Q5D913_SCHJA	Q5D913_schistosoma	343	37	82.2	474	2	Q5T186_HUMAN	Q5T186_homo sapien
271	37	82.2	326	2	Q60ZV5_CAEBR	Q60ZV5_caenorhabdi	344	37	82.2	474	2	Q5T186_HUMAN	Q5T186_homo sapien
272	37	82.2	330	2	Q60JD2_CAEBR	Q60JD2_caenorhabdi	345	37	82.2	477	2	Q6GMX7_HUMAN	Q6GMX7_homo sapien
273	37	82.2	331	2	Q6LLI2_CAEBR	Q6LLI2_caenorhabdi	346	37	82.2	478	2	Q7Z379_HUMAN	Q7Z379_homo sapien
274	37	82.2	331	2	Q8L672_ORYSA	Q8L672_oryza sativ	347	37	82.2	478	2	Q6NYH3_HUMAN	Q6NYH3_homo sapien
275	37	82.2	333	2	Q4PEL4_USITWA	Q4PEL4_ustilago ma	348	37	82.2	479	2	Q6MZV6_HUMAN	Q6MZV6_homo sapien
276	37	82.2	337	2	Q8N2B0_HUMAN	Q8N2B0_homo sapien	349	37	82.2	479	2	Q5R9S9_PONPY	Q5R9S9_pongo pygma
277	37	82.2	340	1	IGHA2_HUMAN	P01877_homo sapien	350	37	82.2	479	2	Q7XFS0_ORYSA	Q7XFS0_oryza sativ
278	37	82.2	341	2	Q743K0_MYCPA	Q743K0_mycobacteri	351	37	82.2	479	2	Q84SV9_ORYSA	Q84SV9_oryza sativ
279	37	82.2	348	2	Q6IMT9_ORYSA	Q6IMT9_oryza sativ	352	37	82.2	479	2	Q8S776_ORYSA	Q8S776_oryza sativ
280	37	82.2	348	2	Q8YJL9_BRUME	Q8YJL9_brucella me	353	37	82.2	479	2	Q9XEV0_ORYSA	Q9XEV0_oryza sativ
281	37	82.2	349	1	PTER_MOUSE	Q96BW5_homo sapien	354	37	82.2	480	2	Q6P089_HUMAN	Q6P089_homo sapien
282	37	82.2	349	1	PTER_MOUSE	Q60866_mus musculu	355	37	82.2	480	2	Q4TAT5_TETNG	Q4TAT5_tetraodon n
283	37	82.2	349	1	PTER_MOUSE	Q63530_rattus norv	356	37	82.2	482	2	Q6JVL1_XENLA	Q6JVL1_xenopus lae
284	37	82.2	349	1	Q5VWM0_HUMAN	Q5VWM0_homo sapien	357	37	82.2	483	2	Q6MZX9_HUMAN	Q6MZX9_homo sapien
285	37	82.2	349	2	Q5S5E9_PONPY	Q5S5E9_pongo pygma	358	37	82.2	483	2	Q8LIX0_ORYSA	Q8LIX0_oryza sativ
286	37	82.2	356	2	Q8SBC0_ORYSA	Q8SBC0_oryza sativ	359	37	82.2	485	2	Q4RWX8_TETNG	Q4RWX8_tetraodon n
287	37	82.2	358	1	PETUA_GAVPO	Q6AYY7_rattus norv	360	37	82.2	485	2	Q5NQ20_ZYMO	Q5NQ20_zymomonas m
288	37	82.2	358	2	Q6YXV7_ORYSA	Q6YXV7_oryza sativ	361	37	82.2	487	2	Q6ZVX0_HUMAN	Q6ZVX0_homo sapien
289	37	82.2	361	2	Q6IMV8_ORYSA	Q6IMV8_oryza sativ	362	37	82.2	490	2	Q4L857_HUMAN	Q4L857_homo sapien
290	37	82.2	361	2	Q7XEA1_ORYSA	Q7XEA1_oryza sativ	363	37	82.2	491	2	Q5RE97_PONPY	Q5RE97_pongo pygma
291	37	82.2	365	2	Q4RR24_TETNG	Q4RR24_tetraodon n	364	37	82.2	492	2	Q7Z374_HUMAN	Q7Z374_homo sapien
292	37	82.2	369	2	Q7JLY2_CABEL	Q7JLY2_caenorhabdi	365	37	82.2	494	2	Q9FXA1_ARATH	Q9FXA1_arabidopsis
293	37	82.2	376	2	Q53N23_ORYSA	Q53N23_oryza sativ	366	37	82.2	496	2	Q8GVZ8_ORYSA	Q8GVZ8_oryza sativ
294	37	82.2	377	2	Q59HB0_HUMAN	Q59HB0_homo sapien	367	37	82.2	498	2	Q6N041_HUMAN	Q6N041_homo sapien
295	37	82.2	377	2	Q84PB9_ORYSA	Q84PB9_oryza sativ	368	37	82.2	500	1	CP46A_HUMAN	Q9Y6A2_homo sapien
296	37	82.2	379	2	Q9SUX2_ARATH	Q9SUX2_arabidopsis	369	37	82.2	500	1	CP46A_MOUSE	Q9WVX8_mus musculu
297	37	82.2	381	2	Q4SUW3_TETNG	Q4SUW3_tetraodon n	370	37	82.2	502	2	Q6N091_HUMAN	Q6N091_homo sapien
298	37	82.2	384	2	Q5T180_HUMAN	Q5T180_homo sapien	371	37	82.2	502	1	UBAP1_MOUSE	Q8BH48_mus musculu
299	37	82.2	384	2	Q6Z8T4_ORYSA	Q6Z8T4_oryza sativ	372	37	82.2	505	2	Q5LRQ6_SILPO	Q5LRQ6_silicibacte
300	37	82.2	388	2	Q9C616_ARATH	Q9C616_arabidopsis	373	37	82.2	506	2	Q9VM36_DROME	Q9VM36_drosophila
301	37	82.2	391	2	Q6FY02_CANGA	Q6FY02_candida gla	374	37	82.2	507	2	Q8FY77_BRUSU	Q8FY77_brucella su
302	37	82.2	393	1	KCNK4_HUMAN	Q9NY98_homo sapien	375	37	82.2	513	2	Q6NUU5_HUMAN	Q6NUU5_homo sapien
303	37	82.2	394	2	Q5KGL5_CRYNE	Q5KGL5_cryptococcu	376	37	82.2	515	2	Q4REX8_TETNG	Q4REX8_tetraodon n
304	37	82.2	395	2	Q7XEV6_ORYSA	Q7XEV6_oryza sativ	377	37	82.2	520	1	WASP_MOUSE	P70315_mus musculu
305	37	82.2	395	2	Q75G68_ORYSA	Q75G68_oryza sativ	378	37	82.2	520	2	Q5VR46_ORYSA	Q5VR46_oryza sativ
306	37	82.2	396	2	Q4QFO6_LEIMA	Q4QFO6_oryza sativ	379	37	82.2	520	2	Q53WY0_MOUSE	Q53WY0_mus musculu
307	37	82.2	397	2	Q6YXT4_ORYSA	Q6YXT4_oryza sativ	380	37	82.2	520	2	Q61078_MOUSE	Q61078_mus musculu
308	37	82.2	407	1	DAF2_MOUSE	Q4QF66_leishmania	381	37	82.2	525	2	Q9LDC2_ORYSA	Q9LDC2_oryza sativ
309	37	82.2	411	2	Q76XB3_PEA	Q61476_mus musculu	382	37	82.2	533	2	Q8ZSX8_PYRAE	Q8ZSX8_pyrobaculum
310	37	82.2	415	2	Q413X8_GIBZE	Q76KB3_pisum sativ	383	37	82.2	536	2	Q5VNI5_ORYSA	Q5VNI5_oryza sativ
311	37	82.2	416	2	Q86U72_HUMAN	Q413X8_gibberella	384	37	82.2	540	2	Q57XW0_9TRYP	Q57XW0_trypanosoma
312	37	82.2	416	2	Q9NPP6_HUMAN	Q86U72_homo sapien	385	37	82.2	540	2	Q7XME8_ORYSA	Q7XME8_oryza sativ
313	37	82.2	417	2	Q8SX17_DROME	Q9NPP6_homo sapien	386	37	82.2	549	1	ATG15_YARLI	Q6C2M7_yarrowia li
314	37	82.2	428	2	Q7PYF3_ANOGA	Q8SX17_drosophila	387	37	82.2	560	1	EFS_MOUSE	Q64355_mus musculu
315	37	82.2	428	2	Q5QLN4_ORYSA	Q7PYF3_anopheles g	388	37	82.2	560	2	Q9P6T8_NEUCR	Q9P6T8_neurospora
316	37	82.2	434	2	Q5OLN4_ASHGO	Q5QLN4_oryza sativ	389	37	82.2	560	2	Q8BSX4_MOUSE	Q8BSX4_mus musculu
317	37	82.2	434	2	Q9SKN2_ARATH	Q750V5_sahyva goss	390	37	82.2	561	2	Q8KOP6_MOUSE	Q8KOP6_mus musculu
318	37	82.2	435	2	Q61Q32_CAEBR	Q9SKN2_arabidopsis	391	37	82.2	570	1	Q5N7Z8_ORYSA	Q5N7Z8_oryza sativ
319	37	82.2	436	1	SHTE6_RAT	Q61Q32_caenorhabdi	392	37	82.2	570	2	STAU2_HUMAN	Q9NUL3_homo sapien
320	37	82.2	439	2	Q6CCC2_YARLI	P31388_rattus norv	393	37	82.2	571	1	STAU2_RAT	Q7XPQ5_ORYSA
321	37	82.2	443	1	EDNRB_HORSE	Q6CCC2_yarrowia li	394	37	82.2	572	2	Q69UE5_ORYSA	Q69UE5_oryza sativ
322	37	82.2	444	2	Q4KLN2_RAT	Q62709_equus cabal	395	37	82.2	576	2	Q4RZV3_TETNG	Q4RZV3_tetraodon n
323	37	82.2	447	2	Q9SUX4_ARATH	Q4KLN2_rattus norv	396	37	82.2	577	2	Q7XRW4_ORYSA	Q7XRW4_oryza sativ
						Q9SUX4_arabidopsis							

397	37	82.2	577	2	Q6DFG1_XENLA	Q6dfg1 xenopus lae	470	37	82.2	893	2	Q6ZCX3_ORYSA	Q6zcx3 oryza sativ
398	37	82.2	578	2	Q59H30_HUMAN	Q59h30 homo sapien	471	37	82.2	895	2	Q9ZUC3_ARATH	Q9zuc3 arabidopsis
399	37	82.2	579	1	SHC1_MOUSE	P98083 mus musculus	472	37	82.2	907	2	Q7Q2T5_ANOGA	Q7q2t5 anopheles g
400	37	82.2	583	1	SHC1_HUMAN	P29353 homo sapien	473	37	82.2	907	2	Q8LIK9_ORYSA	Q8lik9 oryza sativ
401	37	82.2	583	2	Q7SDU6_NEUCR	Q7sdu6 neurospora	474	37	82.2	909	2	Q7XMC9_ORYSA	Q7xmc9 oryza sativ
402	37	82.2	583	2	Q5T184_HUMAN	Q5t184 homo sapien	475	37	82.2	912	2	Q7Z4G8_HUMAN	Q7z4g8 homo sapien
403	37	82.2	583	2	Q5R7W7_PONPY	Q5r7w7 pongo pygma	476	37	82.2	914	2	Q57X17_9TRYP	Q57x17 trypanosoma
404	37	82.2	583	2	Q5T183_HUMAN	Q5t183 homo sapien	477	37	82.2	914	2	Q6GF05_ORYSA	Q6gf05 oryza sativ
405	37	82.2	593	2	Q8LMC6_ORYSA	Q8lmc6 oryza sativ	478	37	82.2	917	2	Q7S285_NEUCR	Q7s285 neurospora
406	37	82.2	602	2	Q42203_BRARE	Q42203 brachydanio	479	37	82.2	926	2	Q4Q523_LEIMA	Q4q523 leishmania
407	37	82.2	604	2	Q5KEV4_CRYNE	Q5kev4 cryptococcus	480	37	82.2	927	2	Q7XSN2_ORYSA	Q7xsn2 oryza sativ
408	37	82.2	606	2	Q5G0V3_CRYNE	Q5g0v3 cryptococcus	481	37	82.2	951	2	Q9M1H0_ARATH	Q9m1h0 arabidopsis
409	37	82.2	609	2	Q7JMB5_TREDE	Q7jmb5 treponema d	482	37	82.2	952	2	Q8I7T3_DICDI	Q8i7t3 dictyosteli
410	37	82.2	615	2	Q4QOL7_LEIMA	Q4qol7 leishmania	483	37	82.2	955	2	Q59LC6_CANAL	Q59lc6 candida alb
411	37	82.2	616	1	SPAST_HUMAN	Q9ubp0 homo sapien	484	37	82.2	964	2	Q571D0_MOUSE	Q571d0 mus musculu
412	37	82.2	616	2	Q6PDK8_MOUSE	Q6pdk8 mus musculu	485	37	82.2	967	2	Q922W3_MOUSE	Q922w3 mus musculu
413	37	82.2	618	2	Q99KV8_MOUSE	Q99kv8 mus musculu	486	37	82.2	979	2	Q9W5A4_DROME	Q9w5a4 drosophila
414	37	82.2	628	2	Q81LK9_MOUSE	Q81lk9 mus musculu	487	37	82.2	984	2	Q6L4M1_ORYSA	Q6l4m1 oryza sativ
415	37	82.2	630	2	Q96AD9_HUMAN	Q96ad9 homo sapien	488	37	82.2	992	2	Q5BG75_EMENI	Q5bg75 aspergillus
416	37	82.2	635	1	VP40_HRV11	P10210 human herpe	489	37	82.2	1000	2	Q5ZBJ7_ORYSA	Q5zbj7 oryza sativ
417	37	82.2	635	2	Q69087_HRV1	Q69087 human herpe	490	37	82.2	1005	2	Q8MQ54_CAEEL	Q8mq54 caenorhabdi
418	37	82.2	637	2	Q9VC38_DROME	Q9vc38 drosophila	491	37	82.2	1011	2	Q5BII2_DROME	Q5bi12 drosophila
419	37	82.2	640	2	Q8WRM5_DROME	Q8wrw5 drosophila	492	37	82.2	1016	2	Q8VRN4_RHOSH	Q8vrn4 rhodobacter
420	37	82.2	640	2	Q8EML4_MOUSE	Q8eml4 mus musculu	493	37	82.2	1018	2	Q9LJKO_ARATH	Q9ljko arabidopsis
421	37	82.2	645	2	Q5ICA3_ENTHI	Q5ica3 entamoeba h	494	37	82.2	1026	2	Q5VR02_ORYSA	Q5vr02 oryza sativ
422	37	82.2	646	2	Q61QV1_CAEER	Q61qv1 caenorhabdi	495	37	82.2	1041	2	Q4I6H3_GIBZE	Q4i6h3 gibberella
423	37	82.2	653	2	Q6S9D7_HUMAN	Q6s9d7 mus sapien	496	37	82.2	1044	2	Q823Z2_CHLCV	Q823z2 chlamydophi
424	37	82.2	668	2	Q8R5A3_MOUSE	Q8r5a3 mus musculu	497	37	82.2	1048	2	Q5AQFO_EMENI	Q5aqfo aspergillus
425	37	82.2	670	1	ATP6A_HUMAN	P18950 homo sapien	498	37	82.2	1062	2	Q63ZY4_HUMAN	Q63zy4 homo sapien
426	37	82.2	675	2	Q8KLY3_MOUSE	Q8kly3 mus musculu	499	37	82.2	1075	1	ATX2L_HUMAN	Q8xwm7 homo sapien
427	37	82.2	676	2	Q9VQSO_DROME	Q9vqso drosophila	500	37	82.2	1079	2	Q5RHJ3_BRARE	Q5rhj3 brachydanio
428	37	82.2	676	2	Q7F730_ORYSA	Q7f730 oryza sativ	501	37	82.2	1083	2	Q6MZK4_HUMAN	Q6mzx4 homo sapien
429	37	82.2	677	2	Q4SZ92_TETNG	Q4sz92 tetraodon n	502	37	82.2	1086	2	Q5TPQ4_ANOGA	Q5tpq4 anopheles g
430	37	82.2	678	2	Q9XF29_ORYSA	Q9xf29 oryza sativ	503	37	82.2	1087	2	Q7Q1T1_ANOGA	Q7q1t1 anopheles g
431	37	82.2	678	2	Q8BZ84_MOUSE	Q8bz84 m mus muscu	504	37	82.2	1099	2	Q4WNT8_ASPFU	Q4wn78 aspergillus
432	37	82.2	692	2	Q5OLT5_ENTHI	Q5olt5 entamoeba h	505	37	82.2	1099	2	Q5RDY2_PONPY	Q5rdt2 pongo pygma
433	37	82.2	715	2	Q9VVD2_DROME	Q9vvd2 drosophila	506	37	82.2	1104	2	Q5SXA9_MOUSE	Q5sxa9 mus musculu
434	37	82.2	716	2	Q6ZWP8_HUMAN	Q6zwp8 homo sapien	507	37	82.2	1113	2	Q8IX03_HUMAN	Q8ix03 homo sapien
435	37	82.2	719	2	Q8VJQ6_MYCTU	Q8vjq6 mycobacteri	508	37	82.2	1114	2	Q8MT16_DROME	Q8mt16 drosophila
436	37	82.2	729	2	Q9XAM0_STRCO	Q9xam0 streptomyce	509	37	82.2	1114	2	Q9NED2_LEIMA	Q9ned2 leishmania
437	37	82.2	732	2	Q95ZV0_CAEEL	Q95zv0 caenorhabdi	510	37	82.2	1114	2	Q7YZA4_DROME	Q7yza4 drosophila
438	37	82.2	736	2	Q5R4Z0_PONPY	Q5r4z0 pongo pygma	511	37	82.2	1115	2	Q4RRV4_TETNG	Q4rrv4 tetraodon n
439	37	82.2	740	2	Q6OF09_ORYSA	Q6of09 oryza sativ	512	37	82.2	1140	2	Q20299_CAEEL	Q20299 caenorhabdi
440	37	82.2	743	1	EXTN2_ARATH	Q9m1g9 arabidopsis	513	37	82.2	1146	2	Q4SVD4_TETNG	Q4svd4 tetraodon n
441	37	82.2	750	2	Q61B96_CAEER	Q61b96 caenorhabdi	514	37	82.2	1146	2	Q4T687_TETNG	Q4t687 tetraodon n
442	37	82.2	754	2	Q9LEU6_ARATH	Q9leu6 arabidopsis	515	37	82.2	1153	2	Q8IRY0_DROME	Q8iry0 drosophila
443	37	82.2	755	2	Q4RRW9_TETNG	Q4rrw9 tetraodon n	516	37	82.2	1159	2	Q69ZC2_MOUSE	Q69zc2 mus musculu
444	37	82.2	757	2	Q94BQ3_ARATH	Q94bq3 arabidopsis	517	37	82.2	1179	2	Q50NAQ_ENTHI	Q50nao entamoeba h
445	37	82.2	758	2	Q7ZYN6_XENLA	Q7zyn6 xenopus lae	518	37	82.2	1183	2	Q5DU14_MOUSE	Q5du14 mus musculu
446	37	82.2	760	2	Q9TOK5_ARATH	Q9tok5 arabidopsis	519	37	82.2	1194	2	Q4Q490_LEIMA	Q4q490 leishmania
447	37	82.2	766	2	Q6C1M0_YARLI	Q6clm0 yarrowia li	520	37	82.2	1197	2	Q5W6I0_ORYSA	Q5w6i0 oryza sativ
448	37	82.2	770	2	Q5Q1C2_BOVIN	Q5q1c2 bos taurus	521	37	82.2	1204	2	Q4S986_TETNG	Q4s986 tetraodon n
449	37	82.2	773	2	Q7XHB6_ORYSA	Q7xhb6 oryza sativ	522	37	82.2	1314	2	Q4RHV8_TETNG	Q4rhv8 tetraodon n
450	37	82.2	773	2	Q8S7Y7_ORYSA	Q8s7y7 oryza sativ	523	37	82.2	1338	2	Q4T1Z9_TETNG	Q4t1z9 tetraodon n
451	37	82.2	776	2	Q4SAJ0_TETNG	Q4saj0 tetraodon n	524	37	82.2	1348	2	Q7XVJ2_ORYSA	Q7xvj2 oryza sativ
452	37	82.2	780	2	Q19790_CAEEL	Q19790 caenorhabdi	525	37	82.2	1417	2	Q9LNI4_ARATH	Q9lnl4 arabidopsis
453	37	82.2	787	2	Q9VEJ1_DROME	Q9vej1 drosophila	526	37	82.2	1455	2	Q7KW17_DROME	Q7kw17 drosophila
454	37	82.2	789	2	Q9YV98_DROME	Q9yv98 drosophila	527	37	82.2	1461	2	Q7S7I0_NEUCR	Q7s7i0 neurospora
455	37	82.2	797	2	Q7XHB9_ORYSA	Q7xhb9 oryza sativ	528	37	82.2	1471	2	Q4Q7G0_LEIMA	Q4q7g0 leishmania
456	37	82.2	797	2	Q8S7Z0_ORYSA	Q8s7z0 oryza sativ	529	37	82.2	1567	1	FMN2_MOUSE	Q9j104 mus musculu
457	37	82.2	802	2	Q4QAM0_LEIMA	Q4qam0 leishmania	530	37	82.2	1578	2	Q505D3_MOUSE	Q505d3 mus musculu
458	37	82.2	812	2	Q8VD17_MOUSE	Q8vd17 mus musculu	531	37	82.2	1604	2	Q4SNA3_TETNG	Q4sna3 tetraodon n
459	37	82.2	815	2	Q7XPC0_ORYSA	Q7xpc0 oryza sativ	532	37	82.2	1608	2	Q59GL0_HUMAN	Q59gl0 homo sapien
460	37	82.2	822	2	Q9G312_ARATH	Q9g312 arabidopsis	533	37	82.2	1647	1	POE1_CAEEL	Q10124 caenorhabdi
461	37	82.2	832	2	Q4SZA6_TETNG	Q4sza6 tetraodon n	534	37	82.2	1779	2	Q53LC9_ORYSA	Q53lc9 oryza sativ
462	37	82.2	864	2	Q8H837_ORYSA	Q8h837 oryza sativ	535	37	82.2	1857	1	R1MB1_HUMAN	Q9s153 homo sapien
463	37	82.2	865	2	Q6TAF5_RAT	Q6taf5 rattus norv	536	37	82.2	1858	2	Q5VYX6_HUMAN	Q5vyx6 homo sapien
464	37	82.2	868	2	Q9SDN6_TOBAC	Q9sdn6 nicotiana t	537	37	82.2	1900	2	Q9Y6X6_HUMAN	Q9y6x6 homo sapien
465	37	82.2	870	2	Q8T3T5_ASCUS	Q8t3t5 ascaris suu	538	37	82.2	1912	2	Q9ERC1_RAT	Q9erc1 rattus norv
466	37	82.2	872	2	Q7XWU7_ORYSA	Q7xwu7 oryza sativ	539	37	82.2	1914	1	RLF_HUMAN	Q13129 homo sapien
467	37	82.2	886	2	Q8H824_ORYSA	Q8h824 oryza sativ	540	37	82.2	1914	2	Q5RCL4_PONPY	Q5rc14 pongo pygma
468	37	82.2	888	2	Q9A946_HUMAN	Q9a946 homo sapien	541	37	82.2	1949	2	Q8UZB6_9VIRU	Q8uzb6 grapevine f
469	37	82.2	891	2	Q7TZX3_CHICK	Q7tzx3 gallus gall	542	37	82.2	2043	2	Q4Q510_LEIMA	Q4q510 leishmania

543	37	82.2	2229	2	Q4RWM8_TETNG	Q4rwm8 tetraodon n	616	36	80.0	144	2	Q94ES5_PEA	Q94es5 pisum sativ
544	37	82.2	2232	2	Q4Q2M1_LEIMA	Q4q2m1 leishmania	617	36	80.0	145	2	Q94ES7_PEA	Q94es7 pisum sativ
545	37	82.2	2241	2	O15850_LEIMA	O15850 leishmania	618	36	80.0	146	2	Q6CVV6_KJULA	Q6cvv6 kluyveromyc
546	37	82.2	2314	1	AKAP6_RAT	Q9wvc7 rattus norv	619	36	80.0	146	2	Q29469_CANFA	Q29469 canis famil
547	37	82.2	2921	2	Q4QF08_LEIMA	Q4qf08 leishmania	620	36	80.0	146	2	Q5ZD77_ORYSA	Q5zd77 oryza sativ
548	37	82.2	3269	2	Q8IR52_DROME	Q8ir52 drosofila	621	36	80.0	148	2	Q5Z6K4_ORYSA	Q5z6k4 oryza sativ
549	37	82.2	3387	2	Q6UDW8_PLAFA	Q6udw8 plasmodium	622	36	80.0	152	2	Q76KW4_PEA	Q76kw4 pisum sativ
550	37	82.2	3571	2	Q4QI22_LEIMA	Q4qi22 leishmania	623	36	80.0	154	2	Q41120_PHAVU	Q41120 phaseolus v
551	37	82.2	3666	2	Q6UDX0_PLAFA	Q6udx0 plasmodium	624	36	80.0	155	2	Q76KW3_PEA	Q76kw3 pisum sativ
552	37	82.2	4391	1	FCBM_HUMAN	Q98160 homo sapien	625	36	80.0	156	2	Q6YX00_ORYSA	Q6yx00 oryza sativ
553	37	82.2	4391	1	FCBM_HUMAN	Q98160 homo sapien	626	36	80.0	157	2	Q6YX01_ORYSA	Q6yx01 oryza sativ
554	36	80.0	30	2	Q7ML14_PHAVU	Q7ml14 phaseolus v	627	36	80.0	157	2	Q6YX05_ORYSA	Q6yx05 oryza sativ
555	36	80.0	35	2	Q9FSY9_CICAR	Q9fsy9 cicar ariet	628	36	80.0	158	2	Q5YLN6_CANFA	Q5yln6 canis famil
556	36	80.0	48	2	O04217_BROFI	O04217 bromheadia	629	36	80.0	159	2	Q5YLN7_CANFA	Q5yln7 canis famil
557	36	80.0	66	2	Q9XIL6_ARATH	Q9xil6 arabidopsis	630	36	80.0	161	2	Q9FSG0_NICSY	Q9fsg0 nicotiana s
558	36	80.0	68	2	Q618A3_CAEBR	Q618a3 caenorhabdi	631	36	80.0	162	2	Q8LN50_ORYSA	Q8ln50 oryza sativ
559	36	80.0	71	2	O04216_BROFI	O04216 bromheadia	632	36	80.0	163	2	Q9FJ12_ARATH	Q9fj12 arabidopsis
560	36	80.0	74	2	Q9M3Q3_HORBU	Q9m3q3 hordeum bul	633	36	80.0	162	2	Q6ZCQ8_ORYSA	Q6zcq8 oryza sativ
561	36	80.0	75	2	O5N843_ORYSA	O5n843 oryza sativ	634	36	80.0	164	2	Q9CVP6_MOUSE	Q9cvp6 mus musculu
562	36	80.0	75	2	Q01944_LYCERS	Q01944 lycopersico	635	36	80.0	165	2	Q5VSA7_ORYSA	Q5vsa7 oryza sativ
563	36	80.0	80	2	Q40146_LYCERS	Q40146 lycopersico	636	36	80.0	168	2	Q6YSS9_ORYSA	Q6yss9 oryza sativ
564	36	80.0	82	2	Q01947_LYCERS	Q01947 lycopersico	637	36	80.0	170	2	Q84MQ2_ORYSA	Q84mq2 oryza sativ
565	36	80.0	84	2	Q5ZAL7_ORYSA	Q5zal7 oryza sativ	638	36	80.0	171	2	Q8LG09_ARATH	Q8lg09 arabidopsis
566	36	80.0	87	2	Q6ERR9_ORYSA	Q6err9 oryza sativ	639	36	80.0	173	2	Q6H484_ORYSA	Q6h484 oryza sativ
567	36	80.0	88	2	Q5Z714_ORYSA	Q5z714 oryza sativ	640	36	80.0	173	2	Q8WOC7_ORYSA	Q8woc7 oryza sativ
568	36	80.0	89	2	Q7XPI1_ORYSA	Q7xpi1 oryza sativ	641	36	80.0	175	2	Q6ZLG2_ORYSA	Q6zlg2 oryza sativ
569	36	80.0	95	2	Q8H7G3_ARATH	Q8h7g3 arabidopsis	642	36	80.0	180	2	Q8DKV7_SYNEL	Q8dkv7 synechococc
570	36	80.0	99	2	Q4PM62_IXOSC	Q4pm62 ixodes scap	643	36	80.0	181	2	Q01943_LYCERS	Q01943 lycopersico
571	36	80.0	100	2	O5BZZ9_SCHJA	O5bzz9 schistosoma	644	36	80.0	181	2	Q94ES6_PEA	Q94es6 pisum sativ
572	36	80.0	101	2	O5AHK9_CANAL	O5ahk9 candida alb	645	36	80.0	181	2	Q9LVH4_ARATH	Q9lvh4 arabidopsis
573	36	80.0	102	2	Q6ZJ49_ORYSA	Q6zj49 oryza sativ	646	36	80.0	182	2	Q7XKV3_ORYSA	Q7xkv3 oryza sativ
574	36	80.0	105	2	Q5SN40_ORYSA	Q5sn40 oryza sativ	647	36	80.0	183	2	Q94ES9_PEA	Q94es9 pisum sativ
575	36	80.0	107	2	O5YLN5_CANFA	O5yln5 canis famil	648	36	80.0	184	2	Q67WC1_ORYSA	Q67wc1 oryza sativ
576	36	80.0	108	2	Q7NHL3_GLOVI	Q7nhl3 gloeobacter	649	36	80.0	186	2	Q7F8Y7_ORYSA	Q7f8y7 oryza sativ
577	36	80.0	110	2	Q6E082_ORYSA	Q6e082 oryza sativ	650	36	80.0	186	2	Q4RDU6_TETNG	Q4rdu6 tetraodon n
578	36	80.0	111	2	Q69QY6_ORYSA	Q69qy6 oryza sativ	651	36	80.0	189	2	Q9KZZ6_STRCO	Q9kzz6 streptomyce
579	36	80.0	111	2	Q9D4P8_MOUSE	Q9d4p8 mus musculu	652	36	80.0	192	2	Q6S760_CICAR	Q6s760 cicar ariet
580	36	80.0	113	2	Q50400_HUMAN	Q50400 homo sapien	653	36	80.0	193	2	Q411U0_GIBZE	Q411u0 gibbrellia
581	36	80.0	113	2	Q5SNA5_ORYSA	Q5sna5 oryza sativ	654	36	80.0	193	2	Q7FIJ4_ORYSA	Q7fij4 oryza sativ
582	36	80.0	113	2	Q8LHG5_ORYSA	Q8lhg5 oryza sativ	655	36	80.0	193	2	Q94D24_ORYSA	Q94d24 oryza sativ
583	36	80.0	114	2	Q7SGN7_NEUCR	Q7sgn7 neurospora	656	36	80.0	194	2	Q6T619_BRARP	Q6t619 brassica ra
584	36	80.0	116	2	Q5SBJ5_HUMAN	Q5sbj5 homo sapien	657	36	80.0	194	2	Q8BR48_MOUSE	Q8br48 mus musculu
585	36	80.0	116	2	Q5SBJ6_HUMAN	Q5sbj6 homo sapien	658	36	80.0	195	2	Q84U10_LUPAN	Q84u10 lupinus ang
586	36	80.0	116	2	Q5SBJ7_HUMAN	Q5sbj7 homo sapien	659	36	80.0	195	2	Q94ES8_PEA	Q94es8 pisum sativ
587	36	80.0	116	2	Q5SBJ8_HUMAN	Q5sbj8 homo sapien	660	36	80.0	196	2	Q29484_HORSE	Q29484 equus cabal
588	36	80.0	116	2	Q5SBJ9_HUMAN	Q5sbj9 homo sapien	661	36	80.0	196	2	Q5I784_BRARE	Q5i784 brachydanio
589	36	80.0	116	2	Q5SBK0_HUMAN	Q5sbk0 homo sapien	662	36	80.0	198	2	Q5CUT4_CRYPV	Q5cut4 cryptospori
590	36	80.0	116	2	Q5SBK1_HUMAN	Q5sbk1 homo sapien	663	36	80.0	198	2	Q5CG00_CRYHO	Q5cg00 cryptospori
591	36	80.0	116	2	Q5SBK2_HUMAN	Q5sbk2 homo sapien	664	36	80.0	198	2	Q60DT1_ORYSA	Q60dt1 oryza sativ
592	36	80.0	116	2	Q5SBK3_HUMAN	Q5sbk3 homo sapien	665	36	80.0	198	2	Q6GUG3_LUPAN	Q6gug3 lupinus ang
593	36	80.0	116	2	Q5SBK4_HUMAN	Q5sbk4 homo sapien	666	36	80.0	199	2	Q8H389_ORYSA	Q8h389 oryza sativ
594	36	80.0	116	2	Q5SBK5_HUMAN	Q5sbk5 homo sapien	667	36	80.0	201	2	Q8LB15_ARATH	Q8lb15 arabidopsis
595	36	80.0	116	2	Q5SBK6_HUMAN	Q5sbk6 homo sapien	668	36	80.0	201	2	Q9XIN6_ARATH	Q9xine arabidopsis
596	36	80.0	118	2	Q5JN11_ORYSA	Q5jnl1 oryza sativ	669	36	80.0	203	2	Q5DLN9_GOSHI	Q5dlng gossypium h
597	36	80.0	119	2	Q4PFI5_USTWA	Q4pfi5 utiilago ma	670	36	80.0	206	2	Q5N3R8_SYNPF	Q5n3r8 synechococc
598	36	80.0	119	2	Q75GV1_ORYSA	Q75gv1 oryza sativ	671	36	80.0	207	1	P53_EQUAS	Q29480 equus asinu
599	36	80.0	120	2	Q94ES4_PEA	Q94es4 pisum sativ	672	36	80.0	212	2	Q59LJ4_CANAL	Q59lj4 candida alb
600	36	80.0	124	2	Q9D992_MOUSE	Q9d992 mus musculu	673	36	80.0	212	2	Q9ZW80_ARATH	Q9zw80 arabidopsis
601	36	80.0	126	2	Q8H604_ORYSA	Q8h604 oryza sativ	674	36	80.0	213	2	Q59X46_CANAL	Q59x46 candida alb
602	36	80.0	126	2	Q80W61_MOUSE	Q80w61 mus musculu	675	36	80.0	214	2	Q6R588_ORYSA	Q6r588 oryza sativ
603	36	80.0	129	2	Q8H2A8_ANACO	Q8h2a8 ananas como	676	36	80.0	214	2	Q9ASP1_ORYSA	Q9asp1 oryza sativ
604	36	80.0	131	2	Q40415_NICSY	Q40415 nicotiana s	677	36	80.0	215	2	Q5Z925_ORYSA	Q5z925 oryza sativ
605	36	80.0	132	2	Q9HB98_HUMAN	Q9hb98 homo sapien	678	36	80.0	216	2	Q6Z138_ORYSA	Q6z138 oryza sativ
606	36	80.0	132	2	Q9HB99_HUMAN	Q9hb99 homo sapien	679	36	80.0	216	2	Q7XGR5_ORYSA	Q7xgr5 oryza sativ
607	36	80.0	132	2	Q9HC54_HUMAN	Q9hc54 homo sapien	680	36	80.0	217	2	Q39600_CATRO	Q39600 catharanthu
608	36	80.0	132	2	Q9HC55_HUMAN	Q9hc55 homo sapien	681	36	80.0	218	2	Q4J7M6_SULAC	Q4j7m6 sulfolobus
609	36	80.0	132	2	Q01942_LYCERS	Q01942 lycopersico	682	36	80.0	219	2	Q61CQ2_CAEBR	Q61cq2 caenorhabdi
610	36	80.0	132	2	Q74YR1_YERPE	Q74yr1 yerisinia pe	683	36	80.0	220	2	Q6ZG44_ORYSA	Q6zg44 oryza sativ
611	36	80.0	134	2	Q9LJ80_ARATH	Q9lj80 arabidopsis	684	36	80.0	223	2	Q6EQX4_ORYSA	Q6eqx4 oryza sativ
612	36	80.0	136	2	Q6ZLJ0_ORYSA	Q6zlj0 oryza sativ	685	36	80.0	224	2	Q40503_TOBAC	Q40503 nicotiana t
613	36	80.0	137	2	Q76KW2_PEA	Q76kw2 pisum sativ	686	36	80.0	224	2	Q9M381_ARATH	Q9m381 arabidopsis
614	36	80.0	137	2	Q94ES3_PEA	Q94es3 pisum sativ	687	36	80.0	224	2	Q7G2C0_ORYSA	Q7g2c0 oryza sativ
615	36	80.0	137	2	Q9XG52_LYCERS	Q9xg52 lycopersico	688	36	80.0	225	1	BRF3_ARATH	Q80339 arabidopsis

689	36	80.0	225	2	Q39599_CATRO	Q39599_catharanthu	762	36	80.0	298	2	Q4PD30_USTMA	Q4pd30_ustilago ma
690	36	80.0	228	2	Q8H543_ORYSA	Q8H543 oryza sativ	763	36	80.0	300	2	Q69M83_ORYSA	Q69m83 oryza sativ
691	36	80.0	229	1	LB011_ARATH	Q9sk08 arabidopsis	764	36	80.0	301	2	Q6L4D1_ORYSA	Q6l4d1 oryza sativ
692	36	80.0	230	1	Q7DMV8_PHAVU	Q7dmv8 phaseolus v	765	36	80.0	302	2	Q9CAC7_ARATH	Q9cac7 arabidopsis
693	36	80.0	230	2	Q9LSN7_ARATH	Q9lsn7 arabidopsis	766	36	80.0	302	2	Q4TW5_TETNG	Q4stw5 tetraodon n
694	36	80.0	231	2	Q89F38_BRAJA	Q89f38 bradyrhizob	767	36	80.0	303	2	Q6ER69_ORYSA	Q6er69 oryza sativ
695	36	80.0	232	2	Q7T0Z7_XENLA	Q7t0z7 xenopus lae	768	36	80.0	304	1	GATAI_CHICK	P17678 gallus gall
696	36	80.0	233	2	Q9FJS9_ARATH	Q9fjs9 arabidopsis	769	36	80.0	304	2	Q60EA4_ORYSA	Q60ea4 oryza sativ
697	36	80.0	236	2	Q5VMZ4_ORYSA	Q5vmz4 oryza sativ	770	36	80.0	304	2	Q651H4_ORYSA	Q651h4 oryza sativ
698	36	80.0	236	2	Q94LF7_ORYSA	Q94lf7 oryza sativ	771	36	80.0	305	2	Q9SH44_ARATH	Q9sh44 arabidopsis
699	36	80.0	238	2	Q5JLD7_ORYSA	Q5jld7 oryza sativ	772	36	80.0	306	1	EXTN_DAUCA	Q96599 daucus caro
700	36	80.0	239	2	Q4X0A3_ASPFU	Q4x0a3 aspergillus	773	36	80.0	306	2	P93845_PEA	P93845 pisum sativ
701	36	80.0	240	2	Q8H8T2_ORYSA	Q8h8t2 oryza sativ	774	36	80.0	307	2	Q9DBES_MOUSE	Q9dbes mus musculu
702	36	80.0	241	2	Q6Z1T9_ORYSA	Q6z1t9 oryza sativ	775	36	80.0	311	2	Q8LQ38_ORYSA	Q8lq38 oryza sativ
703	36	80.0	242	2	Q83B87_VIGUN	Q83b87 vigna ungui	776	36	80.0	311	2	Q9FSG1_NICSY	Q9fsg1 nicotiana s
704	36	80.0	244	2	Q4BBV2_9VIRU	Q4bbv2 garlic viru	777	36	80.0	312	2	Q4QF88_LEIMA	Q4qf88 leishmania
705	36	80.0	246	2	Q9TUX4_CANFA	Q9tux4 canis famil	778	36	80.0	312	2	Q9S174_ARATH	Q9s174 arabidopsis
706	36	80.0	247	2	Q4WX19_ASPFU	Q4wx19 aspergillus	779	36	80.0	312	2	Q440V7_XENLA	Q440v7 xenopus lae
707	36	80.0	247	2	Q9LDY5_ARATH	Q9ldy5 arabidopsis	780	36	80.0	312	2	Q4V810_XENLA	Q4v810 xenopus lae
708	36	80.0	247	2	Q75HX9_ORYSA	Q75hx9 oryza sativ	781	36	80.0	313	2	Q9LZJ7_ARATH	Q9lztj7 arabidopsis
709	36	80.0	247	2	Q8S136_ORYSA	Q8s136 oryza sativ	782	36	80.0	313	2	Q9M7N9_ARATH	Q9m7n9 arabidopsis
710	36	80.0	249	2	Q4PSF3_ARATH	Q4psf3 arabidopsis	783	36	80.0	314	2	Q9L1V7_ORYSA	Q9l1v7 oryza sativ
711	36	80.0	250	2	Q7XEM4_ORYSA	Q7xew4 oryza sativ	784	36	80.0	315	2	Q5Z5Z1_CRYNE	Q5z5z1 cryptococcu
712	36	80.0	250	2	Q94125_ORYSA	Q94125 oryza sativ	785	36	80.0	315	2	Q5KNG6_CRYNE	Q5kng6 cryptococcu
713	36	80.0	252	2	Q8GYZ7_ARATH	Q8gyz7 arabidopsis	786	36	80.0	316	2	Q7EY23_ORYSA	Q7ey23 oryza sativ
714	36	80.0	254	2	Q5U4U7_DICDI	Q5u4u7 dictyosteli	787	36	80.0	317	2	Q8H4Q2_ORYSA	Q8h4q2 oryza sativ
715	36	80.0	254	2	Q6F2M2_ORYSA	Q6f2m2 oryza sativ	788	36	80.0	317	2	Q4NK76_9MICC	Q4nk76 arabidacte
716	36	80.0	255	2	Q6F2M2_ORYSA	Q6f2m2 oryza sativ	789	36	80.0	318	2	Q68002_TOBAC	Q68002 nicotiana t
717	36	80.0	258	2	Q9HA86_HUMAN	Q9ha86 homo sapien	790	36	80.0	318	2	Q8CD25_MOUSE	Q8cd25 mus musculu
718	36	80.0	258	2	Q6YTX3_ORYSA	Q6ytx3 oryza sativ	791	36	80.0	319	1	TTP_MOUSE	T22893 mus musculu
719	36	80.0	259	2	Q40793_PETCR	Q40793 petroselinu	792	36	80.0	320	1	TTP_RAT	P47973 rattus norv
720	36	80.0	259	2	Q8LK15_BRANA	Q8lk15 brassica na	793	36	80.0	320	2	Q6H613_ORYSA	Q6h613 oryza sativ
721	36	80.0	260	2	Q61R97_CABBR	Q61r97 caenorhabdi	794	36	80.0	320	2	Q54AH1_RAT	Q54ahl rattus norv
722	36	80.0	260	2	Q7KW87_DROME	Q7kw87 drosophila	795	36	80.0	320	2	Q6GNE8_XENLA	Q6gne8 xenopus lae
723	36	80.0	260	2	Q69K97_ORYSA	Q69k97 oryza sativ	796	36	80.0	322	2	Q9J084_LYCES	Q9j084 lycopersico
724	36	80.0	260	2	Q6ZJ43_ORYSA	Q6zj43 oryza sativ	797	36	80.0	324	1	TTP_BOVIN	P53781 bos taurus
725	36	80.0	261	2	Q4RIY2_TETNG	Q4riy2 tetraodon n	798	36	80.0	325	1	TTP_SHEEP	Q68960 ovis aries
726	36	80.0	262	2	Q69Q72_ORYSA	Q69q72 oryza sativ	799	36	80.0	325	2	Q6EQG2_ORYSA	Q6eqg2 oryza sativ
727	36	80.0	263	2	Q39949_HELAN	Q39949 helianthus	800	36	80.0	326	2	Q82BG7_STRAW	Q82bg7 streptomyce
728	36	80.0	264	2	Q69Q88_ORYSA	Q69qr8 oryza sativ	801	36	80.0	326	1	TTP_HUMAN	P26651 homo sapien
729	36	80.0	264	2	Q9ZQZ0_ORYSA	Q9zqz0 oryza sativ	802	36	80.0	326	2	Q5ZAJ5_ORYSA	Q5za75 oryza sativ
730	36	80.0	265	2	Q9C7V8_ARATH	Q9c7v8 arabidopsis	803	36	80.0	327	2	Q9M6R7_PEA	Q9mcr7 pisum sativ
731	36	80.0	267	2	Q4WND3_ASPFU	Q4wnd3 aspergillus	804	36	80.0	328	2	Q5VQ11_ORYSA	Q5vq11 oryza sativ
732	36	80.0	268	1	NO20_MEDTR	P93329 medicago tr	805	36	80.0	328	2	Q6Z846_ORYSA	Q6z846 oryza sativ
733	36	80.0	269	2	Q615V3_ORYSA	Q615v3 oryza sativ	806	36	80.0	329	1	CLH1_CITSI	Q9mw14 citrus sine
734	36	80.0	269	2	Q75GB4_ORYSA	Q75gb4 oryza sativ	807	36	80.0	329	1	CLH1_CITUN	Q941x1 citrus unsh
735	36	80.0	270	2	Q05994_ACTNA	Q05994 actinomycet	808	36	80.0	330	2	Q7PNE1_ANOGA	Q7pnf1 anopheles g
736	36	80.0	271	2	Q9AV18_ORYSA	Q9av18 oryza sativ	809	36	80.0	334	2	Q9LHS1_ARATH	Q9lhs1 arabidopsis
737	36	80.0	273	2	Q53M04_ORYSA	Q53m04 oryza sativ	810	36	80.0	335	2	Q4SWD7_TETNG	Q4sbd7 tetraodon n
738	36	80.0	274	2	Q5B505_EMENI	Q5b505 aspergillus	811	36	80.0	338	2	Q7Y033_ARATH	Q7y033 arabidopsis
739	36	80.0	274	2	Q60970_LEIMA	Q60970 leishmania	812	36	80.0	340	2	Q7F8U5_ORYSA	Q7f8u5 oryza sativ
740	36	80.0	274	2	Q8LNG5_ORYSA	Q8lng5 oryza sativ	813	36	80.0	343	2	Q6K6Z4_ORYSA	Q6k6z4 oryza sativ
741	36	80.0	278	2	Q40768_PRUDU	Q40768 prunus dulc	814	36	80.0	348	2	Q86JW4_DICDI	Q86jw4 dictyosteli
742	36	80.0	279	2	Q4ER91_CAMUP	Q4hr91 campylobact	815	36	80.0	348	2	Q8RZ42_ORYSA	Q8rz42 oryza sativ
743	36	80.0	279	2	Q4RA01_TETNG	Q4ra01 tetraodon n	816	36	80.0	349	2	Q6Z136_ORYSA	Q6z136 oryza sativ
744	36	80.0	280	1	P53_HORSE	P79892 equus cabal	817	36	80.0	349	2	Q81P97_ORYSA	Q81p97 oryza sativ
745	36	80.0	280	2	Q6ZTD7_HUMAN	Q6ztd7 homo sapien	818	36	80.0	350	2	Q61TS9_CABBR	Q61ts9 caenorhabdi
746	36	80.0	280	2	Q40502_TOBAC	Q40502 nicotiana t	819	36	80.0	350	2	Q9STN1_ARATH	Q9stn1 arabidopsis
747	36	80.0	281	2	Q29475_CANFA	Q29475 canis famil	820	36	80.0	354	2	Q9SRV2_ARATH	Q9srv2 arabidopsis
748	36	80.0	281	2	Q6ZGC3_ORYSA	Q6zgc3 oryza sativ	821	36	80.0	356	2	Q4Q8Z8_LEIMA	Q4q8z8 leishmania
749	36	80.0	282	2	Q4RI62_TETNG	Q4ri62 tetraodon n	822	36	80.0	357	2	Q9LVK2_ARATH	Q9lvk2 arabidopsis
750	36	80.0	283	1	EXTN_SORBI	P24152 sorghum bic	823	36	80.0	358	2	Q4P569_USTMA	Q4p569 ustilago ma
751	36	80.0	284	2	Q6UDL8_9HERP	Q6udl8 psittacid h	824	36	80.0	358	2	Q9AAV7_CAUCR	Q9aav7 caulobacter
752	36	80.0	285	2	Q95326_CANFA	Q95326 canis famil	825	36	80.0	359	2	Q7FAP4_ORYSA	Q7fap4 oryza sativ
753	36	80.0	286	2	Q61KY7_DROME	Q61ky7 drosophila	826	36	80.0	359	2	Q7XP48_ORYSA	Q7xp48 oryza sativ
754	36	80.0	287	2	Q5EB31_ORYSA	Q5eb31 oryza sativ	827	36	80.0	360	2	Q68DD1_HUMAN	Q68dd1 homo sapien
755	36	80.0	287	2	Q6K2H9_ORYSA	Q6k2h9 oryza sativ	828	36	80.0	362	2	Q940U3_ARATH	Q940u3 arabidopsis
756	36	80.0	287	2	Q4RPT4_TETNG	Q4rpt4 tetraodon n	829	36	80.0	362	2	Q6AXI3_BRARE	Q6axi3 brachydanio
757	36	80.0	289	2	Q5Z572_ORYSA	Q5z572 oryza sativ	830	36	80.0	366	2	Q58CR1_BOVIN	Q58cr1 bos taurus
758	36	80.0	290	2	Q6ZGY7_ORYSA	Q6zgy7 oryza sativ	831	36	80.0	367	2	Q5B0H1_EMENI	Q5b0h1 aspergillus
759	36	80.0	291	2	Q06446_SOLTU	Q06446 solanum tub	832	36	80.0	367	2	Q4T471_TETNG	Q4t471 tetraodon n
760	36	80.0	292	2	Q53LG8_ORYSA	Q53lg8 oryza sativ	833	36	80.0	369	2	Q5KNM7_CRYNE	Q5knm7 cryptococcu
761	36	80.0	294	2	Q642Y2_FUGRU	Q642y2 fugu rubrip	834	36	80.0	369	2	Q7Q6Y2_ANOGA	Q7q6y2 anopheles g

835	36	80.0	373	1	EXTN1_ARATH	Q38913 arabidopsis	908	36	80.0	438	2	Q5TXQ2_ANOGA	Q5txq2 anopheles g
836	36	80.0	374	2	Q6ZBF0_ORISA	Q6zbf0 oryza sativ	909	36	80.0	440	2	Q9LMU8_ARATH	Q9lmu8 arabidopsis
837	36	80.0	375	1	Q6K9M2_ORISA	Q6k9m2 oryza sativ	910	36	80.0	440	2	Q9SM19_MAIZE	Q9sm19 zea mays m
838	36	80.0	374	2	Q6SYB4_ORISA	Q6syb4 oryza sativ	911	36	80.0	441	2	Q5SKH6_CRYNE	Q5skh6 cryptococcu
839	36	80.0	375	1	SOX3_MOUSE	P53784 mus musculu	912	36	80.0	441	2	Q8T8E3_TRICA	Q8t8e3 tribolium c
840	36	80.0	375	2	Q5ZB2_CRYNE	Q5z2b2 cryptococcu	913	36	80.0	442	2	Q5K933_CRYNE	Q5k933 cryptococcu
841	36	80.0	375	2	Q5VPG5_ORISA	Q5vpg5 oryza sativ	914	36	80.0	443	2	Q9C669_ARATH	Q9c669 arabidopsis
842	36	80.0	375	2	Q80XF1_MOUSE	Q80xf1 mus musculu	915	36	80.0	444	2	Q872E7_NEUCR	Q872e7 neurospora
843	36	80.0	378	2	Q7XDQ7_ORISA	Q7xdq7 oryza sativ	916	36	80.0	444	2	Q7PS47_ANOGA	Q7ps47 anopheles g
844	36	80.0	381	1	P53_CANFA	Q29537 canis famil	917	36	80.0	445	2	Q7X8S1_ORISA	Q7x8s1 oryza sativ
845	36	80.0	381	2	Q6ZBB6_ORISA	Q6zbb6 oryza sativ	918	36	80.0	446	1	SOX3_HUMAN	P41225 homo sapien
846	36	80.0	385	2	Q6CGL6_YARLI	Q6cgl6 varrowia li	919	36	80.0	446	2	Q5JWI3_HUMAN	Q5jwi3 homo sapien
847	36	80.0	386	1	P53_PIG	Q3tub2 sus crofa	920	36	80.0	446	2	Q8DLB1_SYNEL	Q8dle1 synecococc
848	36	80.0	387	2	Q3B694_EMENI	Q3b694 aspergillus	921	36	80.0	447	2	Q7QLB8_ANOGA	Q7qlb8 anopheles g
849	36	80.0	387	2	Q8SPZ3_DELLE	Q8spz3 delphinapce	922	36	80.0	448	2	Q6P564_MOUSE	Q6p564 mus musculu
850	36	80.0	388	2	Q09082_LYCES	Q09082 lycopersico	923	36	80.0	449	2	Q5SRK0_MOUSE	Q5srk0 mus musculu
851	36	80.0	388	2	Q5Z6M4_ORISA	Q5z6m4 oryza sativ	924	36	80.0	452	2	Q4TB69_TETNG	Q4tb69 tetraodon n
852	36	80.0	390	1	DAF1_MOUSE	Q61475 mus musculu	925	36	80.0	455	2	Q60UX9_CAEBR	Q60ux9 caenorhabdi
853	36	80.0	390	2	Q921P0_MOUSE	Q921p0 mus musculu	926	36	80.0	457	2	Q60WS8_CAEBR	Q60ws8 caenorhabdi
854	36	80.0	390	2	Q4FJ84_MOUSE	Q4fj84 mus musculu	927	36	80.0	457	2	Q9BHL0_CAEBL	Q9bhl0 caenorhabdi
855	36	80.0	393	2	Q6Z2B1_ORISA	Q6z2b1 oryza sativ	928	36	80.0	458	2	Q56W89_ARATH	Q56w89 arabidopsis
856	36	80.0	394	2	Q5S8G3_CRYNE	Q5s8g3 cryptococcu	929	36	80.0	460	2	Q5TT70_ANOGA	Q5tt70 anopheles g
857	36	80.0	396	2	Q67UT0_ORISA	Q67ut0 oryza sativ	930	36	80.0	460	2	Q8LIF0_ORISA	Q8lif0 oryza sativ
858	36	80.0	397	2	Q8TPB0_TRIVE	Q8tpb0 trichoderma	931	36	80.0	461	2	Q9VRQ6_DROME	Q9vrq6 drosophila
859	36	80.0	398	2	Q7S946_NEUCR	Q7s946 neurospora	932	36	80.0	461	2	Q49986_NICAL	Q49986 nicotiana a
860	36	80.0	398	2	Q9U909_DROYA	Q9u909 drosophila	933	36	80.0	463	2	Q5VMB4_ORISA	Q5vmb4 oryza sativ
861	36	80.0	398	2	Q6SGG3_9BACT	Q6sgg3 uncultured	934	36	80.0	463	2	Q8LI07_ARATH	Q8li07 arabidopsis
862	36	80.0	399	2	Q6YFP3_ORISA	Q6yfp3 oryza sativ	935	36	80.0	463	2	Q8LGI7_ARATH	Q8lgi7 arabidopsis
863	36	80.0	400	2	Q9U908_DROER	Q9u908 drosophila	936	36	80.0	463	2	Q9LYT9_ARATH	Q9lyt9 arabidopsis
864	36	80.0	401	2	Q7S4Q1_NEUCR	Q7s4q1 neurospora	937	36	80.0	464	2	Q41645_VOLCA	Q41645 volvox cart
865	36	80.0	404	2	Q4SMW3_TETNG	Q4smw3 tetraodon n	938	36	80.0	466	2	Q41911_GIBZE	Q41911 gibberella
866	36	80.0	406	2	Q6VL01_DROME	Q6vl01 drosophila	939	36	80.0	467	2	Q919C5_CHICK	Q919c5 gallus gall
867	36	80.0	406	2	Q86P88_DROME	Q86p88 drosophila	940	36	80.0	468	2	Q5W6X4_ORISA	Q5w6x4 oryza sativ
868	36	80.0	407	2	Q551Y4_CRYNE	Q551y4 cryptococcu	941	36	80.0	472	2	Q67U47_ORISA	Q67u47 oryza sativ
869	36	80.0	407	2	Q5KCR9_CRYNE	Q5kcr9 cryptococcu	942	36	80.0	473	2	Q869M2_DICDI	Q869m2 dictyosteli
870	36	80.0	407	2	Q5E925_ARATH	Q5e925 arabidopsis	943	36	80.0	474	2	Q5KCT0_CRYNE	Q5kct0 cryptococcu
871	36	80.0	408	2	Q4Q423_LEIMA	Q4q423 leishmania	944	36	80.0	475	2	Q96EK3_HUMAN	Q96ek3 homo sapien
872	36	80.0	408	2	Q4RRF7_TETNG	Q4rrf7 tetraodon n	945	36	80.0	475	2	Q8IYU4_HUMAN	Q8iyu4 homo sapien
873	36	80.0	409	1	CRD1_ARATH	Q9m591 a magnesium	946	36	80.0	477	2	Q5BIU0_EMENI	Q5biu0 aspergillus
874	36	80.0	409	2	Q69QB4_ORISA	Q69qb4 oryza sativ	947	36	80.0	477	2	Q716P6_9CAUD	Q716p6 mycobacteri
875	36	80.0	410	2	Q5AKY2_CANAL	Q5aky2 candida alb	948	36	80.0	477	2	Q851M1_ORISA	Q851m1 oryza sativ
876	36	80.0	411	1	CPRF1_PETCR	Q99089 petroselinu	949	36	80.0	478	2	Q9C668_ARATH	Q9c668 arabidopsis
877	36	80.0	412	2	Q8Z869_ORISA	Q8z869 oryza sativ	950	36	80.0	486	1	COBB_SFRCO	Q8rj16 streptomyce
878	36	80.0	412	2	Q8ZH83_STRAW	Q8zh83 streptomyce	951	36	80.0	487	2	Q8H1D7_ARATH	Q8h1d7 arabidopsis
879	36	80.0	414	2	Q9UBU2_DROSI	Q9ub2 drosophila	952	36	80.0	487	2	Q93ZU2_ARATH	Q93zu2 arabidopsis
880	36	80.0	414	2	Q94AS1_ARATH	Q94as1 arabidopsis	953	36	80.0	489	2	Q4SEF7_TETNG	Q4sef7 tetraodon n
881	36	80.0	414	2	Q9SEB5_ARATH	Q9see5 arabidopsis	954	36	80.0	490	2	Q5AAN3_CANAL	Q5aan3 candida alb
882	36	80.0	415	2	Q7RWV1_NEUCR	Q7rvw1 neurospora	955	36	80.0	490	2	O14670_HUMAN	O14670 homo sapien
883	36	80.0	415	2	Q6S9B6_VOLCA	Q6s9b6 volvox cart	956	36	80.0	491	2	Q4Q3F4_LEIMA	Q4q3f4 leishmania
884	36	80.0	415	2	Q4S8M8_TETNG	Q4s8m8 tetraodon n	957	36	80.0	492	2	Q9FK84_ARATH	Q9fk84 arabidopsis
885	36	80.0	416	2	Q9UBU0_DROTE	Q9ubu0 drosophila	958	36	80.0	492	2	O5NWA2_AZOSE	O5nwa2 azoarcus sp
886	36	80.0	416	2	Q40402_NICPL	Q40402 nicotiana p	959	36	80.0	492	2	Q5P428_AZOSE	Q5p428 azoarcus sp
887	36	80.0	417	2	Q8H035_ORISA	Q8h035 oryza sativ	960	36	80.0	492	2	Q6ZPP8_MOUSE	Q6zpp8 mus musculu
888	36	80.0	417	2	Q67ZC3_ARATH	Q67zc3 arabidopsis	961	36	80.0	494	2	Q9LHF1_ARATH	Q9lhf1 arabidopsis
889	36	80.0	418	2	Q9UBT8_DROOR	Q9ubt8 drosophila	962	36	80.0	497	2	Q8CE96_MOUSE	Q8ce96 m mus muscu
890	36	80.0	418	2	Q82H63_STRAW	Q82h63 streptomyce	963	36	80.0	498	1	VGLX_FRVRI	P07562 pseudorabie
891	36	80.0	419	2	Q9P7C0_AZOSE	Q9p7c0 azoarcus sp	964	36	80.0	498	2	Q5A7M4_CANAL	Q5a7m4 candida alb
892	36	80.0	422	2	Q6S9W6_9ACTO	Q6s9w6 streptomyce	965	36	80.0	498	2	Q6BJD0_DEBHA	Q6bjd0 debaryomyce
893	36	80.0	423	1	ATL2C_ARATH	Q9zv53 arabidopsis	966	36	80.0	498	2	O55XG2_CRYNE	O55xg2 cryptococcu
894	36	80.0	424	2	Q6Z7A0_ORISA	Q6z7a0 oryza sativ	967	36	80.0	498	2	Q8S3D4_ARATH	Q8s3d4 arabidopsis
895	36	80.0	427	1	EXTN3_ARATH	Q9fs16 arabidopsis	968	36	80.0	498	2	Q9FUL4_ARATH	Q9ful4 arabidopsis
896	36	80.0	427	2	Q4HVQ4_GIBZE	Q4hvq4 gibberella	969	36	80.0	498	2	Q5PP79_9ALPH	Q5pp79 suid herpes
897	36	80.0	427	2	Q75GQ8_ORISA	Q75gq8 oryza sativ	970	36	80.0	499	2	O5KMH1_CRYNE	O5kmh1 cryptococcu
898	36	80.0	429	2	Q23046_CABEL	Q23046 caenorhabdi	971	36	80.0	503	2	Q598E2_CANAL	Q598e2 candida alb
899	36	80.0	429	2	Q7T0L0_ARATH	Q7t0l0 arabidopsis	972	36	80.0	503	2	Q7PYZ3_ANOGA	Q7pyz3 anopheles g
900	36	80.0	430	2	Q60WS2_CAEBR	Q60ws2 caenorhabdi	973	36	80.0	503	2	Q8LJ87_ORISA	Q8lj87 oryza sativ
901	36	80.0	432	2	Q39835_SOYBN	Q39835 glycine max	974	36	80.0	503	2	Q8CSU4_MOUSE	Q8csu4 mus musculu
902	36	80.0	433	2	Q5TXQ3_ANOGA	Q5txq3 anopheles g	975	36	80.0	504	2	Q5N800_ORISA	Q5n800 oryza sativ
903	36	80.0	434	2	Q9HEL2_NEUCR	Q9hel2 neurospora	976	36	80.0	504	2	Q7UVP2_RHOBA	Q7uvp2 rhodopirell
904	36	80.0	434	2	Q9FG07_ARATH	Q9fg07 arabidopsis	977	36	80.0	504	2	Q68FV4_RAT	Q68fv4 rattus norv
905	36	80.0	436	2	Q51P87_MAGGR	Q51p87 magnaporthe	978	36	80.0	505	2	O5CJU2_CRYHO	O5cju2 cryptospori
906	36	80.0	436	2	Q33ZD7_ARATH	Q33zd7 arabidopsis	979	36	80.0	508	2	Q6H559_ORISA	Q6h559 oryza sativ
907	36	80.0	436	2	Q4VBD8_MOUSE	Q4vbd8 mus musculu	980	36	80.0	509	2	O01792_CABEL	O01792 caenorhabdi

Q5txq2 anopheles g	Q9lmu8 arabidopsis	Q9sm19 zea mays m	Q5skh6 cryptococcu	Q8t8e3 tribolium c	Q5k933 cryptococcu	Q9c669 arabidopsis	Q872e7 neurospora	Q7ps47 anopheles g	Q7x8s1 oryza sativ	P41225 homo sapien	Q5jwi3 homo sapien	Q8dle1 synecococc	Q7qlb8 anopheles g	Q6p564 mus musculu	Q5srk0 mus musculu	Q4tb69 tetraodon n	Q60ux9 caenorhabdi	Q60ws8 caenorhabdi	Q9bhl0 caenorhabdi	Q56w89 arabidopsis	Q5tt70 anopheles g	Q8lif0 oryza sativ	Q9vrq6 drosophila	Q49986 nicotiana a	Q5vmb4 oryza sativ	Q8li07 arabidopsis	Q8lgi7 arabidopsis	Q9lyt9 arabidopsis	Q41645 volvox cart	Q41911 gibberella	Q919c5 gallus gall	Q5w6x4 oryza sativ	Q67u47 oryza sativ	Q869m2 dictyosteli	Q851m1 oryza sativ	Q9c668 arabidopsis	Q8rj16 streptomyce	Q8h1d7 arabidopsis	Q93zu2 arabidopsis	Q4sef7 tetraodon n	Q5aan3 candida alb	O14670 homo sapien	Q4q3f4 leishmania	Q9fk84 arabidopsis	Q5nwa2 azoarcus sp	Q5p428 azoarcus sp	Q6zpp8 mus musculu	Q9lhf1 arabidopsis	Q8ce96 m mus muscu	P07562 pseudorabie	Q5a7m4 candida alb	Q6bjd0 debaryomyce	O55xg2 cryptococcu	Q8s3d4 arabidopsis	Q9ful4 arabidopsis	Q5pp79 suid herpes	O5kmh1 cryptococcu	Q598e2 candida alb	O7pyz3 anopheles g	Q8lj87 oryza sativ	Q8csu4 mus musculu	Q5n800 oryza sativ	Q7uvp2 rhodopirell	Q68fv4 rattus norv	O5cju2 cryptospori	Q6h559 oryza sativ	O01792 caenorhabdi
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981 36 80.0 510 2 Q60ER5_ORYSA
982 36 80.0 511 2 Q55R29_CRYNE
983 36 80.0 511 2 Q5KGF1_CRYNE
984 36 80.0 511 2 Q9S231_ARYTH
985 36 80.0 511 2 Q6NX29_XENTR
986 36 80.0 512 2 Q6NRE3_XENLA
987 36 80.0 512 2 Q6NRE3_XENLA
988 36 80.0 513 2 Q5STM8_ARYTH
989 36 80.0 514 2 Q5UCV6_CRYPV
990 36 80.0 515 2 Q51WB6_MAGGR
991 36 80.0 517 2 Q9PSU0_NEUCR
992 36 80.0 517 2 Q54MB1_DICDI
993 36 80.0 520 2 Q92H62_RICCN
994 36 80.0 522 2 Q7XJN9_ARYTH
995 36 80.0 523 2 Q8LA02_ARYTH
996 36 80.0 523 2 Q9C8L9_ARYTH
997 36 80.0 530 2 Q5AU94_EMENI
998 36 80.0 532 2 Q6YWA3_ORYSA
999 36 80.0 532 2 Q9XEP1_SORBI
1000 36 80.0 533 2 Q810Z7_CABEL
1000 36 80.0 534 2 Q6ZG81_ORYSA

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## ALIGNMENTS

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RESULT 1
Q5TOW7_ANOGA
ID Q5TOW7_ANOGA PRELIMINARY; PRT; 205 AA.
AC Q5TOW7_2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DE ENSANGP0000027848 (Fragment).
OS ORFNames=ENSANGS0000023582;
GN Anopheles gambiae str. F85T.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=F85T;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=F85T;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008960; EAL40096.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 205
SQ SEQUENCE 205 AA; 19442 MW; 2DDF9DC7A78F3D64 CRC64;

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Query Match 100.0%; Score 45; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SGPSPPC 7
Db 41 SGPSPPC 47

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RESULT 2
Q5ZDR5_ORYSA
ID Q5ZDR5_ORYSA PRELIMINARY; PRT; 759 AA.
AC Q5ZDR5_
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

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DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Putative polygalacturonase PG2.
GN Name=P0554D10.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsunoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilmaru Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Ito S., Ito T., Ito Y., Ito Y., Iwabuchi A., Kamiya K.,
RA Karasawa M., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshinara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Bun M.-Y.,
RA Yano M., Jiang J., Gojobori T.
RT "The genome sequence and structure of rice chromosome 1."
RL Nature 420:312-316(2002).
DR EMBL; AP002869; BAD54709.1; -; Genomic DNA.
DR GO; GO:0004650; F:polygalacturonase activity; IEA.
DR GO; GO:0005975; F:carbohydrate metabolism; IEA.
DR InterPro; IPR00743; Glyco_hydro_28.
DR InterPro; IPR006626; PbH1.
DR Pfam; PF00295; Glyco_hydro_28; 1.
DR SMART; SM00710; PbH1; 5.
SQ SEQUENCE 759 AA; 77704 MW; BE489C9551AAEE7B CRC64;

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Query Match 100.0%; Score 45; DB 2; Length 759;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SGPSPPC 7
Db 329 SGPSPPC 335

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RESULT 3
Q5NCY0_MOUSE
ID Q5NCY0_MOUSE PRELIMINARY; PRT; 1641 AA.
AC Q5NCY0;
DT 01-FEB-2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE Novel protein.
GN Name=RP23-5023.5; ORFNames=RP23-5023.5-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wallis J.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL596125; CAI35996.1; -; Genomic_DNA.
DR InterPro; IPR003347; TF_JmJC.
DR Pfam; PF02373; JmJC; 1.
DR SMART; SM00558; JmJC; 1.
SQ SEQUENCE 1641 AA; 176353 MW; 6CBE3620998427EA CRC64;

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```

Query Match 100.0%; Score 45; DB 2; Length 1641;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ID Q8AXW5_9TELE PRELIMINARY; PRT; 1617 AA.
AC Q8AXW5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE NMDA receptor subunit NR2B.
OS Apterontotus leptorhynchus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Gymnotiformes;
OC Apterontotidae; Apterontotus.
OX NCBI_TaxID=36674;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Harvey-Girard E., Dunn R.;
RT "Excitatory amino acid receptors of the electrosensory system.";
RL J. Neurophysiol. 0:0-0(2003).
DR EMBL; AY166701; AAN65280.1; -; mRNA.
DR HSSP; P19491; 1FTK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005234; F:glutamate-gated ion channel activity; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0004970; F:ionotropic glutamate receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0008811; F:ion transport; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR001320; Ion_glu_receptor.
DR InterPro; IPR001508; NMDA_receptor.
DR InterPro; IPR000169; Pect_cys_AS.
DR InterPro; IPR001311; SBP/Glu_receptor.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF00060; Lig_chan; 1.
DR PRINTS; PR00177; NMDARECEPTOR.
DR SMART; SM00079; PRPE; 1.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 1617 AA; 176830 MW; DC8CA0851ED9C920 CRC64;

Query Match 93.3%; Score 42; DB 2; Length 1617;
Best Local Similarity 85.7%; Pred. No. 2.2e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 1046 SAPPPPC 1052
|:|||||

RESULT 8
ID Q6YX71_ORYSA PRELIMINARY; PRT; 124 AA.
AC Q6YX71;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein OSUNBa0028A18.8.
GN Names=OSUNBa0028A18.8;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005726; BAD03832.1; -; Genomic_DNA.
DR Gramene; Q6YX71; -.
KW Hypothetical protein.
SQ SEQUENCE 124 AA; 13406 MW; 11EB0792B1C7157D CRC64;

Query Match 91.1%; Score 41; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID Q8AXW5_9TELE PRELIMINARY; PRT; 1617 AA.
AC Q8AXW5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE NMDA receptor subunit NR2B.
OS Apterontotus leptorhynchus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Gymnotiformes;
OC Apterontotidae; Apterontotus.
OX NCBI_TaxID=36674;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Harvey-Girard E., Dunn R.;
RT "Excitatory amino acid receptors of the electrosensory system.";
RL J. Neurophysiol. 0:0-0(2003).
DR EMBL; AY166701; AAN65280.1; -; mRNA.
DR HSSP; P19491; 1FTK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005234; F:glutamate-gated ion channel activity; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0004970; F:ionotropic glutamate receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0008811; F:ion transport; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR001320; Ion_glu_receptor.
DR InterPro; IPR001508; NMDA_receptor.
DR InterPro; IPR000169; Pect_cys_AS.
DR InterPro; IPR001311; SBP/Glu_receptor.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF00060; Lig_chan; 1.
DR PRINTS; PR00177; NMDARECEPTOR.
DR SMART; SM00079; PRPE; 1.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 1617 AA; 176830 MW; DC8CA0851ED9C920 CRC64;

Query Match 93.3%; Score 42; DB 2; Length 1617;
Best Local Similarity 85.7%; Pred. No. 2.2e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 1046 SAPPPPC 1052
|:|||||

RESULT 8
ID Q6YX71_ORYSA PRELIMINARY; PRT; 124 AA.
AC Q6YX71;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein OSUNBa0028A18.8.
GN Names=OSUNBa0028A18.8;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005726; BAD03832.1; -; Genomic_DNA.
DR Gramene; Q6YX71; -.
KW Hypothetical protein.
SQ SEQUENCE 124 AA; 13406 MW; 11EB0792B1C7157D CRC64;

Query Match 91.1%; Score 41; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 SPPPPC 7
Db 13 SPPPPC 18
|||||

RESULT 9
Q657J3_ORYSA PRELIMINARY; PRT; 215 AA.
ID Q657J3;
AC Q657J3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein P0002B05.30.
GN Name=P0002B05.30;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Ito S., Ito Y., Ito Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP003141; BAD45024.1; -; Genomic_DNA.
DR Gramene; Q657J3; -.
KW Hypothetical protein.
SQ SEQUENCE 215 AA; 23191 MW; 19C74A68532182C3 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
Db 181 SPPPPC 186
|||||

RESULT 10
Q52KH0_MOUSE PRELIMINARY; PRT; 234 AA.
ID Q52KH0;
AC Q52KH0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE LOC435965 protein.
GN Name=LOC435965;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6; TISSUE=Brain;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinska M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.",  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RG NIH MGC Project;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
DR ENBL: BC094349; AAH94349.1; -: mRNA  
SQ SEQUENCE 234 AA; 25214 MW; 52F3DDFB1FE0F5F CRC64;  
Query Match 91.1%; Score 41; DB 2; Length 234;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 SPPTPC 7  
DB 214 SPPTPC 219  
RESULT 11  
Q6Y783 ORYSA  
ID Q6Y783\_ORYSA PRELIMINARY; PRT; 300 AA.  
AC Q6Y783;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein OSJNBa006015.15.  
GN Name=OSJNBa006015.15;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Sasaki T., Matsumoto T., Katayose Y.;  
RT "Oryza sativa nipponbare (G3) genomic DNA, chromosome 2, BAC  
RT clone OSJNBa006015.",  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR ENBL: AP005640; BA017417.1; -: Genomic DNA.  
DR Gramene; Q6Y783; -  
DR GO; GO:0008415; P:acyltransferase activity; IEA.  
DR GO; GO:0004607; P:phosphatidylcholine-sterol O-acyltransferase. . .; IEA.  
DR GO; GO:0016740; P:transferase activity; IEA.  
DR GO; GO:0006629; P:lipid metabolism; IEA.  
DR GO; GO:0006629; P:lipid metabolism; IEA.  
DR InterPro; IPR003386; LACT.  
DR Pfam; PF02450; LACT; 1.  
DR Acyltransferase; Hypothetical protein; Lipid metabolism; Transferase.  
SQ SEQUENCE 300 AA; 32422 MW; 9916D1616F3519A0 CRC64;  
Query Match 91.1%; Score 41; DB 2; Length 300;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 SPPTPC 7  
DB 214 SPPTPC 219

DB 112 SPPTPC 117  
RESULT 12  
O22534 ORYSA  
ID O22534\_ORYSA PRELIMINARY; PRT; 343 AA.  
AC O22534;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Glyceraldehyde-3-phosphate dehydrogenase subunit (Fragment).  
GN Name=GAPDH;  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Milyang 23; TISSUE=Seed;  
RA Lee M.C., Kim C.S., Eun M.Y.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
-1- SIMILARITY: Belongs to the glyceraldehyde-3-phosphate  
CC dehydrogenase family.  
DR ENBL: AF022730; AAB82133.1; -: mRNA.  
DR FIR; T02071; T02071.  
DR HSSP; P19866; INBO.  
DR SMR; O22534; 66-337.  
DR Gramene; O22534; -  
DR GO; GO:0004365; P:glyceraldehyde-3-phosphate dehydrogenase (p. . .; IEA.  
DR GO; GO:0051287; P:NAD binding; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006096; P:glycolysis; IEA.  
DR InterPro; IPR000173; GAP dehydrogenase.  
DR PANTHER; PTHR10836; GAP dehydrogenase; 1.  
DR Pfam; PF00800; Gp\_dh\_C1.  
DR Pfam; PF00044; Gp\_dh\_N; 1.  
DR PRINTS; PR00078; G3PDHGRNASE.  
DR PROSITE; PS00071; GAPDH; 1.  
KW Oxidoreductase.  
FT NON\_TER 343  
SQ SEQUENCE 343 AA; 36444 MW; BAB4F76566B6DB57 CRC64;  
Query Match 91.1%; Score 41; DB 2; Length 343;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 SPPTPC 7  
DB 6 SPPTPC 11  
RESULT 13  
Q9LHU9 ORYSA  
ID Q9LHU9\_ORYSA PRELIMINARY; PRT; 366 AA.  
AC Q9LHU9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Putative cytochrome proteinase Mir3.  
GN Name=P0515G01.47; Synonym=P0665D10.6;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,  
RA Wu J., Nishimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,  
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,  
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,  
RA Hijishita S., Honda M., Ichikawa Y., Ikonuma A., Iijima M., Ikeda M.,

RA Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,  
RA Karsawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,  
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,  
RA Nagasaki H., Nakaahima M., Nakama Y., Nakamichi Y., Nakamura M.,  
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,  
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,  
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,  
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,  
RA Yano M., Jiang J., Gojobori T.,  
RT "The genome sequence and structure of rice chromosome 1.";  
RL Nature 420:312-316(2002).  
CC -1- SIMILARITY: Belongs to the peptidase C1 family.  
DR EMBL; AF001633; BAA94209.1; -; Genomic DNA.  
DR EMBL; AF002861; BAB16481.1; -; Genomic DNA.  
DR HSSP; P80067; 1JQP.  
DR Granene; Q9LH9; -.  
DR GO; GO:0004197; Fcysteine-type endopeptidase activity; IEA.  
DR GO; GO:0006508; Proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000170; Hipot\_ironsulf.  
DR InterPro; IPR000668; Peptidase C1.  
DR InterPro; IPR000169; Pept\_cys\_A5.  
DR Pfam; PF00112; Peptidase\_C1; 1.  
DR PRINTS; PR00705; PAPAIN.  
DR ProDom; PD000158; Peptidase\_C1; 1.  
DR SMART; SM00645; Pept C1; 1.  
DR PROSITE; PS00596; HIPIP; UNKNOWN 1.  
DR PROSITE; PS00640; THIOL\_PROTEASE\_ASN; 1.  
SQ SEQUENCE 366 AA; 39292 MW; 0E245AFB8604EB3C CRC64;

Query Match 91.1%; Score 41; DB 2; Length 366;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPTCC 7  
DB 33 SPPTCC 38  
|||||

RESULT 10  
Q9DCD9 MOUSE  
ID Q9DCD9\_MOUSE PRELIMINARY; PRT; 426 AA.  
AC Q9DCD9;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Mus musculus adult male kidney cDNA, RIKEN full-length enriched  
DE library, clone:0610041A01 product:immunoglobulin heavy chain 6 (heavy  
DE chain of IgM), full insert sequence.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Kidney;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.,  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Kidney;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyoko-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
[3]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Kidney;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
[4]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Kidney;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
[5]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Kidney;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
[6]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Kidney;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
[6]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Kidney;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
[6]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Kidney;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
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DR InterPro; IPR003006; Ig MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00407; IgC1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Immune response; Immunoglobulin domain; MHC I.
SQ SEQUENCE 426 AA; 45920 MW; 56E1275BA48F6FB1 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 426;
Best Local Similarity 85.7%; Pred. No. 8.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 183 SGPPPPC 189

RESULT 15
Q9STN0_ARATH PRELIMINARY; PRT; 437 AA.
AC Q9STN0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Extensin-like protein.
GN Name=Y28D5.70; Synonyms=AT4G08380;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.,
RA Barrell B.G., Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K.,
RA Schueller C.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL109819; CAB52560.1; -; Genomic DNA.
DR EMBL; AL161511; CAB77963.1; -; Genomic DNA.
DR PIR; T14192.
DR GO; GO:000928; C:cell surface (sensu Magnoliophyta); IEA.
DR GO; GO:0005199; F:structural constituent of cell wall; IEA.
DR GO; GO:0009664; P:cell wall organization and biogenesis (sens. .); IEA.
DR InterPro; IPR006706; Extensin_2.
DR Pfam; PF04554; Extensin_2; 1.
SQ SEQUENCE 437 AA; 48622 MW; D5CD9474423D949F CRC64;

Query Match 91.1%; Score 41; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SPPPPC 7
Db 390 SPPPPC 395

RESULT 16
Q58561_MOUSE PRELIMINARY; PRT; 485 AA.
ID Q58561_MOUSE PRELIMINARY;
AC Q58561;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

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DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCES.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Vallalon D.K., Muray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092056; AAH92056.1; -; mRNA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; Ig; 3.
DR SMART; SM00407; Ig; 3.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 485 AA; 52628 MW; F08C1FB47C4E44EC CRC64;

Query Match 91.1%; Score 41; DB 2; Length 485;
Best Local Similarity 85.7%; Pred. No. 9.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 242 SGPPPPC 248

RESULT 17
Q91207_MOUSE PRELIMINARY; PRT; 486 AA.
ID Q91207_MOUSE PRELIMINARY;
AC Q91207;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

```

GN Name=Igh-VJ558;  
 OS Mus musculus (Musae).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RX [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RP  
 RC STRAIN=CZECH II;  
 RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;  
 RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.M., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=CZECH II;  
 RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;  
 RA Submitted MGC Project;  
 RL Director (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; BC004786; AAH04786.1; -; mRNA.  
 DR HSP; P01810; 2FBJ.  
 DR Ensembl; ENSMUSG0000021155; Mus musculus.  
 DR MGI; MGI:96486; Igh-VJ558.  
 DR GO; GO:0003823; Frantigen binding; IEA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Immunoglobulin domain.  
 SQ SEQUENCE 487 AA; 52555 MW; 7DC8E96DB33077B CRC64;  
  
 Query Match 91.1%; Score 41; DB 2; Length 487;  
 Best Local Similarity 85.7%; Pred. No. 9.3e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 Qy 1 SSPPPPC 7  
 Db 244 SGPPPPC 250  
  
 RESULT 19  
 Q874V7\_PODAN  
 ID Q874V7\_PODAN PRELIMINARY; PRT; 494 AA.  
 AC Q874V7;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein Pa5D0091.  
 OS Podosporea anserina.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podosporea.

OX NCBI\_TaxID=5145;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA Genoscope;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, BX088700; CAD60778.1; -, Genomic DNA.  
 GO, GO:0008233; P:peptidase activity; IEA.  
 KW Hydrolase; Hypothetical protein; Protease.  
 SQ SEQUENCE 494 AA; 55692 MW; 38F260C3CD7423AD CRC64;

Query Match 91.1%; Score 41; DB 2; Length 494;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SPPPPC 7  
 Db 119 SPPPPC 124

## RESULT 20

Q4SHL4 TETNG PRELIMINARY; PRT; 519 AA.

AC Q4SHL4;  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
 DE Chromosome 5 SCAP14581, whole genome shotgun sequence.  
 GN ORFNames=GSTENG00018098001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodonidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Blemont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype."  
 RL Nature 431:946-957(2004).  
 RN [2]

NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.

CC EMBL; CAER01014581; CAF99868.1; -, Genomic DNA.  
 DR InterPro; IPR001132; Dwarfin.  
 DR InterPro; IPR003619; Dwarf1n\_A.

DR InterPro; IPR013019; MAD\_MH1.

DR Pfam; PF03165; MH1; 1.

DR Pfam; PF03166; MH2; 1.

DR SMART; SM00523; DWA; 1.

DR SMART; SM00524; DWA; 1.

DR PROSITE; PSS1075; MH1; 1.

DR PROSITE; PSS1076; MH2; 1.

KW Transcription; Transcription regulation.

SQ SEQUENCE 519 AA; 57095 MW; CBD79858DB468DF2 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 519;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 SPPPPC 7  
 Db 237 SPPPPC 242

## RESULT 21

OB1849 ARATH PRELIMINARY; PRT; 532 AA.

AC OB1849;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)  
 DE Hypothetical protein T16H5.30 (Hypothetical protein AT4g19670).  
 GN Name=T16H5.30; Synonyms=AT4g19670;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC Rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsi.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA De Haan M., Maarse A.C., Grivell L.A., Bancroft I., Mewes H.W.,  
 RA Mayer K., Schueller C., Bevan M.; EMBL/GenBank/DBJ databases.  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K.,  
 RA Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]

NUCLEOTIDE SEQUENCE.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL024486; CAI19684.1; -, Genomic DNA.  
 DR EMBL; AL161551; CAB78969.1; -, Genomic DNA.  
 DR PIR; T04748; T04748.  
 DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.  
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.  
 DR GO; GO:0008270; P:zinc ion binding; IEA.  
 DR GO; GO:0016567; P:protein ubiquitination; IEA.  
 DR InterPro; IPR012337; RNaseH fold.  
 DR InterPro; IPR002867; Znf C6HC.  
 DR InterPro; IPR001841; Znf\_RING.  
 DR Pfam; PF01485; IBR; 2.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR SMART; SM00647; IBR; 2.

DR SMART; SM00184; RING; 2.  
 DR PROSITE; PS00518; ZF\_RING\_1; 1.  
 DR PROSITE; PS00889; ZF\_RING\_2; 1.  
 KW Hypothetical protein.

SQ SEQUENCE 532 AA; AC1AFDPEDC74B3F CRC64;  
 Query Match 91.1%; Score 41; DB 2; Length 532;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SPPPPC 7  
 Db 490 SPPPPC 495

## RESULT 22

Q4S8D5 TETNG PRELIMINARY; PRT; 612 AA.

ID Q4S8D5 TETNG PRELIMINARY;  
 AC Q4S8D5;  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)  
DE Chromosome undetermined SCAF14706, whole genome shotgun sequence.  
DE (Fragment).  
GN ORFNames=GSTENG00022379001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet P., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
RA Blemont C., Skalli Z., Cattolico L., Foulain J., De Berardinis V.,  
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nuebaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schacher V., Quetier F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAEE01014706; CAG03097.1; -; Genomic\_DNA.  
FT NON\_TER 1  
SQ SEQUENCE 612 AA; 68400 MW; 4630680260963C57 CRC64;  
Query Match 91.1%; Score 41; DB 2; Length 612;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 SPSPPC 7  
DB 174 SPSPPC 179  
RESULT 23  
ID Q55WY8\_CRYNE PRELIMINARY; PRT; 643 AA.  
AC Q55WY8;  
DT 13-SEP-2005 (TReMBLrel. 31, Created)  
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)  
DE 13-SEP-2005 (TReMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=CNRC0040;  
OS Cryptococcus neoformans var. neoformans B-3501A.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
OX NCBI\_TaxID=283643;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Funke B., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,  
RA Wickes B.L., Fu J., Davis R.W.;  
RT "Cryptococcus neoformans serotype D sequencing.";  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAEX01000012; EAL22290.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 643 AA; 72190 MW; 49C9C12102AC46BF CRC64;

Query Match 91.1%; Score 41; DB 2; Length 643;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 SPSPPC 7  
DB 347 SPSPPC 352  
RESULT 24  
ID Q5KJB1\_CRYNE PRELIMINARY; PRT; 643 AA.  
AC Q5KJB1;  
DT 10-MAY-2005 (TReMBLrel. 30, Created)  
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)  
DE 5' flap endonuclease, putative.  
GN ORFNames=CNCR07150;  
OS Cryptococcus neoformans var. neoformans JEC21.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
OX NCBI\_TaxID=214684;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JEC21;  
RA Loftus B., Fraser C.;  
RA Van Aken S., Fraser C.;  
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX PubMed=15653466; DOI=10.1126/science.1103773;  
RC Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,  
RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,  
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,  
RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,  
RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,  
RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,  
RA Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,  
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,  
RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,  
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,  
RA Fraser C.M., Hyman R.W.;  
RT "The genome of the basidiomycetous yeast and human pathogen  
RT Cryptococcus neoformans.";  
RL Science 307:1321-1324(2005).  
DR EMBL; AE017343; AA42538.1; -; Genomic\_DNA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0004519; F:endonuclease activity; IEA.  
DR GO; GO:0006281; F:DNA repair; IEA.  
DR InterPro; IPR000513; Exo\_N\_I.  
DR InterPro; IPR008918; HhH2.  
DR InterPro; IPR006086; XPG\_I.  
DR InterPro; IPR006085; XPG\_N.  
DR InterPro; IPR006084; XPG\_Rad.  
DR Pfam; PF00867; XPG\_I; 1.  
DR Pfam; PF00752; XPG\_N; 1.  
DR PRINTS; PR00853; XPG\_RADSUPER.  
DR SMART; SM00484; XPGI; 1.  
DR SMART; SM00485; XPGN; 1.  
KW Complete proteome; Endonuclease.  
SQ SEQUENCE 643 AA; 72191 MW; 49C9C12102AC46BF CRC64;  
Query Match 91.1%; Score 41; DB 2; Length 643;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 SPSPPC 7  
DB 347 SPSPPC 352

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RESULT 25
O65375 ARATH
ID O65375 ARATH PRELIMINARY; PRT; 744 AA.
AC O65375;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE F12F1.9 protein (leucine-rich repeat/extensin 1).
GN Name=F12F1.9; Synonyms=LRX1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Vysotskaia V.S., Osborne B.I., Schwartz J.R., Toriumi M., Yu G.,
RA Kwan A., Oji O., Liu S., Buehler G., Conway A.B., Conway A.R.,
RA Dewar K., Peng J., Kim C., Kurtz D., Palm C.J., Li Y., Shinn P.,
RA Sun H., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=21231189; PubMed=11331608; DOI=10.1101/gad.200201;
RA Baumberger N., Ringli C., Keller B.;
RT "The chimeric leucine-rich repeat/extensin cell wall protein LRX1 is
RT required for root hair morphogenesis in Arabidopsis thaliana.";
RL Genes Dev. 15:1128-1139(2001).
DR EMBL; AC002131; AAC17609.1; -; Genomic_DNA.
DR EMBL; AY026364; AAC07681.1; -; mRNA.
DR PIR; E86255; E86255.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR Pfam; PF00560; LRR_1; 5.
DR PRINTS; PR00019; LEURICHRPT.
KW Leucine-rich repeat; Repeat.
SQ SEQUENCE 744 AA; 80394 MW; 3C75174DBBB91F6F CRC64;

Query Match 91.1%; Score 41; DB 2; Length 744;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SPPTPC 7
Db 528 SPPTPC 533

RESULT 26
Q5W6L7 ORYSA
ID Q5W6L7 ORYSA PRELIMINARY; PRT; 752 AA.
AC Q5W6L7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Zinc knuckle containing protein.
GN Name=OSJNB0085A04.2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Wang A., Maiti R., Jones K.M.,
RA Tallon L.J., Feldblyum T.V., Teairin T., Bera J.J., Kim M.M., Jin S.,
RA Padrosh D., Vuong H., Overton II L.L., Reardon M., Weaver B., Jin S.,
RA Johri S., Utterback T.R., Pai G., Smith S., Wortman J., Haas B.J.,
RA Zhu W., Yang Q., Koo H., Ziemann V., Hsiao J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RL "Oryza sativa chromosome 3 BAC OSJNB0085A04 genomic sequence.";
RT Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.

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RA Buell R.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC135502; AAV35795.1; -; Genomic_DNA.
DR GO; GO:0003676; F:nuclieic acid binding; IEA.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 1.
DR PRINTS; PR00939; CZHCZNFINGER.
DR PROSITE; PS0158; 2P_CCHC; 1.
SQ SSSEQUENCE 752 AA; 78925 MW; 9F4765B1607D30EE CRC64;

Query Match 91.1%; Score 41; DB 2; Length 752;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SPPTPC 7
Db 543 SPPTPC 548

RESULT 27
Q5ZD97 ORYSA
ID Q5ZD97 ORYSA PRELIMINARY; PRT; 849 AA.
AC Q5ZD97;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein P0681B11.44.
GN Name=P0681B11.44;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niumura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijehita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Ito S., Ito T., Ito Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Taji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP003022; BAD52672.1; -; Genomic_DNA.
DR InterPro; IPR000270; OPR_PB1.
DR Pfam; PF00564; PB1; 1.
KW Hypothetical protein.
SQ SEQUENCE 849 AA; 91952 MW; 984F13BED938900D CRC64;

Query Match 91.1%; Score 41; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SPPTPC 7
Db 227 SPPTPC 232

RESULT 28
Q4RQ54 TETNG
ID Q4RQ54 TETNG PRELIMINARY; PRT; 855 AA.
AC Q4RQ54;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

```

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Chromosome 17 SCAR15006, whole genome shotgun sequence.  
 DN (Fragment).  
 GN ORFNames=GSTENG00030765001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,  
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
 RA Farré G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Volff J.N., Guigio R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;  
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 RT the early vertebrate proto-karyotype";  
 RL Nature 431:946-957 (2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -! CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAAB01015006; CAG09478.1; -; Genomic\_DNA.  
 FT NON\_TER 1 855  
 FT NON\_TER 855 855  
 FT SEQUENCE 855 AA; 92576 MW; 5DC7E5A7908B7126 CRC64;  
 SQ SEQUENCE 855 AA; 92576 MW; 5DC7E5A7908B7126 CRC64;  
  
 Query Match 91.1%; Score 41; DB 2; Length 855;  
 Best Local Similarity 85.7%; Pred. No. 1.6e+03;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 SSPPPPC 7  
 Db 753 SDPPPPC 759  
  
 RESULT 29  
 Q6H8G9 ORYSA  
 ID Q6H8G9\_ORYSA PRELIMINARY; PRT; 60 AA.  
 AC Q6H8G9;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein P0491E01.25.  
 GN Names=P0491E01.25;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzeae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, PAC  
 RT clone: P0491E01.";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF002485; BAD24980.1; -; Genomic\_DNA.  
 DR Gramene; Q6H8G9; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 60 AA; 6060 MW; 3EA74FBD1313F74C CRC64;

Query Match 88.9%; Score 40; DB 2; Length 60;  
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 SSPPPPC 7  
 Db 34 SPDPPPC 40  
  
 RESULT 30  
 Q87616 SIVCZ  
 ID Q87616\_SIVCZ PRELIMINARY; PRT; 71 AA.  
 AC Q87616;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Rev protein (Fragment).  
 GN Name=rev;  
 OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).  
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
 OC Lentivirus; Primate lentivirus group.  
 OX NCBI\_TaxID=11723;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=97138325; PubMed=8985351;  
 RA Bibollat-Ruche F., Brengues C., Galat-Luong A., Galat G., Pourrut X.,  
 RA Vidal N., Veas F., Durand J.P., Cuny G.;  
 RT "Genetic diversity of simian immunodeficiency viruses from West  
 RT African green monkeys: evidence of multiple genotypes within  
 RT populations from the same geographical locale.";  
 RL J. Virol. 71:307-313 (1997).  
 DR EMBL; U37215; AAC56174.1; -; Genomic\_DNA.  
 DR GO; GO:0042025; C:host cell nucleus; IEA.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR000625; REV\_protein.  
 DR Pfam; PF00424; REV; 1.  
 FT NON\_TER 1 71  
 FT NON\_TER 71 71  
 FT SEQUENCE 71 AA; 8123 MW; E064765F8AD50515 CRC64;  
 SQ SEQUENCE 71 AA; 8123 MW; E064765F8AD50515 CRC64;  
  
 Query Match 88.9%; Score 40; DB 2; Length 71;  
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 SSPPPPC 7  
 Db 57 SPDPPPC 63  
  
 RESULT 31  
 Q4TDU0 TETNG  
 ID Q4TDU0\_TETNG PRELIMINARY; PRT; 136 AA.  
 AC Q4TDU0;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Chromosome undetermined SCAP6040, whole genome shotgun sequence.  
 GN ORFNames=GSTENG0002628001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,

RA Bionet C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.,  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RN the early vertebrate proto-karyotype.";  
RN Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAAB01006040; CAF88942.1; -; Genomic DNA.  
SQ SEQUENCE 136 AA; 14950 MW; 6ELB6A859FC2EFA7 CRC64;  
  
Query Match 88.9%; Score 40; DB 2; Length 136;  
Best Local Similarity 85.7%; Pred. No. 3.6e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 SSPPPPC 7  
Db 31 SPPPPPC 37  
  
RESULT 32  
Q9XG80\_ORYSA  
ID Q9XG80\_ORYSA PRELIMINARY; PRT; 138 AA.  
AC Q9XG80;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Putative phospholipase A2 precursor (EC 3.1.1.4).  
GN Name=pla2-i;  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN NCBI\_TaxID=4530;  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Nipponbare; TISSUE=Green shoot;  
EX PubMed=10608658; DOI=10.1023/A:1006323405788;  
RA Stahl U., Lee M., Sjodahl S., Acher D., Cellini F., Ek B.,  
RA Iannaccone R., Mackenzie D.A., Semeraro L., Tramontano E., Stymne S.;  
RT "Plant low-molecular-weight phospholipase A2s (PLA2s) are structurally  
RT related to the animal secretory PLA2s and are present as a family of  
RT isoforms in rice (Oryza sativa).";  
RL Plant Mol. Biol. 41:481-490(1999).  
DR EMBL; AJ238116; CAB40841.1; -; mRNA.  
DR HSPF; P00592; I18S.  
DR Gramene; Q9XG80; -;  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.  
DR GO; GO:0016042; F:lipid catabolism; IEA.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR ProDom; PD000303; PhospholipaseA2; 1.  
DR PROSITE; PS00118; PA2\_HIS; 1.  
KW Hydrolase; Signal.  
FT SIGNAL 1 19 Potential.  
FT CHAIN 20 138 putative phospholipase A2.  
SQ SEQUENCE 138 AA; 14884 MW; CC0BC0F87A966C0B CRC64;  
  
Query Match 88.9%; Score 40; DB 2; Length 136;  
Best Local Similarity 85.7%; Pred. No. 3.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 SSPPPPC 7  
Db 130 SPPPPPC 136

Db 23 SPPPPPC 29  
  
RESULT 33  
Q6K970\_ORYSA  
ID Q6K970\_ORYSA PRELIMINARY; PRT; 138 AA.  
AC Q6K970;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Putative phospholipase A2.  
GN Name=OJ1149\_C12.15;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN NCBI\_TaxID=39947;  
RP NUCLEOTIDE SEQUENCE.  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to the phospholipase A2 family.  
DR EMBL; AP004082; BAD23008.1; -; Genomic DNA.  
DR HSP; P00608; IAE7.  
DR Gramene; Q6K970; -;  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.  
DR GO; GO:0016042; F:lipid catabolism; IEA.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR ProDom; PD000303; PhospholipaseA2; 1.  
DR PROSITE; PS00118; PA2\_HIS; 1.  
SQ SEQUENCE 138 AA; 14884 MW; CC0BC0F87A966C0B CRC64;  
  
Query Match 88.9%; Score 40; DB 2; Length 138;  
Best Local Similarity 85.7%; Pred. No. 3.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 SSPPPPC 7  
Db 23 SPPPPPC 29  
  
RESULT 34  
O22480\_ORYSA  
ID O22480\_ORYSA PRELIMINARY; PRT; 157 AA.  
AC O22480;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Low molecular early light-inducible protein.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN NCBI\_TaxID=4530;  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Milyang 23;  
RA Lee M.C., Kim C.S., Eun M.Y.;  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF017356; AAB70536.1; -; mRNA.  
DR PIR; T02034; T02034.  
DR Gramene; O22480; -;  
SQ SEQUENCE 157 AA; 15977 MW; D0594E93596CB335 CRC64;  
  
Query Match 88.9%; Score 40; DB 2; Length 157;  
Best Local Similarity 85.7%; Pred. No. 4.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 SSPPPPC 7  
Db 130 SPPPPPC 136



RA Schnersch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RG NIH MSC Project;  
 RA Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 RL SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL; BC095947; AAH95947.1; -; mRNA.  
 DR MGI; MGI:96185; Hoxb4.  
 DR InterPro; IPR001827; Antennapedia.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR012287; Homeodomain-rel.  
 DR Pfam; PF00046; Homeobox; 1.  
 DR PRINTS; PR00025; ANTENNAPEDIA.  
 DR PRINTS; PR00024; HOMEBOX2; 1.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00032; ANTENNAPEDIA; UNKNOWN 1.  
 DR PROSITE; PS00027; HOMEBOX1; 1.  
 DR PROSITE; PS00071; HOMEBOX2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein; Transcription;  
 KW Transcription regulation.  
 SQ SEQUENCE 250 AA; 27563 MW; 70984779D5333650 CRC64;

Query Match 89.9%; Score 40; DB 2; Length 250;  
 Best Local Similarity 85.7%; Pred. No. 6.5e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
 Db 115 SPPPPPC 121

RESULT 38  
 HXB4 HUMAN  
 ID HXB4 HUMAN STANDARD; PRT; 251 AA.  
 AC F17483; Q9NTA0;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Homeobox protein Hox-B4 (Hox-2P) (Hox-2.6).  
 GN Name=HoxB4; Synonym=Hox2P;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 OX 1  
 RN NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=91153613; PubMed=1981366;  
 RA Peverali P.A., D'Esposito M., Acampora D., Bunone G., Negri M.,  
 RA Faiella A., Stornaiuolo A., Pannese M., Migliaccio E., Simeone A.,  
 RA Valle G.D., Boncinelli E.;  
 RT "Expression of HOX homeobox genes in human neuroblastoma cell culture  
 RL lines.";  
 RL Differentiation 45:61-69(1990).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RP Kidd K.K., Busygina V., DeMille M.M.C., Speed W.C., Ruggeri V.,  
 RA Kidd J.R., Pakstis A.J.;  
 RT "Overall linkage disequilibrium in 33 populations for highly  
 RL informative multiallelic haplotypes spanning the HOXB gene cluster.";  
 RN Am. J. Hum. Genet. 67:235-235(2000).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20538492; PubMed=11085749; DOI=10.1084/jem.192.10.1479;  
 RA Giannola D.M., Shlonschik W.D., Jegathesan M., Liebowitz D.,  
 RA Abrams C.S., Kadesch T., Dancis A., Emerson S.G.;  
 RT "Hematopoietic expression of HOXB4 is regulated in normal and leukemic  
 RT stem cells through transcriptional activation of the HOXB4 promoter by

RT upstream stimulating factor (USF)-1 and USP-2."; J. Exp. Med. 192:1479-1490(2000).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Uterus;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL [5]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 6-251.  
 RC TISSUE=Testis;  
 RG The German cDNA Consortium;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE OF 160-227.  
 RC TISSUE=Placenta;  
 RX MEDLINE=89378558; PubMed=2570724;  
 RA Giampaolo A., Acampora D., Zappavigna V., Pannese M., D'Esposito M.,  
 RA Care A., Faiella A., Stornaiuolo A., Russo G., Simeone A.,  
 RA Boncinelli E., Peschle C.;  
 RT "Differential expression of human HOX-2 genes along the anterior-  
 RL posterior axis in embryonic central nervous system."; Differentiation 40:191-197(1989).  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE OF 162-227.  
 RX MEDLINE=90215256; PubMed=2576652;  
 RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,  
 RA Gaudino G., Stornaiuolo A., Cafiero M., Faiella A., Simeone A.;  
 RT "Organization of human class I homeobox genes."; Genome 31:745-756(1989).  
 RL -1- FUNCTION: Sequence-specific transcription factor which is part of  
 CC a developmental regulatory system that provides cells with  
 CC specific positional identities on the anterior-posterior axis.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DEVELOPMENTAL STAGE: Expressed in whole embryos and fetuses at 5-9  
 CC weeks from conception.  
 CC -1- SIMILARITY: Belongs to the Antp homeobox family. Deformed  
 CC subfamily.  
 CC -1- SIMILARITY: Contains 1 homeobox DNA-binding domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; X16174; CAA34296.1; -; Genomic DNA.  
 CC EMBL; AF287967; AAG31554.1; -; Genomic DNA.  
 CC EMBL; AF307160; AAG45052.1; -; Genomic DNA.  
 CC EMBL; BC049204; AAB49204.1; -; mRNA.  
 CC EMBL; AL137449; CAB70742.1; -; mRNA.  
 CC PIR; B60492; B60492.  
 CC PIR; T46446; T46446.  
 CC HSP; P02833; 9ANT.  
 CC SNR; P17483; 163-222.

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DR TRANSFAC; T01727; -.
DR Ensembl; ENSG00000182742; Homo sapiens.
DR HGNC; HGNC:1115; HOBX4.
DR MIM; 142965; -.
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003770; F:transcription factor activity; NAS.
DR GO; GO:0007275; P:development; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR012287; Homeodomain-rel.
DR Efam; PF00046; Homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRODOM; PD000010; Homeobox; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEBOX; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;
KW Transcription; Transcription regulation.
FT DNA_BIND 162 221 Homeobox.
FT MOTIF 141 146 Antp-type hexapeptide.
FT COMBIAS 15 139 Pro-rich (part of the transcriptional
FT activation domain).
FT COMBIAS 71 87 Poly-Pro.
SQ SEQUENCE 251 AA; 27604 MW; 23BE1DDDCCE2DB4 CRC64;

Query Match 88.9%; Score 40; DB 1; Length 251;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 116 SPPPPPC 122

RESULT 39
Q51Z5 MAGGR
ID Q51Z5 MAGGR PRELIMINARY; PRT; 327 AA.
AC Q51Z5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MG05901.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthaceae.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen T., An P., Anderson M., Anderson S.,
RA Arachi H., Ambruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Caliste N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Grandbois E., Gnerre S.,
RA Gnrke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysysselis M., Karlsson E.,
RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokvitsang T., Lokvitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,

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RA Mesirov J., Mihalov A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA Mozes J., Mullrain L., Munson G., Naylor J., Neves C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotohso B.,
RA O'Neill K., Oseman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Ruman M., Schupbach R., Seaman C., Settippalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Tsamila T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe grisea.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACU01000838; EAA522773.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 327 AA; 36399 MW; 6E0374031EDAF956 CRC64;

Query Match 88.9%; Score 40; DB 2; Length 327;
Best Local Similarity 85.7%; Pred. No. 8.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 202 SPPPPPC 208

RESULT 40
Q4SZ13 TETNG
ID Q4SZ13 TETNG PRELIMINARY; PRT; 341 AA.
AC Q4SZ13;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 2 SCAP11863, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00010063001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lufalla G., Dossat C., Segreus B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Kattinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat G., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

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RA Laudet V., Schachter V., Quetier P., Saurin W., Scarpelli C.,  
RA Winkler P., Lander S.S., Weissenbach J., Roest Crolius H.;  
RT "genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype";  
RN Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope, Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL, CAZ01011663; CAF94119.1; -; Genomic\_DNA.  
FT NON\_TER 1  
SQ SEQUENCE 341 AA; 36696 MW; CAC7D7F9D8A38512 CRC64;  
Query Match 88.9%; Score 40; DB 2; Length 341;  
Best Local Similarity 85.7%; Pred. No. 8.8e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SSPPPPC 7  
Db 280 SPPPPPC 286  
RESULT 41  
Q5BLI6 BRARE PRELIMINARY; PRT; 357 AA.  
AC Q5BLI6;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Wu:fj84d09 protein (Fragment).  
GN Name=wu:fj84d09;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OC NCBI\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Singapore local strain; TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Frange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.B.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Singapore local strain; TISSUE=Embryo;  
RG NIH MGC Project;  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL, BC090421; AAH90421.1; -; mRNA.  
DR Ensembl, ENSDARG00000011360; Danio rerio.  
DR GO, GO:0006464; P-protein modification; IEA.  
DR InterPro, IPR000626; Ubiquitin.  
DR SMART, SM00213; UBQ; 1.

FT NON\_TER 1  
SQ SEQUENCE 357 AA; 39640 MW; 3BFB8D5654D604CA CRC64;  
Query Match 88.9%; Score 40; DB 2; Length 357;  
Best Local Similarity 85.7%; Pred. No. 9.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SSPPPPC 7  
Db 114 SPPPPPC 120  
RESULT 42  
Q9NP08 HUMAN PRELIMINARY; PRT; 373 AA.  
AC Q9NP08;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE H5 homeodomain protein.  
GN Name=HMx1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Grainofacial;  
RX MEDLINE=93087572; PubMed=1360670;  
RA Stadler H.S., Padanilam B.J., Buetow K., Murray J.C., Solursh M.;  
RT "Identification and genetic mapping of a homeobox gene to the 4p16.1  
RT region of human chromosome 4.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:11579-11583(1992).  
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
DR EMBL, M95587; AAF70205.1; -; mRNA.  
DR PIR, A47234; A47234.  
DR HSP, P13297; IIG7.  
DR TRANSFAC; T04443; -.  
DR Ensembl; ENSG00000188749; Homo sapiens.  
DR HGNC; HGNC:5017; HMx1.  
DR GO, GO:0003700; F:transcription factor activity; NAS.  
DR InterPro, IPR001356; Homeobox.  
DR InterPro, IPR012287; Homeodomain-rel.  
DR InterPro, IPR000047; HTH\_lambdrepreser.  
DR Pfam, PF00046; Homeobox; 1.  
DR PRINTS; PR00024; HOMEBOX.  
DR PRINTS; PR00031; HTHREPRESSR.  
DR ProDom; PD000010; Homeobox; 1.  
DR SMART; SM00389; Hox; 1.  
DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS50071; HOMEBOX\_2; 1.  
KW DNA-binding; Homeobox; Nuclear protein.  
SQ SEQUENCE 373 AA; 39225 MW; 8BF9EB1722660A76 CRC64;  
Query Match 88.9%; Score 40; DB 2; Length 373;  
Best Local Similarity 85.7%; Pred. No. 9.6e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SSPPPPC 7  
Db 327 SRPPPPC 333  
RESULT 43  
Q6C595 YARLI PRELIMINARY; PRT; 402 AA.  
AC Q6C595;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Similarity.  
GN OrderedLocusNames=YAL10B19965g;

OS Yarrowia lipolytica (Candida lipolytica).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Dipodascaceae; Yarrowia.  
 OX NCBI\_TaxID=4952;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=CLIB 122 / B 150;  
 RX PubMed15229592; DOI=10.1038/nature025579;  
 RA Lafontaine I., de Montigny J., Marck C., Neveuglise C., Tallia E.,  
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
 RA Goffard N., Frangaul L., Agie M., Anthouard V., Babour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
 RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Koszul R., Lemaire M., Leur I., Ma L., Muller H.,  
 RA Nicaud J.-M., Nikolski M., Ostas S., Ozier-Kalogeropoulos O.,  
 RA Pellien S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissbach J.,  
 RA Wincker P., Souciet J.-L.,  
 RT "Genome evolution in yeasts."  
 RL Nature 430:35-44(2004).  
 DR EMBL; CR382131; CAG79762.1; -; Genomic\_DNA.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0046872; P:metal ion binding; IEA.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR Pfam; PF00096; zf-C2H2; 1.  
 DR SMART; SM00355; Znf\_C2H2; 3.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 1.  
 DR PROSITE; PS0157; ZINC\_FINGER\_C2H2\_2; 1.  
 KW Complete proteome; Metal-binding; Nuclear protein; zinc; zinc-finger.  
 SQ SEQUENCE 402 AA; 43889 MW; 0BAC7170DDEAE444 CRC64;

Query Match 88.9%; Score 40; DB 2; Length 402;  
 Best Local Similarity 85.7%; Pred. No. 1e+03;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 | | | | |  
 Db 29 SPPPPPC 35

RESULT 44  
 Q7ZX99 XENLA PRELIMINARY; PRT; 427 AA.  
 AC Q7ZX99;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Tial protein (Fragment).  
 GN Name=Tial;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Abramson P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullány S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT Initiative."  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RA Klein S., Strausberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC045086; AAH45086.1; -; mRNA.  
 DR HSP; P11940; 1CVJ.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR InterPro; IPR000504; RNPI\_RRM.  
 DR Pfam; PF00076; RRM\_1; 3.  
 DR SMART; SM00360; RRM; 3.  
 DR PROSITE; PS01102; RRM; 3.  
 FT NON\_TER 1  
 SQ SEQUENCE 427 AA; 47172 MW; 4C2E5EA5884DA333 CRC64;

Query Match 88.9%; Score 40; DB 2; Length 427;  
 Best Local Similarity 85.7%; Pred. No. 1.1e+03;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 | | | | |  
 Db 15 SPPPPPC 21

RESULT 45  
 Q69TY6 ORYSA PRELIMINARY; PRT; 667 AA.  
 AC Q69TY6;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Putative receptor protein kinase PERK1.  
 GN Name=OSJNBa0029G06.37; Synonym=OSJNBa0072A21.6;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzoideae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC  
 clone:OSJNBa0029G06."  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC  
 clone:OSJNBa0072A21."  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP004680; BAD35691.1; -; Genomic\_DNA.  
 DR EMBL; AP004737; BAD37736.1; -; Genomic\_DNA.  
 DR Gramene; Q69TY6; -.

DR GO; GO:0005524; P:ATP binding; IEA.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0004872; P:receptor activity; IEA.  
 DR GO; GO:0016998; P:cell wall catabolism; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR002482; LysM.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF01476; LysM; 2.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Kinase; Receptor.  
 SQ SEQUENCE 667 AA; 70964 MW; DB3BB0BEC7AC743D CRC64;

Query Match 88.9%; Score 40; DB 2; Length 667;  
 Best Local Similarity 85.7%; Pred. No. 1.7e+03;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
 | |||||  
 Db 51 SPPPPPC 57

## RESULT 46

O15054 HUMAN  
 ID Q15054\_HUMAN PRELIMINARY; PRT; 1682 AA.  
 AC O15054;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE KIAA0346 protein (Fragment).  
 GN Name=JMJD3; Synonyms=KIAA0346;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=97349984; PubMed=9205841;  
 RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,  
 Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. VII.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro.";  
 RL DNA Res. 4:141-150(1997).  
 DR EMBL; AB002344; BAA21572.2; -; mRNA.  
 DR Ensembl; ENSG00000132510; Homo sapiens.  
 DR HGNC; HGNC:29012; JMJD3.  
 DR InterPro; IPR003347; TP\_JmJC.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR InterPro; IPR011990; TPR-like\_helical.  
 DR Pfam; PF02373; JmJC; 1.  
 DR SMART; SM00558; JmJC; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 1682 AA; 180749 MW; 2FD120F8336845A3 CRC64;

Query Match 88.9%; Score 40; DB 2; Length 1682;  
 Best Local Similarity 85.7%; Pred. No. 4.1e+03;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
 | |||||  
 Db 467 SPPPPPC 473

## RESULT 47

Q850N7 ORYSA  
 ID Q850N7\_ORYSA PRELIMINARY; PRT; 80 AA.  
 AC Q850N7;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Hypothetical protein P0692C11.30 (Hypothetical protein  
 DE P0510F09.8).  
 GN Name=P0692C11.30; Synonyms=P0510F09.8;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OC NCBI\_TaxID=39947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,  
 Wu J., Nimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,  
 Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,  
 Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,  
 Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,  
 Ikono M., Itoh S., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,  
 Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,  
 Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,  
 Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,  
 Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,  
 Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,  
 Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,  
 Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,  
 Yano M., Jiang J., Gojobori T.;  
 RT "The genome sequence and structure of rice chromosome 1.";  
 RL Nature 420:312-316(2002).  
 DR EMBL; AF003381; BAB86525.1; -; Genomic DNA.  
 DR EMBL; AF003273; BAB92334.1; -; Genomic DNA.  
 DR Gramene; Q850N7; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 80 AA; 7710 MW; 028E97A5088144FF CRC64;

Query Match 86.7%; Score 39; DB 2; Length 80;  
 Best Local Similarity 71.4%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
 | |||||  
 Db 18 ANPPPPC 24

## RESULT 48

Q8CC63\_MOUSE  
 ID Q8CC63\_MOUSE PRELIMINARY; PRT; 117 AA.  
 AC Q8CC63;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Mus musculus adult male epididymis cDNA, RIKEN full-length enriched  
 DE library, clone:9230116M18 product:Hypothetical protein, full insert  
 DE sequence.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Epididymis;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Epididymis;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Guscinich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberte P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-P.,  
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,  
RA Hayashizaki Y.;  
RA "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
[3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Epididymis;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
[4]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Epididymis;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
[5]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Epididymis;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
[6]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Epididymis;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK033831; BAC29489.1; -; mRNA.  
KW Hypothetical protein.  
SQ SEQUENCE 117 AA; 12583 MW; BDE48398D1CCEA77 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 117;  
Best Local Similarity 85.7%; Pred. No. 4.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SSPPPPC 7  
| | | | |  
DB 78 SVPPPPC 84

## RESULT 49

O69Q83\_ORYSA PRELIMINARY; PRT; 162 AA.  
AC O69Q83\_ORYSA PRELIMINARY; PRT; 162 AA.  
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)  
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)  
DE Hypothetical protein P0463D04.9 (Hypothetical protein  
DE P0463G11.24).  
GN Name=P0463D04.9; Synonyms=P0463G11.24;  
OS Oryza sativa (Japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Sasaki T., Matsumoto T., Katayose Y.;  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, PAC  
RT clone:P0463D04.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Sasaki T., Matsumoto T., Katayose Y.;  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, PAC  
RT clone:P0463G11.";  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP005392; BAD33389.1; -; Genomic\_DNA.  
DR EMBL; AP005633; BAD46336.1; -; Genomic\_DNA.  
DR GRL; O69Q83; -;  
KW Hypothetical protein.  
SQ SEQUENCE 162 AA; 16686 MW; B4B8C83EB56FCD6 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 162;  
Best Local Similarity 71.4%; Pred. No. 5.8e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPPPPC 7  
| | | | |  
DB 30 AAPPPPC 36

## RESULT 50

O8VPN4\_9MICC PRELIMINARY; PRT; 249 AA.  
AC O8VPN4\_9MICC PRELIMINARY; PRT; 249 AA.  
DT 01-MAR-2002 (TRENBLrel. 20, Created)  
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
DE Putative proline-rich extensin-like protein.  
OS Micrococcus sp. 28.  
OG Plasmid pSD10.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Micrococccineae; Micrococccaceae; Micrococcus.  
OX NCBI\_TaxID=161213;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=28;  
RA Zhong Z., Caspi R., Mincer T., Helinski D., Knauf V., Boardman K.,  
RA Wilkinson J.E., Shea T., Deloughery C., Toudkarian A.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY034092; AAK62513.1; -; Genomic\_DNA.  
KW Plasmid.  
SQ SEQUENCE 249 AA; 26247 MW; 4AB620F0004B5F7D CRC64;

Query Match 86.7%; Score 39; DB 2; Length 249;  
Best Local Similarity 71.4%; Pred. No. 8.8e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPC 7  
:|||||  
Db 198 ATPPPC 204

Search completed: January 3, 2006, 09:50:21  
Job time : 101.667 secs

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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:05 ; Search time 70.6667 Seconds  
(without alignments)  
43.523 Million cell updates/sec

Title: US-10-759-832-10  
Perfect score: 45  
Sequence: 1 SSPPPPC 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	7	2	AAR78289
2	45	100.0	7	2	AAR74296
3	45	100.0	7	2	AAR95392
4	45	100.0	7	3	AAW49310
5	45	100.0	7	3	AAW51307
6	45	100.0	7	5	AAW66089
7	45	100.0	7	5	ABH82193
8	45	100.0	7	7	ADP42661
9	45	100.0	7	8	ADH82115
10	45	100.0	7	8	ADH82115
11	45	100.0	13	8	ADH82118
12	45	100.0	16	2	AAR74295
13	45	100.0	16	3	AAW49309
14	45	100.0	16	6	ABP73035
15	45	100.0	17	2	AAR78283
16	45	100.0	17	3	AAW58140
17	45	100.0	17	3	AAW99519
18	45	100.0	17	5	AAW66085
19	45	100.0	17	7	ADP42680
20	45	100.0	17	7	ADP42674
21	45	100.0	17	7	ADP42672
22	45	100.0	17	7	ADP42678
23	45	100.0	17	7	ADP42676
24	45	100.0	17	7	ADP42682

98	39	86.7	1664	9	ADY15167	Adv15167 PRO polyp	171	37	82.2	10	3	AA51311	Aay51311 Human gas
99	38	84.4	9	4	AAU09145	Aau09145 Ena/VASP	172	37	82.2	10	6	ABP73034	Abp73034 Peptide s
100	38	84.4	23	4	ABG79181	Abg79181 Synthetic	173	37	82.2	10	9	ADY37662	Ady37662 Human G17
101	38	84.4	84	5	ABP01326	Abp01326 Human ORF	174	37	82.2	11	2	AA06247	Aar06247 Antigenic
102	38	84.4	100	2	AAV60293	Aay60293 Human end	175	37	82.2	11	3	AAV49304	Aay49304 Human hep
103	38	84.4	100	4	AAW94217	Aaw94217 Human rep	176	37	82.2	11	3	AAV51310	Aay51310 Human gas
104	38	84.4	107	5	ABP00921	Abp00921 Human ORF	177	37	82.2	11	6	ABP73033	Abp73033 Peptide s
105	38	84.4	125	7	ABM88411	Abm88411 Rice abio	178	37	82.2	11	6	ABU61404	Abu61404 Peptide 1
106	38	84.4	130	4	AAU43766	Aau43766 Propionib	179	37	82.2	11	8	ADP21628	Adp21628 Artificial
107	38	84.4	130	6	ABM40285	Abm40285 Propionib	180	37	82.2	11	9	ADY37661	Ady37661 Human G17
108	38	84.4	142	4	AAO09303	Aao09303 Human pol	181	37	82.2	12	2	AA06246	Aar06246 Antigenic
109	38	84.4	179	7	ABO78158	Abot78158 Pseudomon	182	37	82.2	12	2	AA06335	Aar06335 Antigenic
110	38	84.4	190	9	ADY65062	Ady65062 S. mansoni	183	37	82.2	12	2	AAW25460	Aaw25460 SH3 domain
111	38	84.4	198	8	ADY59601	Ady59601 Plant pol	184	37	82.2	12	3	AAV49307	Aay49307 Human tet
112	38	84.4	201	7	ABM87745	Abm87745 Rice abio	185	37	82.2	12	3	AAV49303	Aay49303 Human hep
113	38	84.4	230	4	ABG60746	Abg60746 Drosophil	186	37	82.2	12	3	AAV49306	Aay49306 Human hep
114	38	84.4	241	7	ADB64163	Adb64163 Human pro	187	37	82.2	12	3	AAV51312	Aay51312 Rat gastr
115	38	84.4	259	8	ADS27306	Ads27306 Bacterial	188	37	82.2	12	3	AAV51306	Aay51306 Human gas
116	38	84.4	259	8	ADS26953	Ads26953 Bacterial	189	37	82.2	12	3	AAV51313	Aay51313 Human gas
117	38	84.4	263	4	ABB69470	Abb69470 Drosophil	190	37	82.2	12	3	AAV51309	Aay51309 Human gas
118	38	84.4	280	8	ADY11773	Ady11773 Plant ful	191	37	82.2	12	6	ABP73032	Abp73032 Peptide s
119	38	84.4	285	8	ADY06704	Ady06704 Plant ful	192	37	82.2	12	9	ADY37663	Ady37663 Rat G17 (
120	38	84.4	316	7	ABM89584	Abm89584 Rice abio	193	37	82.2	12	9	ADY37660	Ady37660 Human G17
121	38	84.4	373	7	ADCL0050	Adcl0050 Human NOV	194	37	82.2	12	9	ADY37664	Ady37664 Human G34
122	38	84.4	373	8	ADQ39459	Adq39459 Human myo	195	37	82.2	15	1	AAV71000	Aav71000 Sequence
123	38	84.4	390	7	ADJ768437	Adj768437 Human hea	196	37	82.2	15	1	AAV71000	Aav71000 Sequence
124	38	84.4	390	8	ADQ39458	Adq39458 Human myo	197	37	82.2	15	1	AAV80034	Aav80034 Beta-huma
125	38	84.4	411	4	ABG12956	Abg12956 Novel hum	198	37	82.2	15	1	AAV91839	Aav91839 Analogue
126	38	84.4	444	8	ADX95338	Adx95338 Plant ful	199	37	82.2	15	2	AA06336	Aar06336 Heptadeca
127	38	84.4	511	7	ABO77332	Abot77332 Pseudomon	200	37	82.2	15	2	AAV74297	Aav74297 Human gas
128	38	84.4	574	7	ABO82122	Abot82122 Pseudomon	201	37	82.2	15	2	AAW39032	Aaw39032 Peptide r
129	38	84.4	644	8	ADR08628	Adr08628 Human pro	202	37	82.2	15	2	AAW37269	Aaw37269 Peptide d
130	38	84.4	688	4	AAW93311	Aam93311 Human pol	203	37	82.2	15	2	AAW69453	Aaw69453 HCG anti
131	38	84.4	688	8	ADL30788	Adl30788 Human pro	204	37	82.2	15	3	AAW93438	Aaw93438 Human hCG
132	38	84.4	770	7	ADRS4355	Ades4355 Human pro	205	37	82.2	15	3	AAV87483	Aay87483 Human cho
133	38	84.4	770	7	ADQ46513	Adq46513 Human pro	206	37	82.2	15	3	AAV49308	Aay49308 Human G34
134	38	84.4	770	7	ADRS4359	Ades4359 Human pro	207	37	82.2	15	3	AAV51314	Aay51314 Human gas
135	38	84.4	770	7	ADDA6517	Adda6517 Human pro	208	37	82.2	15	3	AAV20560	Aav20560 Human cho
136	38	84.4	770	8	ADJ769418	Adj769418 Human hea	209	37	82.2	15	4	AAU01143	Aau01143 Structure
137	38	84.4	770	8	ADJ27175	Adj27175 Human LRP	210	37	82.2	15	4	AAV48389	Aav48389 Human cho
138	38	84.4	770	8	ADQ39601	Adq39601 Human myo	211	37	82.2	15	4	AAU02841	Aau02841 Human cho
139	38	84.4	785	7	ADQ93395	Adq93395 Human lip	212	37	82.2	15	4	AAU04125	Aau04125 Peptide f
140	38	84.4	814	4	ABG04441	Abg04441 Novel hum	213	37	82.2	15	8	ADS18291	Ads18291 Human int
141	38	84.4	987	3	AAV43064	Aav43064 Human ORF	214	37	82.2	15	9	ADY37665	Ady37665 Human G34
142	38	84.4	1006	8	ADU20559	Adu20559 A. thalia	215	37	82.2	16	2	AAV78285	Aav78285 GnRH immu
143	38	84.4	1006	8	ADU20561	Adu20561 A. thalia	216	37	82.2	16	3	AAV58141	Aay58141 Gonadotro
144	38	84.4	1253	3	AAV29663	Aav29663 Human tyr	217	37	82.2	16	5	AAV66081	Aav66081 Gonadotro
145	38	84.4	1264	3	AAV29664	Aav29664 Human tyr	218	37	82.2	16	8	ADH89222	Adh89222 Human cho
146	38	84.4	1274	2	AAW89253	Aaw89253 Human ALP	219	37	82.2	25	8	ADS13554	Ads13554 Human rhe
147	38	84.4	1329	5	ABB90782	Abb90782 Mouse Tum	220	37	82.2	26	2	AAV31607	Aav31607 Sequence
148	38	84.4	1329	5	ABB90728	Abb90728 Mouse Tum	221	37	82.2	27	2	AAV69446	Aav69446 HCG anti
149	38	84.4	1329	6	ABU54489	Abu54489 Mouse tum	222	37	82.2	27	2	AAV69448	Aav69448 HCG anti
150	38	84.4	1329	6	ABU54435	Abu54435 Mouse tum	223	37	82.2	27	2	AAW93472	Aaw93472 Synthetic
151	38	84.4	1329	8	ADO29669	Ado29669 Mouse GPC	224	37	82.2	27	2	AAW93469	Aaw93469 Synthetic
152	38	84.4	1403	8	ADX91854	Adx91854 Plant ful	225	37	82.2	27	2	AAW93470	Aaw93470 Synthetic
153	38	84.4	1487	6	ABR52735	Abv52735 Protein s	226	37	82.2	27	4	AAU01178	Aau01178 Synthetic
154	38	84.4	1487	7	ADK61978	Adk61978 Disease t	227	37	82.2	27	4	AAU01179	Aau01179 Synthetic
155	38	84.4	1583	3	AAV29662	Aav29662 Human tyr	228	37	82.2	27	4	AAU01181	Aau01181 Human cho
156	38	84.4	1636	3	AAV29661	Aav29661 Human his	229	37	82.2	27	4	AAU01182	Aau01182 Human cho
157	38	84.4	1636	5	AAV25081	Aav25081 Human kin	230	37	82.2	27	4	AAU01180	Aau01180 Synthetic
158	38	84.4	1636	6	AAV99782	Aav99782 Antagonis	231	37	82.2	28	4	AAV64636	Aav64636 Immunoglo
159	37	82.2	1636	8	AAW99682	Aaw99682 Human IGA	232	37	82.2	28	4	AAV64637	Aav64637 Immunoglo
160	37	82.2	6	5	AAV66083	Aav66083 Amino aci	233	37	82.2	29	1	AAV71004	Aav71004 Sequence
161	37	82.2	6	7	ADP42663	Adp42663 Spacer pe	234	37	82.2	29	1	AAV71004	Aav71004 Sequence
162	37	82.2	6	7	ADP42662	Adp42662 Spacer pe	235	37	82.2	29	1	AAV80038	Aav80038 Beta-huma
163	37	82.2	6	8	ADH89214	Adh89214 Spacer pe	236	37	82.2	29	1	AAV91844	Aav91844 Analogue
164	37	82.2	6	8	ADH89217	Adh89217 Novel inf	237	37	82.2	29	2	AAW42211	Aaw42211 Peptide d
165	37	82.2	6	8	ADSL18218	Adsl18218 Novel inf	238	37	82.2	29	2	AAW69457	Aaw69457 HCG anti
166	37	82.2	6	8	ADH89216	Adh89216 Spacer pe	239	37	82.2	29	2	AAW93442	Aaw93442 Human hCG
167	37	82.2	9	2	AAV37993	Aav37993 IGA2 allo	240	37	82.2	29	3	AAV87487	Aay87487 Human cho
168	37	82.2	9	4	AAU09144	Aau09144 Ena/VASP	241	37	82.2	29	3	AAV20551	Aav20551 Human cho
169	37	82.2	10	2	AAR06248	Aar06248 Antigenic	242	37	82.2	29	3	AAU01147	Aau01147 Structure
170	37	82.2	10	3	AAV49305	Aay49305 Human hep	243	37	82.2	29	4	AAV48393	Aav48393 Human cho

244	37	82.2	29	4	AAU02845	Aau02845 Human Cho	317	99	5	ABP07908	Abp07908 Human ORF
245	37	82.2	29	4	AAU04129	Aab04129 Peptide f	318	100	8	ADY23743	Ady23743 Plant ful
246	37	82.2	38	5	AAU79547	Aau79547 Rice rubi	319	101	4	AAH85263	Aam85263 Human imm
247	37	82.2	41	1	AAU10196	Aap10196 Sequence	320	101	8	ADY22787	Ady22787 Plant ful
248	37	82.2	41	1	ABM88054	Abm88054 Rice abio	321	102	4	AAO00629	Aao00629 Human pol
249	37	82.2	42	1	AAU71006	Aap71006 Sequence	322	102	7	ADG63870	Adg63870 Human pro
250	37	82.2	42	1	AAU80040	Aap80040 Beta-huma	323	106	8	ADG66954	Adg66954 Novel hum
251	37	82.2	42	1	AAU91846	Aap91846 Analogue	324	108	4	AAO07118	Aao07118 Human pol
252	37	82.2	42	2	AAW42213	Aaw42213 Peptide d	325	109	7	ADB55322	Adb55322 Human pro
253	37	82.2	42	2	AAW69459	Aaw69459 HCG antig	326	110	3	AAU35327	Aau35327 Zea maye
254	37	82.2	42	2	AAW93444	Aaw93444 Human hCG	327	110	4	AAO03790	Aao03790 Human pol
255	37	82.2	42	3	AAU87489	Aay87489 Human cho	328	110	5	ABP03767	Abp03767 Human ORF
256	37	82.2	42	3	AAU20553	Aab20553 Human cho	329	112	7	ABM88815	Abm88815 Rice abio
257	37	82.2	42	4	AAU01149	Aau01149 Structure	330	113	8	ADY25127	Adi25127 Corn gamm
258	37	82.2	42	4	AAU48395	Aab48395 Human cho	331	114	4	AAO05912	Aao05912 Human pol
259	37	82.2	42	4	AAU02847	Aau02847 Human cho	332	114	8	ADT60422	Adt60422 Plant pol
260	37	82.2	42	4	AAU04131	Aab04131 Peptide f	333	116	6	ADA54184	Ada54184 Human pro
261	37	82.2	42	6	ADA48220	Ada48220 Rice prot	334	116	8	ADG65612	Adg65612 Novel hum
262	37	82.2	43	5	AAU50788	Aam50788 Human cho	335	116	8	ADX79203	Adx79203 Plant ful
263	37	82.2	46	4	AAU14423	Aam14423 Peptide #	336	120	4	ABG00847	Abg00847 Novel hum
264	37	82.2	46	4	ABU33371	Abb33371 Peptide #	337	121	4	AAO03310	Aao03310 Human pol
265	37	82.2	46	4	AAU26836	Aam26836 Peptide #	338	122	4	AAU29615	Aau29615 Novel hum
266	37	82.2	46	4	ABU28196	Abb28196 Human pep	339	126	9	AEA90462	Aea90462 Human lun
267	37	82.2	46	4	ABU18830	Abb18830 Protein #	340	129	4	ABU67541	Abb67541 Drosophil
268	37	82.2	46	4	AAU66550	Aam66550 Human bon	341	130	4	AAO01894	Aao01894 Human pol
269	37	82.2	46	4	AAU54156	Aam54156 Human bra	342	132	4	AAO03532	Aao03532 Human pol
270	37	82.2	46	4	ABU48218	Abb48218 Human liv	343	134	5	AAU47988	Aam47988 Simian IT
271	37	82.2	46	4	AAU02150	Aam02150 Peptide #	344	136	8	ADX79242	Adx79242 Plant ful
272	37	82.2	46	5	ABU36202	Abb36202 Human pep	345	138	4	ABU11959	Abu11959 Novel hum
273	37	82.2	47	5	AAU79555	Aap79555 Rice rubi	346	139	8	ADG66947	Adg66947 Novel hum
274	37	82.2	48	1	AAU10195	Aap10195 Sequence	347	141	7	ADH87155	Adh87155 Enterococ
275	37	82.2	48	1	AAU71005	Aap71005 Sequence	348	142	8	ADX67165	Adx67165 Plant ful
276	37	82.2	48	1	AAU80039	Aap80039 Beta-huma	349	143	4	AAO13070	Aao13070 Human pol
277	37	82.2	48	1	AAU91845	Aap91845 Analogue	350	147	8	ADX77660	Adx77660 Plant ful
278	37	82.2	48	2	AAU4212	Aaw4212 Peptide d	351	147	8	ABM89585	Abm89585 Rice abio
279	37	82.2	48	2	AAU69458	Aaw69458 HCG antig	352	148	7	ABM89585	Abm89585 Rice abio
280	37	82.2	48	2	AAU93443	Aaw93443 Human hCG	353	155	3	AAU26908	Aau26908 Zea maye
281	37	82.2	48	3	AAU87488	Aay87488 Human cho	354	159	4	AAU67370	Aau67370 Propionib
282	37	82.2	48	3	AAU20552	Aab20552 Human cho	355	159	6	ABM63889	Abm63889 Propionib
283	37	82.2	48	4	AAU01148	Aau01148 Structure	356	161	4	ABU14726	Abu14726 Novel hum
284	37	82.2	48	4	AAU48394	Aab48394 Human cho	357	162	4	ABU11958	Abu11958 Novel hum
285	37	82.2	48	4	AAU02846	Aau02846 Human cho	358	162	7	ADP05400	Adp05400 Bacterial
286	37	82.2	48	4	AAU04130	Aab04130 Peptide f	359	162	7	ADI60122	Adi60122 Secreted
287	37	82.2	52	4	ABU15061	Abb15061 Human ner	360	162	8	ADU01112	Adu01112 Human pro
288	37	82.2	53	4	AAU08643	Aao08643 Human pol	361	162	8	ADU15494	Adu15494 Novel hum
289	37	82.2	56	4	AAU06362	Aao06362 Human pol	362	164	3	AAU44836	Aay44836 Human per
290	37	82.2	63	3	AAU38594	Aab38594 Gene 15 h	363	164	4	AAU27698	Aau27698 Full-leng
291	37	82.2	64	3	AAU39289	Aab39289 Gene 38 h	364	165	7	ADD12567	Add12567 Human ENZ
292	37	82.2	66	2	AAU48333	Aay48333 Human pro	365	170	8	ADU020389	Adu020389 Human PRO
293	37	82.2	67	4	ABU22828	Abg22828 Novel hum	366	170	9	ADY18559	Ady18559 PRO polyp
294	37	82.2	70	4	AAU07626	Aao07626 Human pol	367	180	4	ABU13101	Abu13101 Novel hum
295	37	82.2	71	2	AAU60051	Aay60051 Human end	368	183	4	ABU90563	Aab90563 Human sec
296	37	82.2	71	8	ADI25129	Adi25129 Corn gamm	369	183	5	ABG65476	Abg65476 Human alb
297	37	82.2	73	8	ADU27804	Adu27804 Human pro	370	183	8	ADL78743	Adl78743 Albumin f
298	37	82.2	73	8	ADU04331	Adn04331 Antipori	371	184	3	AAU14315	Aab14315 Human sec
299	37	82.2	78	4	AAU51463	Aau51463 Propionib	372	184	8	ABU85237	Aab85237 Human sec
300	37	82.2	78	6	ABU47982	Abm47982 Propionib	373	184	8	ADI45227	Adi45227 Rice isop
301	37	82.2	79	4	AAU51194	Aau51194 Propionib	374	186	8	ADX97029	Adx97029 Plant ful
302	37	82.2	79	6	ABU47713	Abm47713 Propionib	375	188	4	AAU88879	Aam88879 Human imm
303	37	82.2	82	5	ABU01686	Abu01686 Human bre	376	190	3	ABU58309	Abu58309 Lung canc
304	37	82.2	85	4	AAU31036	Aau31036 Novel hum	377	198	7	ABU67162	Abu67162 Klebsiell
305	37	82.2	85	4	ABU55498	Abo55498 Human gen	378	198	8	ADX79833	Adx79833 Plant ful
306	37	82.2	86	4	AAU00489	Aao00489 Human pol	379	198	8	ADY09004	Ady09004 Plant ful
307	37	82.2	88	4	AAU03120	Aao03120 Human gen	380	199	8	ADY09775	Ady09775 Plant ful
308	37	82.2	88	4	AAU32799	Aau32799 Novel hum	381	201	4	AAU32714	Aau32714 Novel hum
309	37	82.2	88	5	ABU63595	Abg63595 Human alb	382	205	8	ADX68802	Adx68802 Plant ful
310	37	82.2	88	5	AAU15868	Aae15868 Mutant po	383	206	4	AAU94533	Aab94533 Human pro
311	37	82.2	88	8	ADL76860	Adl76860 Albumin f	384	206	4	AAU93090	Aab93090 Human pro
312	37	82.2	91	5	ADG79469	Adg79469 Human sec	385	207	4	AAU27870	Aau27870 Contig po
313	37	82.2	91	5	ADG79571	Adg79571 Human sec	386	213	6	ADA54493	Ada54493 Human pro
314	37	82.2	92	8	ADI25128	Adi25128 Corn gamm	387	214	4	AAU25738	Aam25738 Human pro
315	37	82.2	97	4	AAU49631	Aau49631 Propionib	388	216	7	ABU78189	Abu78189 Pseudomon
316	37	82.2	97	6	ABU46150	Abm46150 Propionib	389	220	4	AAU41487	Aam41487 Human pol

390	37	82.2	224	8	AD125126	Adi25126	Corn gamm	463	37	82.2	404	4	ABG25984	Novel hum
391	37	82.2	224	8	ADY09470	Plant ful	464	37	82.2	404	4	ABG25619	Novel hum	
392	37	82.2	227	8	ADX72143	Plant ful	465	37	82.2	404	4	ABG04912	Novel hum	
393	37	82.2	230	2	AAW22525	H45-gamma	466	37	82.2	404	4	ABG25076	Novel hum	
394	37	82.2	233	8	ADs10938	Human the	467	37	82.2	415	2	AAr28638	UL26 prot	
395	37	82.2	234	8	ADX72915	Plant ful	468	37	82.2	419	5	AAg78406	Amino aci	
396	37	82.2	235	7	ABO80880	Pseudomon	469	37	82.2	419	7	AAe38597	Human pot	
397	37	82.2	236	4	AAm39701	Human pol	470	37	82.2	419	7	ADK52550	Hematolog	
398	37	82.2	236	4	ABG08436	Novel hum	471	37	82.2	419	8	ADH51639	Human 123	
399	37	82.2	240	2	AAW22526	P20-gamma	472	37	82.2	419	8	ADi27936	Human TWI	
400	37	82.2	240	6	ABP78606	N_gonorr	473	37	82.2	419	8	ADr44894	Polypepti	
401	37	82.2	242	6	ABU70401	Human adi	474	37	82.2	419	9	AEa23359	Tumor ant	
402	37	82.2	249	4	AAU17400	Novel sig	475	37	82.2	422	7	ABO81879	Pseudomon	
403	37	82.2	249	7	ABD94108	Human nov	476	37	82.2	424	7	ABM86265	Rice abio	
404	37	82.2	249	8	ADX91862	Plant ful	477	37	82.2	432	8	ABM84663	Human dia	
405	37	82.2	251	7	ADJ70277	Human hea	478	37	82.2	439	8	ADY07573	Plant ful	
406	37	82.2	251	8	ADX68208	Plant ful	479	37	82.2	449	4	ABG08435	Novel hum	
407	37	82.2	252	4	AA890595	Human sec	480	37	82.2	453	8	ABM83965	Human dia	
408	37	82.2	252	4	ABG03386	Novel hum	481	37	82.2	455	8	ADX87802	Plant ful	
409	37	82.2	252	5	ABG65477	Human alb	482	37	82.2	456	7	ADC65688	Mutant re	
410	37	82.2	252	8	ADL78744	Albumin f	483	37	82.2	457	7	ADC65687	Mutant re	
411	37	82.2	261	7	ABM89090	Rice abio	484	37	82.2	457	7	ADC65686	Wild type	
412	37	82.2	271	3	AA828444	Human fra	485	37	82.2	457	7	ADC65689	Mutant re	
413	37	82.2	271	5	ABP62934	Human pol	486	37	82.2	457	7	ADC65690	Mutant re	
414	37	82.2	271	9	AEb11267	Amino aci	487	37	82.2	458	8	ADX87713	Plant ful	
415	37	82.2	271	9	AEb11766	Human FOS	488	37	82.2	464	3	AAy68739	Amino aci	
416	37	82.2	277	8	ADC87503	Human GPC	489	37	82.2	465	7	ADB81330	Human cyt	
417	37	82.2	279	8	ADr10339	Human pro	490	37	82.2	467	2	AAW75057	Human sec	
418	37	82.2	280	7	ABW01568	Mouse for	491	37	82.2	467	2	AAy13378	Amino aci	
419	37	82.2	291	3	AA856390	Human pro	492	37	82.2	467	3	AAy94860	Human pro	
420	37	82.2	294	4	ABG15400	Novel hum	493	37	82.2	467	3	ADC78515	Human PRO	
421	37	82.2	294	8	ADY58369	Plant pol	494	37	82.2	467	4	AAAB80246	Human PRO	
422	37	82.2	297	3	AA826753	Rice bzfp	495	37	82.2	467	4	AAW78342	Human pro	
423	37	82.2	299	7	ADB64638	Human pro	496	37	82.2	467	4	AAU29031	Human PRO	
424	37	82.2	301	8	ADr21602	Human enz	497	37	82.2	467	4	AA888401	Human mem	
425	37	82.2	302	7	ADW04491	Human pro	498	37	82.2	467	6	ABU58407	Human PRO	
426	37	82.2	302	8	ADH35325	ENZM prot	499	37	82.2	467	6	ABU71624	Human PRO	
427	37	82.2	311	2	AAW90248	Human FAS	500	37	82.2	467	6	ABU87955	Novel hum	
428	37	82.2	323	8	ADU02384	Novel hum	501	37	82.2	467	6	ABU84270	Human sec	
429	37	82.2	325	4	ABG21919	Novel hum	502	37	82.2	467	6	ABR66144	Human sec	
430	37	82.2	332	7	ABM88621	Rice abio	503	37	82.2	467	6	ABR65534	Human sec	
431	37	82.2	340	5	AAW47855	Human Ig-	504	37	82.2	467	6	ABU99474	Human sec	
432	37	82.2	340	7	ADY97349	Human Iga	505	37	82.2	467	6	ABU82713	Human PRO	
433	37	82.2	340	9	ADW24782	Human var	506	37	82.2	467	6	ABU89834	Novel hum	
434	37	82.2	340	9	ADW24740	Human var	507	37	82.2	467	6	ABU71479	Human PRO	
435	37	82.2	340	9	ADZ08938	Mammalian	508	37	82.2	467	6	ABR68083	Human sec	
436	37	82.2	340	9	ADZ08807	Mammalian	509	37	82.2	467	6	ABU96136	Novel hum	
437	37	82.2	340	9	ADZ44464	Human imm	510	37	82.2	467	6	ABU92567	Human sec	
438	37	82.2	340	9	AEa16539	Human MCP	511	37	82.2	467	6	ABO08644	Human sec	
439	37	82.2	340	9	AEb72774	Anti-Ltal	512	37	82.2	467	6	ABO02696	Human sec	
440	37	82.2	344	4	AAU28019	Human con	513	37	82.2	467	6	ABR74850	Human sec	
441	37	82.2	349	2	AAW06416	Phosphotr	514	37	82.2	467	6	ABR94612	Human sec	
442	37	82.2	349	4	AAW39747	Human pol	515	37	82.2	467	6	ABU85585	Human PRO	
443	37	82.2	349	5	ABD07525	Human dru	516	37	82.2	467	6	ABU98745	Novel hum	
444	37	82.2	349	8	ADP30135	Human sec	517	37	82.2	467	6	ABU97960	Novel hum	
445	37	82.2	349	8	ADP25013	PRO polyyp	518	37	82.2	467	6	ABU91666	Novel hum	
446	37	82.2	349	9	AEa24001	Human PRO	519	37	82.2	467	6	ABU71925	Human sec	
447	37	82.2	353	8	ADP30134	Human sec	520	37	82.2	467	6	ABU89359	Human PRO	
448	37	82.2	354	9	ADY19020	PRO polyyp	521	37	82.2	467	6	ABU86200	Human sec	
449	37	82.2	361	8	ADY59637	Plant pol	522	37	82.2	467	6	ABU67413	Human sec	
450	37	82.2	362	2	AAW69717	Herpesvir	523	37	82.2	467	6	ABU80441	Human PRO	
451	37	82.2	367	7	ABM87729	Rice abio	524	37	82.2	467	6	ABO01808	Novel hum	
452	37	82.2	371	8	ADN99556	Novel hum	525	37	82.2	467	6	ABR99359	Human sec	
453	37	82.2	372	7	ABO71362	Pseudomon	526	37	82.2	467	6	ABR98749	Human sec	
454	37	82.2	380	4	AAW41533	Human pol	527	37	82.2	467	6	ABO16272	Human sec	
455	37	82.2	380	8	ADs12175	Human the	528	37	82.2	467	6	ABR92172	Human sec	
456	37	82.2	385	8	ABO84836	Murine ca	529	37	82.2	467	6	ABO18813	Human sec	
457	37	82.2	390	6	AAO29751	Human 326	530	37	82.2	467	6	ABr78234	Human sec	
458	37	82.2	392	3	AAy60891	Human G p	531	37	82.2	467	6	ABU84970	Novel hum	
459	37	82.2	393	3	AAy94426	Human h-T	532	37	82.2	467	6	ABO00109	Novel hum	
460	37	82.2	393	3	AAy94425	Human h-T	533	37	82.2	467	6	ABO11441	Human sec	
461	37	82.2	393	4	AA667777	Human mec	534	37	82.2	467	6	ABO02086	Human sec	
462	37	82.2	393	9	AEa62073	Human pot	535	37	82.2	467	6	ABU54381	Human sec	



682	37	82.2	467	6	ABR94307	Human sec	755	37	82.2	467	6	ABO20240	Human sec
683	37	82.2	467	6	ABR75814	Human sec	756	37	82.2	467	6	ABO21155	Human sec
684	37	82.2	467	6	ADA18256	Human sec	757	37	82.2	467	6	ABO22070	Human sec
685	37	82.2	467	6	ABO32790	Human sec	758	37	82.2	467	6	ABR96504	Human sec
686	37	82.2	467	6	ABR71190	Human sec	759	37	82.2	467	6	ABR85682	Human sec
687	37	82.2	467	6	ABR93087	Human sec	760	37	82.2	467	6	ABR99664	Human sec
688	37	82.2	467	6	ABR93392	Human sec	761	37	82.2	467	6	ABM00215	Human sec
689	37	82.2	467	6	ABR87817	Human sec	762	37	82.2	467	6	ABM00520	Human sec
690	37	82.2	467	6	ABO27817	Human sec	763	37	82.2	467	6	ABO29647	Human sec
691	37	82.2	467	6	ABO29952	Human sec	764	37	82.2	467	6	ABM23513	Human sec
692	37	82.2	467	6	ABO33161	Human PRO	765	37	82.2	467	6	ABM29308	Human sec
693	37	82.2	467	6	ABM04849	Human sec	766	37	82.2	467	6	ABO38239	Human sec
694	37	82.2	467	6	ABM08809	Human sec	767	37	82.2	467	6	ABO45539	Human PRO
695	37	82.2	467	6	ABO36409	Human sec	768	37	82.2	467	6	ABM20463	Human sec
696	37	82.2	467	6	ABO35494	Human PRO	769	37	82.2	467	6	ADA42376	Human sec
697	37	82.2	467	6	ABO39459	Human sec	770	37	82.2	467	6	ADA81287	Human sec
698	37	82.2	467	6	ABM10334	Human sec	771	37	82.2	467	6	ABO16577	Human sec
699	37	82.2	467	6	ABM11859	Human sec	772	37	82.2	467	6	ABO18203	Human sec
700	37	82.2	467	6	ABO52005	Human PRO	773	37	82.2	467	6	ABO22630	Human PRO
701	37	82.2	467	6	ABO52310	Human PRO	774	37	82.2	467	6	ABO22935	Human PRO
702	37	82.2	467	6	ABO23628	Human sec	775	37	82.2	467	6	ABR92477	Human sec
703	37	82.2	467	6	ABR97114	Human sec	776	37	82.2	467	6	ABR81434	Human sec
704	37	82.2	467	6	ABR86902	Human sec	777	37	82.2	467	6	ABO17528	Human PRO
705	37	82.2	467	6	ABM10944	Human sec	778	37	82.2	467	6	ABM77858	Human sec
706	37	82.2	467	6	ABM28088	Human sec	779	37	82.2	467	6	ABR89647	Human sec
707	37	82.2	467	6	ABO32087	Human sec	780	37	82.2	467	6	ABM26563	Human sec
708	37	82.2	467	6	ABM15214	Human sec	781	37	82.2	467	6	ABM13689	Human sec
709	37	82.2	467	6	ABM06369	Human sec	782	37	82.2	467	6	ABO28427	Human sec
710	37	82.2	467	6	ABM04180	Human sec	783	37	82.2	467	6	ABO30257	Human sec
711	37	82.2	467	6	ABM22293	Human sec	784	37	82.2	467	6	ABM07284	Human sec
712	37	82.2	467	6	ABM07589	Human sec	785	37	82.2	467	6	ABM03875	Human sec
713	37	82.2	467	6	ABO40679	Human sec	786	37	82.2	467	6	ABO37019	Human sec
714	37	82.2	467	6	ABM35326	Human sec	787	37	82.2	467	6	ABO41594	Human sec
715	37	82.2	467	6	ABM33089	Human PRO	788	37	82.2	467	6	ABO35189	Human PRO
716	37	82.2	467	6	ABO52615	Human PRO	789	37	82.2	467	6	ABM25038	Human sec
717	37	82.2	467	6	ABO50175	Human sec	790	37	82.2	467	6	ABO47430	Human sec
718	37	82.2	467	6	ABU99169	Human sec	791	37	82.2	467	6	ABO47735	Human sec
719	37	82.2	467	6	ABO04221	Human sec	792	37	82.2	467	6	ABO48345	Human sec
720	37	82.2	467	6	ABO05951	Human sec	793	37	82.2	467	6	ABO51395	Human PRO
721	37	82.2	467	6	ABO34850	Human PRO	794	37	82.2	467	6	ABO51700	Human PRO
722	37	82.2	467	6	ABM18391	Human sec	795	37	82.2	467	6	ABO50480	Human sec
723	37	82.2	467	6	ADA16231	Human sec	796	37	82.2	467	6	ABR79604	Human sec
724	37	82.2	467	6	ABR97419	Human sec	797	37	82.2	467	6	ABM16866	Human sec
725	37	82.2	467	6	ABR80519	Human sec	798	37	82.2	467	6	ABO17898	Human sec
726	37	82.2	467	6	ABM01130	Human sec	799	37	82.2	467	6	ABO20850	Human sec
727	37	82.2	467	6	ABR88732	Human sec	800	37	82.2	467	6	ABR96809	Human sec
728	37	82.2	467	6	ABM13384	Human sec	801	37	82.2	467	6	ABM12164	Human sec
729	37	82.2	467	6	ABM20768	Human sec	802	37	82.2	467	6	ABM16256	Human sec
730	37	82.2	467	6	ABO41899	Human sec	803	37	82.2	467	6	ABM24123	Human sec
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732	37	82.2	467	6	ABM10029	Human sec	805	37	82.2	467	6	ABM04485	Human sec
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734	37	82.2	467	6	ABM32784	Human sec	807	37	82.2	467	6	ABM09114	Human sec
735	37	82.2	467	6	ABM22598	Human sec	808	37	82.2	467	6	ABO39154	Human sec
736	37	82.2	467	6	ABM74809	Human sec	809	37	82.2	467	6	ABM75419	Human sec
737	37	82.2	467	6	ADA79560	Human sec	810	37	82.2	467	6	ABM25343	Human sec
738	37	82.2	467	6	ABR96199	Human sec	811	37	82.2	467	6	ABM19853	Human sec
739	37	82.2	467	6	ABM02350	Human sec	812	37	82.2	467	6	ABO46759	Human PRO
740	37	82.2	467	6	ABR86922	Human sec	813	37	82.2	467	6	ABO47064	Human PRO
741	37	82.2	467	6	ABR86597	Human sec	814	37	82.2	467	6	ABR83085	Human sec
742	37	82.2	467	6	ABM16561	Human sec	815	37	82.2	467	6	ABR71495	Human sec
743	37	82.2	467	6	ABM29613	Human sec	816	37	82.2	467	6	ABR72105	Human sec
744	37	82.2	467	6	ABO29037	Human sec	817	37	82.2	467	6	ABR98444	Human sec
745	37	82.2	467	6	ABM23818	Human sec	818	37	82.2	467	6	ABO06814	Human sec
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748	37	82.2	467	6	ABO37629	Human sec	821	37	82.2	467	6	ABR76419	Human sec
749	37	82.2	467	6	ABM28393	Human sec	822	37	82.2	467	6	ABR73020	Human sec
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751	37	82.2	467	6	ABM66342	Human sec	824	37	82.2	467	6	ABO20545	Human sec
752	37	82.2	467	6	ABM75724	Human sec	825	37	82.2	467	6	ABO25288	Human PRO
753	37	82.2	467	6	ABM34004	Human sec	826	37	82.2	467	6	ABO25593	Human PRO
754	37	82.2	467	6	ABM34309	Human sec	827	37	82.2	467	6	ABR94002	Human sec

828	37	82.2	467	6	ABR79909	Human sec	901	37	82.2	467	7	ABO23933	Human sec
829	37	82.2	467	6	ABM11249	Human sec	902	37	82.2	467	7	ABR93697	Human sec
830	37	82.2	467	6	ABO32856	Human PRO	903	37	82.2	467	7	ABM01740	Human sec
831	37	82.2	467	6	ABO30562	Human sec	904	37	82.2	467	7	ABM78163	Human sec
832	37	82.2	467	6	ABO30867	Human sec	905	37	82.2	467	7	ABR89952	Human sec
833	37	82.2	467	6	ABM27173	Human sec	906	37	82.2	467	7	ABM27478	Human sec
834	37	82.2	467	6	ABM29918	Human sec	907	37	82.2	467	7	ABM13079	Human sec
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837	37	82.2	467	6	ABM08504	Human sec	910	37	82.2	467	7	ABM08199	Human sec
838	37	82.2	467	6	ABO42204	Human sec	911	37	82.2	467	7	ABO40069	Human sec
839	37	82.2	467	6	ABO37934	Human sec	912	37	82.2	467	7	ABM74504	Human sec
840	37	82.2	467	6	ABO45844	Human PRO	913	37	82.2	467	7	ABM33699	Human sec
841	37	82.2	467	6	ABM66647	Human sec	914	37	82.2	467	7	ABM20158	Human sec
842	37	82.2	467	6	ADB20128	Human sec	915	37	82.2	467	7	ABO48650	Human sec
843	37	82.2	467	6	ABM19548	Human sec	916	37	82.2	467	7	ABR72715	Human sec
844	37	82.2	467	6	ABO49260	Human sec	917	37	82.2	467	7	ABO15357	Human sec
845	37	82.2	467	6	ABO49565	Human sec	918	37	82.2	467	7	ABR85072	Human sec
846	37	82.2	467	6	ADA78380	Human sec	919	37	82.2	467	7	ABO15052	Human sec
847	37	82.2	467	6	ABR88122	Human sec	920	37	82.2	467	7	ABO17187	Human sec
848	37	82.2	467	6	ABM26868	Human sec	921	37	82.2	467	7	ABM17476	Human sec
849	37	82.2	467	6	ABM03265	Human sec	922	37	82.2	467	7	ABR85377	Human sec
850	37	82.2	467	6	ABO39764	Human sec	923	37	82.2	467	7	ABO17589	Human PRO
851	37	82.2	467	7	ABO49870	Human sec	924	37	82.2	467	7	ABM76943	Human sec
852	37	82.2	467	7	ABO50785	Human sec	925	37	82.2	467	7	ABO28122	Human sec
853	37	82.2	467	7	ABO05241	Human sec	926	37	82.2	467	7	ABM22903	Human sec
854	37	82.2	467	7	ABR74545	Human sec	927	37	82.2	467	7	ABM30223	Human sec
855	37	82.2	467	7	ABR77024	Human sec	928	37	82.2	467	7	ABM21683	Human sec
856	37	82.2	467	7	ADA16655	Human sec	929	37	82.2	467	7	ABM21378	Human sec
857	37	82.2	467	7	ABM17781	Human sec	930	37	82.2	467	7	ABM14909	Human sec
858	37	82.2	467	7	ABR95832	Human sec	931	37	82.2	467	7	ABO40984	Human sec
859	37	82.2	467	7	ADA13084	Human sec	932	37	82.2	467	7	ABO36714	Human sec
860	37	82.2	467	7	ABO21765	Human sec	933	37	82.2	467	7	ABO37324	Human sec
861	37	82.2	467	7	ABO19935	Human sec	934	37	82.2	467	7	ABM75114	Human sec
862	37	82.2	467	7	ABO24238	Human sec	935	37	82.2	467	7	ABM33394	Human sec
863	37	82.2	467	7	ABR85987	Human sec	936	37	82.2	467	7	ABO46149	Human PRO
864	37	82.2	467	7	ABM10639	Human sec	937	37	82.2	467	7	ADA82451	Human sec
865	37	82.2	467	7	ABM76638	Human sec	938	37	82.2	467	7	ABM311748	Human sec
866	37	82.2	467	7	ABR89342	Human sec	939	37	82.2	467	7	ABM31138	Human sec
867	37	82.2	467	7	ABM12469	Human sec	940	37	82.2	467	7	ADB77721	Human sec
868	37	82.2	467	7	ABM05759	Human PRO	941	37	82.2	467	7	ADB74857	Human sec
869	37	82.2	467	7	ABO34884	Human sec	942	37	82.2	467	7	ADB85759	Human sec
870	37	82.2	467	7	ABM02960	Human sec	943	37	82.2	467	7	ABM32053	Human sec
871	37	82.2	467	7	ABM18938	Human sec	944	37	82.2	467	7	ABM32358	Human sec
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873	37	82.2	467	7	ABO46454	Human PRO	946	37	82.2	467	7	ABM30833	Human sec
874	37	82.2	467	7	ABO48955	Human sec	947	37	82.2	467	7	ADC28503	Human sec
875	37	82.2	467	7	ADA11952	Human sec	948	37	82.2	467	7	ADC39703	Human sec
876	37	82.2	467	7	ABR68998	Human sec	949	37	82.2	467	7	ADC40217	Human sec
877	37	82.2	467	7	ABR89037	Human sec	950	37	82.2	467	7	ADC19041	Human sec
878	37	82.2	467	7	ABR72410	Human sec	951	37	82.2	467	7	ADC34341	Human sec
879	37	82.2	467	7	ABR74240	Human sec	952	37	82.2	467	7	ADC29396	Human sec
880	37	82.2	467	7	ABO18508	Human sec	953	37	82.2	467	7	ADC28927	Human sec
881	37	82.2	467	7	ADA17299	Human sec	954	37	82.2	467	7	ADC40812	Human sec
882	37	82.2	467	7	ABR80214	Human sec	955	37	82.2	467	7	ADC19469	Human sec
883	37	82.2	467	7	ABM01435	Human sec	956	37	82.2	467	7	ADC33917	Human sec
884	37	82.2	467	7	ABM02045	Human sec	957	37	82.2	467	7	ADC12987	Human sec
885	37	82.2	467	7	ABR87207	Human sec	958	37	82.2	467	7	ADC12439	Human sec
886	37	82.2	467	7	ABM12774	Human sec	959	37	82.2	467	7	ADD05489	Human sec
887	37	82.2	467	7	ABM30528	Human sec	960	37	82.2	467	7	ADD04994	Human sec
888	37	82.2	467	7	ABM24428	Human sec	961	37	82.2	467	7	ADD04000	Human sec
889	37	82.2	467	7	ABO29342	Human sec	962	37	82.2	467	7	ADD03576	Human sec
890	37	82.2	467	7	ABO31172	Human sec	963	37	82.2	467	7	ADG34828	Human sec
891	37	82.2	467	7	ABM14299	Human sec	964	37	82.2	467	7	ADG02484	Novel hum
892	37	82.2	467	7	ABM09724	Human sec	965	37	82.2	467	7	ADG01191	Novel hum
893	37	82.2	467	7	ABO39849	Human sec	966	37	82.2	467	7	ADP95366	Novel hum
894	37	82.2	467	7	ABM34614	Human sec	967	37	82.2	467	7	ADG12181	Novel hum
895	37	82.2	467	7	ABO51090	Human sec	968	37	82.2	467	7	ADH08841	Human PRO
896	37	82.2	467	7	ADA42802	Human sec	969	37	82.2	467	7	ADH59311	Human sec
897	37	82.2	467	7	ABO03916	Human sec	970	37	82.2	467	7	ADJ38090	Human sec
898	37	82.2	467	7	ABO10386	Human PRO	971	37	82.2	467	7	ADJ26358	Human sec
899	37	82.2	467	7	ABR77629	Human sec	972	37	82.2	467	7	ADL32622	Novel hum
900	37	82.2	467	7	ABR78839	Human sec	973	37	82.2	467	7	ADM30156	Novel hum

974 37 82.2 467 8 ADE79273 Human sec  
 975 37 82.2 467 8 ADE79697 Human sec  
 976 37 82.2 467 8 ADE73373 Human sec  
 977 37 82.2 467 8 ADE74153 Human sec  
 978 37 82.2 467 8 ADE73908 Human sec  
 979 37 82.2 467 8 ADE74765 Human sec  
 980 37 82.2 467 8 ADE99462 Human sec  
 981 37 82.2 467 8 ADE98581 Human sec  
 982 37 82.2 467 8 ADE99008 Human sec  
 983 37 82.2 467 8 ADE40478 Human sec  
 984 37 82.2 467 8 ADE73872 Human sec  
 985 37 82.2 467 8 ADE95978 Novel hum  
 986 37 82.2 467 8 ADE73448 Human sec  
 987 37 82.2 467 8 ADE73448 Human sec  
 988 37 82.2 467 8 ADG04249 Novel hum  
 989 37 82.2 467 8 ADG00409 Novel hum  
 990 37 82.2 467 8 ADG82665 Human PRO  
 991 37 82.2 467 8 ADG92291 Human sec  
 992 37 82.2 467 8 ADG92718 Human sec  
 993 37 82.2 467 8 ADH25946 Novel hum  
 994 37 82.2 467 8 ADH32915 Human PRO  
 995 37 82.2 467 8 ADH20507 Human sec  
 996 37 82.2 467 8 ADH07362 Human sec  
 997 37 82.2 467 8 ADH59907 Human sec  
 998 37 82.2 467 8 ADH06935 Human sec  
 999 37 82.2 467 8 ADI18677 Human sec  
 1000 37 82.2 467 8 ADI65397 Human sec  
 ADI37660 Human sec

## ALIGNMENTS

RESULT 1  
 AAR78289  
 ID AAR78289 standard; peptide; 7 AA.  
 AC AAR78289;  
 DT 13-MAR-1996 (first entry)  
 DE Spacer #3 used to construct GnRH immunomimetic.  
 KW Immunomimetic; gonadotropin releasing hormone; GnRH; LHRH; vaccine;  
 KW luteinising hormone releasing hormone; GnRH; immunomimetic; uterine;  
 KW diphtheria toxoid; DT; gynaecological; endometriosis; uterine fibroids;  
 KW gonadal steroid hormone associated dependent disease; gonadotropin;  
 KW immunological contraception; mammal; breast; cancer; prostate;  
 KW benign prostatic hypertrophy.  
 OS Synthetic.  
 OS WO9520600-A1.  
 PN WO9520600-A1.  
 XX 03-AUG-1995.  
 XX 26-JAN-1995; 95WO-US001225.  
 XX 27-JAN-1994; 94US-00188223.  
 XX (APHT-) APHTON CORP.  
 PA Grimes S, Scibienski R;  
 PI WPI; 1995-275410/36.  
 DR New anti-gonadotropin releasing hormone immunogenic composition(s) - used  
 XX for treating gonadotropin and gonadal steroid hormone dependent  
 PT disease(s) and providing contraception.  
 PT Example 1; Page 5; 39pp; English.  
 PS The sequences given in AAR78287-89 represent spacer peptides which were  
 CC used in the contraction of the immunomimetics to gonadotropin releasing

CC hormone (GnRH) of the invention. The mimetic peptides comprise the wild  
 CC type GnRH sequence and a spacer attached to either the N- or C- terminal.  
 CC The spacer molecules serve as a link through which the immunomimetic is  
 CC attached to an immunological carrier such as diphtheria toxoid (DT) and  
 CC also affects the immune response generated by the vaccinated mammal  
 CC against the immunomimetic. Compositions comprising these peptides may be  
 CC used for treating a mammal for gonadotropin and gonadal steroid hormone  
 CC associated dependent disease or for providing immunological contraception  
 CC in mammals. They can also be used for treating breast cancer, uterine and  
 CC other gynaecological cancers, endometriosis, uterine fibroids, prostate  
 CC cancer, or benign prostatic hypertrophy  
 XX Sequence 7 AA;

Query Match 100.0%; Score 45; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 |||||  
 Db 1 SSPPPPC 7

RESULT 2  
 AAR74296  
 ID AAR74296 standard; peptide; 7 AA.  
 XX AAR74296;

DT 10-JAN-1996 (first entry)  
 DE Human gastrin 17 antigenic peptide Ser spacer peptide.  
 KW Human gastrin 17; antigenic peptide; immunisation; treatment;  
 KW gastro-oesophageal reflux disease; gastric; duodenal; ulceration; cancer;  
 KW Ser spacer peptide.  
 OS Synthetic.  
 OS WO9513297-A2.  
 PN 18-MAY-1995.  
 XX 10-NOV-1994; 94WO-US013205.  
 XX 12-NOV-1993; 93US-00151219.  
 XX (APHT-) APHTON CORP.

PI Gevas PC, Grimes S, Karr SL, Michaeli D, Scibienski R;  
 DR WPI; 1995-194034/25.  
 XX Immunogenic compen. for producing anti-human gastrin 17 antibodies - used  
 PT for treating e.g. gastro-oesophageal reflux disease, gastric and duodenal  
 PT ulceration or cancer.  
 XX Claim 7; Page 14; 17pp; English.

CC AAR74295 is the human gastrin 17 (hg17) hg17(1-9)-Ser9 antigenic peptide,  
 CC it comprises a 9 amino acid hg17 immunomimetic followed by the Ser spacer  
 CC peptide AAR74296. The antigenic peptide is used to produce anti-hg17  
 CC antibodies (Abs). The Abs can be induced in a patient, or used for  
 CC passive immunisation, for the treatment of diseases in which hg17 is  
 CC involved, e.g. Gastric and duodenal ulceration; gastro-oesophageal reflux  
 CC disease and cancer  
 XX Sequence 7 AA;

Query Match 100.0%; Score 45; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 DB 1 SSPPPPC 7

RESULT 3  
 AAW95392  
 ID AAW95392 standard; peptide; 7 AA.

AC AAW95392;

DT 17-MAR-1999 (first entry)

DE Spacer sequence used in an immunogenic peptide.

OS Cholecystokinin-B; CCK-B/gastrin-receptor; immunogen; gastrin; tumour;  
 KW colorectal; scintigraphic scanning; gastrointestinal, colorectal;  
 KW stomach; pancreatic; hepatocellular; cancer.

XX Synthetic.

PN WO9851337-A2.

PD 19-NOV-1998.

PF 12-MAY-1998; 98WO-US0009957.

PR 12-MAY-1997; 97US-0046201P.

XX (APHT-) APHTON CORP.

PI Michael D, Caplin M, Watson SA, Grimes S;

DR WPI; 1999-045194/04.

XX Use of a cholecystokinin-gastrin receptor - for producing antibodies for  
 PT the detection and treatment of gastrin-dependent tumours, e.g.  
 PT gastrointestinal cancer.

PS Claim 4; Page 40; 60pp; English.

XX The invention relates to an immunogen comprising a peptide from the  
 CC cholecystokinin (CCK)-B/gastrin-receptor conjugated to an immunogenic  
 CC carrier. The invention provides methods (1) for treating a malignant  
 CC condition caused by gastrin-dependent malignant cell growth that  
 CC comprises administering to an animal an anti-CCK-B/gastrin-receptor  
 CC immunogen; (2) for treating a gastrin-dependent tumour that comprises  
 CC administering to an animal anti-CCK-B/gastrin antibodies which recognise  
 CC and bind to the CCK-B/gastrin-receptors in the tumour cells; (3) for  
 CC detecting a gastrin-responsive tumour containing CCK-B/gastrin-receptors,  
 CC that comprises exposing an anti-gastrin-receptor antibody to cells  
 CC isolated from a tumour biopsy sample and detecting the CCK-B/gastrin-  
 CC receptor in the sample; and (4) a method for diagnosing a gastrin-  
 CC dependent tumour, comprising administering radiolabelled anti-CCK-B/  
 CC gastrin-receptor antibodies to a patient possessing a colorectal tumour  
 CC and imaging the tumour by scintigraphic scanning. The methods can be used  
 CC for the detection and treatment of tumours such as gastrointestinal,  
 CC colorectal, stomach, pancreatic and hepatocellular cancers. The present  
 CC sequence represents a specifically claimed spacer sequence of the  
 CC immunogen. This sequence is used in order to make the immunogens capable  
 CC of inducing specific immune responses

XX Sequence 7 AA;

Query Match 100.0%; Score 45; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 DB 1 SSPPPPC 7

RESULT 4

AA49310

XX AAY49310 standard; peptide; 7 AA.

XX AAY49310;

DT 06-MAR-2000 (first entry)

DE Carboxy terminal spacer peptide.

XX Gastroesophageal reflux disease; GERD; gastrin; anti-gastrin antibody;  
 KW histamine H2; proton pump inhibitor; acid output; stomach; therapy;  
 KW esophagitis; immunogen; human; heptadecagastrin; immunomimic; G17.

OS Synthetic.

PN WO959612-A1.

PD 25-NOV-1999.

PF 14-MAY-1999; 99WO-US010734.

PR 15-MAY-1998; 98US-0085610P.

XX (APHT-) APHTON CORP.

PI Gevas PC, Grimes S, Karr S, Michael D;

DR WPI; 2000-062378/05.

PT Method for treatment of gastroesophageal reflux disease (GERD).

PS Example 5; Page 14; 24pp; English.

XX The invention relates to the treatment of gastroesophageal reflux disease  
 CC (GERD) that comprises administering to a patient an immunogenic  
 CC composition which generates anti-gastrin antibodies, which bind to  
 CC gastrin, in a patient; and administering histamine H2 antagonist or a  
 CC proton pump inhibitor. The method provides a more effective method for  
 CC controlling acid output by the stomach. The therapy is less costly. High  
 CC gastrin levels associated with standard therapies are neutralized and  
 CC undesirable side effects are reduced. The method permits a reduced dosage  
 CC of acid reducing agent both at the acid producing level as well as the  
 CC acid production stimulating level (gastrin). Reduction of dosages is  
 CC desirable for prolonged treatment of GERD. In a combination therapy with  
 CC H2 agonists or proton pump inhibitors, anti-gastrin 17 antibody titers  
 CC can be maintained by occasional booster shots while gastric acid  
 CC inhibitor dosing is reduced. Immunization allows a sufficient time for  
 CC the esophagitis to completely heal and no surgery is required. The  
 CC present sequence represents a carboxy-terminal spacer used along with a  
 CC human heptadecagastrin (G17) immunomimic

XX Sequence 7 AA;

Query Match 100.0%; Score 45; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 DB 1 SSPPPPC 7

RESULT 5

AA451307

XX AAY51307 standard; peptide; 7 AA.

XX AAY51307;

DT 14-APR-2000 (first entry)

DE Human gastrin spacer peptide.

KW Immunogenic; treatment; hypergastrinemia; gastrin G17; gastrin G34;  
 KW pernicious anemia; anti-ulcer; proton pump inhibitor; colorectal disease.

OS Homo sapiens.

PN WO9559631-A1.

XX 25-NOV-1999.

XX 14-MAY-1999; 99WO-US010751.

XX 15-MAY-1998; 98US-0085714P.

XX (APHT-) APHTON CORP.

XX Gevas PC, Grimes S, Karr S, Michaeli D, Watson S;

XX WPI; 2000-116301/10.

XX Treating or preventing hypergastrinemia comprising administration of,  
 PT e.g. anti-gastrin antibodies.

XX Disclosure; Page 11; 44pp; English.

CC This invention describes a novel method for the treatment or preventing  
 CC hypergastrinemia by administering to a patient a gastrin G17 and/or G34  
 CC peptide fragment linked by an amino acid spacer to an immunogenic  
 CC carrier. The methods are used to treat hypergastrinemic patients,  
 CC particularly those with pernicious anemia, those receiving treatment with  
 CC anti-ulcer agents such as proton pump inhibitors (particularly omeprazole  
 CC or lansoprazole) or H<sub>2</sub> receptor blocking agents or antagonists, or those  
 CC having colorectal disorders or diseases. This sequence represents a  
 CC spacer peptide used in the construction of the immunogenic construct  
 CC described in the method of the invention

XX Sequence 7 AA;

Query Match 100.0%; Score 45; DB 3; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7

DB 1 SSPPPPC 7

RESULT 6

AAG66089

ID AAG66089 standard; peptide; 7 AA.

XX AAG66089;

XX 27-FEB-2002 (first entry)

XX Amino acid sequence of spacer Ser 10.

XX GnRH; gonadotropin hormone; gonadal steroid hormone; cytostatic; cancer;  
 KW gonadotropin releasing hormone; endometriosis; prostatic hypertrophy;  
 KW spacer.

XX Synthetic.

XX Key Location/Qualifiers

XX 1..7

XX /note= "spacer"

XX US6303123-B1.

XX 16-OCT-2001.

XX 07-JUN-1995; 95US-00478546.

XX 27-JAN-1994; 94US-00188223.

XX

PA (APHT-) APHTON CORP.

XX Grimes S, Scibienski R;

XX WPI; 2002-048293/06.

XX Administering antibodies or immunogenic compositions against gonadotropin  
 PT releasing hormone is useful to treat gonadotropin hormone-dependent or  
 PT gonadal steroid hormone-dependent disorders such as breast and prostate  
 PT cancer.

XX Example 1; Col 5; 24pp; English.

XX The invention relates to treating a gonadotropin hormone-dependent or  
 CC gonadal steroid hormone-dependent cancer. The method comprises  
 CC administering anti-GnRH antibodies which bind and neutralize Gonadotropin  
 CC Releasing Hormone (GnRH) in vivo. The anti-GnRH immunogenic composition  
 CC comprises a GnRH immunogenic peptide conjugated through the terminal Cys  
 CC of the spacer peptide to an immunogenic carrier, preferably diphtheria or  
 CC tetanus toxoid, with carrier/peptide ratio being in the range of 4.7 to  
 CC 30.1 peptide molecules per carrier molecule. The method is used to treat  
 CC GnRH-dependent cancer, particularly of the breast, uterus or prostate,  
 CC oestrogen-dependent cancer, endometriosis or prostatic hypertrophy. The  
 CC present sequence represents a spacer sequence

XX Sequence 7 AA;

Query Match 100.0%; Score 45; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7

DB 1 SSPPPPC 7

RESULT 7

ABB82193

ID ABB82193 standard; peptide; 7 AA.

XX ABB82193;

XX 23-DEC-2002 (first entry)

XX Synthetic peptide spacer.

XX Gastrin; immunogenic; chemotherapeutic; cancer; cytostatic; pancreatic;

XX CCK-B; chemokine; spacer.

XX Synthetic.

XX WO200276499-A2.

XX 03-OCT-2002.

XX 22-MAR-2002; 2002WO-US008756.

XX 23-MAR-2001; 2001US-0278294P.

XX (APHT-) APHTON CORP.

XX Michaeli D, Caplin M, Gevas PC, Grimes S;

XX WPI; 2002-713604/77.

XX Combination useful in the treatment of pancreatic cancer or in the  
 PT prevention of cancer cell metastasis, comprises an anti-gastrin effective  
 PT immunogenic composition, and at least one chemotherapeutic agent.

XX Disclosure; Page 12; 42pp; English.

XX The invention relates to a combination treatment for pancreatic cancer.

CC The combination comprises: (a) either an anti-gastrin effective  
 CC immunogenic composition (A) or an anti-gastrin and/or anti-gastrin  
 CC receptor effective immunological agent; and (b) at least one  
 CC chemotherapeutic agent for inhibiting cancer growth. The immunological  
 CC agent is a monoclonal or polyclonal antibody derived from antisera  
 CC produced in patients by immunization with (A). The combination is used  
 CC for the treatment of pancreatic cancer or in the prevention of cancer  
 CC cell metastasis. The present sequence represents a synthetic peptide  
 CC spacer  
 CC XX  
 CC SQ Sequence 7 AA;

Query Match 100.0%; Score 45; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 DB 1 SSPPPPC 7  
 |||||

RESULT 8  
 ADP42661  
 ID ADF42661 standard; peptide; 7 AA.  
 XX  
 AC ADF42661;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Spacer peptide SEQ ID NO:39.  
 XX  
 KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;  
 KW vaccine; asthma; allergy; allergic disease; human; spacer.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FN WO2003082349-A1.  
 XX  
 PD 09-OCT-2003.  
 XX  
 PF 24-MAR-2003; 2003WO-US008970.  
 XX  
 XX 25-MAR-2002; 2002US-0367591P.  
 PR  
 PA (MERC-) MERCIA PHARMA LLC.  
 PI Drivas DT;  
 XX  
 DR WPI; 2003-803977/75.  
 XX  
 PT Treating a subject for a condition mediated by eotaxin, e.g. asthma,  
 PT allergy or allergic disease by generating an active immune response in  
 PT the subject to eotaxin.  
 XX  
 PS Disclosure; SEQ ID NO 39; 40pp; English.  
 XX  
 CC The present invention describes a method for treating a subject for a  
 CC condition mediated by eotaxin comprising generating an active immune  
 CC response in the subject to eotaxin. Also described: (1) an immunogenic  
 CC composition (C) comprising eotaxin or its peptide fragment coupled to an  
 CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical  
 CC formulation for use as a vaccine comprising (C) and an adjuvant and a  
 CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be  
 CC used in vaccines. The method is useful for treating a subject for a  
 CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.  
 CC The present sequence represents a spacer peptide, which is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 45; DB 7; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 DB 1 SSPPPPC 7  
 |||||

RESULT 9  
 ADH89215  
 ID ADH89215 standard; peptide; 7 AA.  
 XX  
 AC ADH89215;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Spacer peptide, SEQ ID 10.  
 XX  
 KW Cytotoxic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;  
 KW gastrin G-34; gonadotropin releasing hormone; GnRH;  
 KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;  
 KW thyroid cancer; lung cancer; reproductive system cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004004687-A2.  
 XX  
 PD 15-JAN-2004.  
 XX  
 PF 03-JUL-2003; 2003WO-US021176.  
 XX  
 PR 03-JUL-2002; 2002US-0394179P.  
 XX  
 PA (APHT-) APHTON CORP.  
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 XX  
 PI Michaeli D, Grimes S, Barenholz Y, Even-Chen S;  
 XX  
 DR WPI; 2004-099340/10.  
 XX  
 PT Injectable liposomal composition for delivery of a water-soluble  
 PT substance e.g. vaccine for preventing pregnancy, comprises several  
 PT liposomal vesicles comprising a high weight ratio of lipid to  
 PT encapsulated water-soluble substance.  
 XX  
 PS Claim 28; SEQ ID NO 10; 73pp; English.  
 XX  
 CC The present invention relates to injectable liposomal compositions (I)  
 CC for delivery of a water-soluble substance e.g. immunomimic peptides. (I)  
 CC comprises several liposomal vesicles comprising a high weight ratio of a  
 CC lipid to an encapsulated water-soluble substance so as to achieve a high  
 CC efficiency of encapsulation. The immunomimic peptide is chosen from  
 CC gastrin G-17 (ADH89206 to ADH89213 and ADH89223), gastrin G-34 (ADH89217-  
 CC ADH89219), gonadotropin releasing hormone (GnRH) peptide (ADH89220 and  
 CC ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-  
 CC ADH89222 and ADH89225). (I) comprising vaccines directed against hormone  
 CC or hormone cognate receptors, where the vaccine comprises at least one:  
 CC hormone-immunomimic peptide such as gastrin G-17 or G-34 is useful for  
 CC treating gastrointestinal malignancy, and non-gastrointestinal tumors  
 CC such as thyroid and lung cancer; or GnRH or hCG immunomimic peptide is  
 CC useful as contraceptive and for treating cancers in male and female  
 CC reproductive systems. The present sequence is a spacer peptide.  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 45; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 DB 1 SSPPPPC 7  
 |||||

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RESULT 10
ADSI18216
ID ADSI18216 standard; peptide; 7 AA.
XX
XX ADSI18216;
XX
DT 30-DEC-2004 (first entry)
XX
DE Novel inflammatory condition treatment-related spacer peptide SeqID39.
XX
KW inflammatory condition; eosinophil accumulation; immune response;
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;
KW allergic disease; spacer peptide.
XX
OS Unidentified.
OS Synthetic.
XX
PN WO2004084837-A2.
XX
PD 07-OCT-2004.
XX
XX 24-MAR-2004; 2004WO-US008901.
XX
PF 24-MAR-2003; 2003US-0457137P.
XX
PA (MERC-) MERCIA PHARMA LLC.
XX
PI Drivas DT, Blackburn P;
XX
XX WPI; 2004-710267/69.
XX
XX Treating inflammatory conditions resulting from eosinophil accumulation
XX (e.g. asthma, allergy or allergic disease) comprises generating an active
XX immune response against eotaxin and interleukin-5.
XX
XX Example 1; SEQ ID NO 39; 55pp; English.
XX
XX This invention relates to a novel method of treating a subject for an
XX inflammatory condition which results from eosinophil accumulation which
XX comprises generating an active immune response in the patient comprising
XX autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-
XX 13). The invention may be useful for the development of compounds with an
XX antiinflammatory, antiasthmatic or antiallergic activity or for the
XX production of a vaccine. The composition and methods are useful for
XX preventing or treating inflammatory conditions resulting from eosinophil
XX accumulation, such as asthma, allergy or allergic diseases. The present
XX sequence is that of a spacer peptide which may be used within the method
XX of the invention.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 45; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSPPPPC 7
Db 1 SSSPPPPC 7
|||||

RESULT 11
ADH89218
ID ADH89218 standard; peptide; 13 AA.
XX
XX ADH89218;
XX
XX 06-MAY-2004 (first entry)
XX
DT Gastrin G-34 peptide fragment, SEQ ID 13.
XX
DE Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;
XX gastrin G-34; gonadotropin releasing hormone; GnRH;
KW
XX

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KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;
KW thyroid cancer; lung cancer; reproductive system cancer.
XX
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Pyroglutamic acid"
XX
XX WO2004004687-A2.
XX
PD 15-JAN-2004.
XX
PF 03-JUL-2003; 2003WO-US021176.
XX
XX 03-JUL-2002; 2002US-0394179P.
XX
XX (APHT-) APHTON CORP.
XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
XX Michaeli D, Grimes S, Barenholz Y, Even-Chen S;
XX
XX WPI; 2004-099340/10.
XX
XX Injectable liposomal composition for delivery of a water-soluble
XX substance e.g. vaccine for preventing pregnancy, comprises several
XX liposomal vesicles comprising a high weight ratio of lipid to
XX encapsulated water-soluble substance.
XX
XX Disclosure; SEQ ID NO 13; 73pp; English.
XX
XX The present invention relates to injectable liposomal compositions (I)
XX for delivery of a water-soluble substance e.g. immunomimic peptides. (I)
XX comprises several liposomal vesicles comprising a high weight ratio of a
XX lipid to an encapsulated water-soluble substance so as to achieve a high
XX efficiency of encapsulation. The immunomimic peptide is chosen from
XX gastrin G-17 (ADH89206 to ADH89213 and ADH89223), gastrin G-34 (ADH89217-
XX ADH89219), gonadotropin releasing hormone (GnRH) peptide (ADH89220 and
XX ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-
XX ADH89222 and ADH89225). (I) comprising vaccines directed against hormone
XX or hormone cognate receptors, where the vaccine comprises at least one:
XX hormone-immunomimic peptide such as gastrin G-17 or G-34 is useful for
XX treating gastrointestinal malignancy, and non-gastrointestinal tumors
XX such as thyroid and lung cancer; or GnRH or hCG immunomimic peptide is
XX useful as contraceptive and for treating cancers in male and female
XX reproductive systems. The present sequence comprises residues 1-6 of G-34
XX linked to a spacer peptide at the C-terminal end.
XX
SQ Sequence 13 AA;
Query Match 100.0%; Score 45; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSPPPPC 7
Db 7 SSSPPPPC 13
|||||

RESULT 12
AAR74295
ID AAR74295 standard; peptide; 16 AA.
XX
XX AAR74295;
XX
XX 10-JAN-1996 (first entry)
XX
DT Human gastrin 17 antigenic peptide hG17(1-9)-Ser9.
XX
DE Human gastrin 17; antigenic peptide hG17(1-9)-Ser9; immunisation;
XX treatment; gastro-oesophageal reflux disease; gastric; duodenal;
XX ulceration; cancer.
XX

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OS Synthetic.  
 XX PN WO9513297-A2.  
 XX PD 18-MAY-1995.  
 XX PP 10-NOV-1994; 94WO-US013205.  
 XX PR 12-NOV-1993; 93US-00151219.  
 XX PA (APHT-) APHTON CORP.  
 XX PI Gevas PC, Grimes S, Karr SL, Michaeli D, Scibienski R;  
 XX PF WPI; 1995-194034/25.  
 XX DR Immunogenic compsn. for producing anti-human gastrin 17 antibodies - used  
 XX PT for treating e.g. gastro-oesophageal reflux disease, gastric and duodenal  
 XX PT ulceration or cancer.  
 XX PS Claim 1; Page 14; 17pp; English.  
 XX CC AAR74295 and AAR74297 are human gastrin 17 (hg17) antigenic peptides,  
 CC used to produce anti-hg17 antibodies (Abs). The Abs can be induced in a  
 CC patient, or used for passive immunisation, for the treatment of diseases  
 CC in which hg17 is involved, e.g. gastric and duodenal ulceration; gastro-  
 CC oesophageal reflux disease and cancer  
 XX SQ Sequence 16 AA;  
 Query Match 100.0%; Score 45; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SSPPPPC 7  
 DB 10 SSPPPPC 16  
 RESULT 13  
 AAY49309  
 ID AAY49309 standard; peptide; 16 AA.  
 XX AC AAY49309;  
 XX DT 06-MAR-2000 (first entry)  
 XX DE Human heptadecagastrin (G17) immunomimic with carboxy terminal spacer.  
 XX KW Gastroesophageal reflux disease; GERD; gastrin; anti-gastrin antibody;  
 KW histamine H2; proton pump inhibitor; acid output; stomach; therapy;  
 KW esophagitis; immunogen; human; heptadecagastrin; immunomimic; G17.  
 XX OS Synthetic.  
 OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Modified-site 1 /label= pGlu  
 FT /note= "pyroglutamate"  
 FT Peptide 10..16  
 FT /note= "carboxy-terminal spacer"  
 XX PN WO9959612-A1.  
 XX PD 25-NOV-1999.  
 XX PF 14-MAY-1999; 99WO-US010734.  
 XX PR 15-MAY-1998; 98US-0085610P.  
 XX PA (APHT-) APHTON CORP.

PI Gevas PC, Grimes S, Karr S, Michaeli D;  
 XX WPI; 2000-062378/05.  
 XX DR Method for treatment of gastroesophageal reflux disease (GERD).  
 XX PS Example 5; Page 13; 24pp; English.  
 XX CC The invention relates to the treatment of gastroesophageal reflux disease  
 CC (GERD) that comprises administering to a patient an immunogenic  
 CC composition which generates anti-gastrin antibodies, which bind to  
 CC gastrin, in a patient; and administering histamine H2 antagonist or a  
 CC proton pump inhibitor. The method provides a more effective method for  
 CC controlling acid output by the stomach. The therapy is less costly. High  
 CC gastrin levels associated with standard therapies are neutralized and  
 CC undesirable side effects are reduced. The method permits a reduced dosage  
 CC of acid reducing agent both at the acid producing level as well as the  
 CC acid production stimulating level (gastrin). Reduction of dosages is  
 CC desirable for prolonged treatment of GERD. In a combination therapy with  
 CC H2 agonists or proton pump inhibitors, anti-gastrin 17 antibody titers  
 CC can be maintained by occasional booster shots while gastric acid  
 CC inhibitor dosing is reduced. Immunization allows a sufficient time for  
 CC the esophagitis to completely heal and no surgery is required. The  
 CC present sequence represents a human heptadecagastrin (G17) immunomimic  
 CC followed by a carboxy-terminal spacer  
 XX SQ Sequence 16 AA;  
 Query Match 100.0%; Score 45; DB 3; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SSPPPPC 7  
 DB 10 SSPPPPC 16  
 RESULT 14  
 ABP73035  
 ID ABP73035 standard; peptide; 16 AA.  
 XX AC ABP73035;  
 XX DT 03-JUN-2003 (first entry)  
 XX DE Peptide specific for the induction of immune response to G17.  
 XX KW Cancer; lung; oesophagus; liver; immunogen; hormone; gastrin 17; G17;  
 KW gastrin receptor; cholecystokinin-B; CCK-B; Barrett's condition;  
 XX KW gastrin-induced tumour; immune response.  
 XX OS Synthetic.  
 OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "pyroglutamic acid"  
 FT Peptide 10..16  
 FT /note= "spacer"  
 XX PN WO2003005955-A2.  
 XX PD 23-JAN-2003.  
 XX PF 09-JUL-2002; 2002WO-US021768.  
 XX PR 09-JUL-2001; 2001US-0303868P.  
 XX PA (APHT-) APHTON CORP.  
 XX PI Gevas PC, Michaeli D, Grimes S;  
 XX WPI; 2003-229433/22.

XX Treating cancerous or pre-cancerous conditions of the lung, esophagus or  
 PT liver, by administering an immunogen which induces antibodies in the  
 PT patient against G17 and/or cholecystokinin-B/gastrin receptors.  
 XX Example 1; Page 7; 27pp; English.  
 XX  
 CC The specification describes a method of treating a cancerous or pre-  
 CC cancerous condition of the lung, esophagus or liver. The method involves  
 CC administering to a patient an immunogen which induces antibodies in the  
 CC patient against peptide hormone gastrin 17 (G17) and/or a gastrin  
 CC receptor, e.g. cholecystokinin (CCK)-B. The method is useful for treating  
 CC cancerous or pre-cancerous condition of lung, esophagus or liver, where  
 CC the condition is cancer, or Barrett's condition. The treatment prevents  
 CC or delays progression of the Barrett's esophagus to a cancerous state.  
 CC The method is also useful for treating the growth of a gastrin-induced  
 CC tumour or pre-cancerous lesion of the lung, liver or esophagus. ASP73032  
 CC -35 represent peptides which induce specific immune responses to G17. The  
 CC peptides comprise an amino terminal fragment of G17 and a carboxy-  
 CC terminal spacer  
 XX  
 SQ Sequence 16 AA;

Query Match 100.0%; Score 45; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 |||||  
 Db 10 SSPPPPC 16

RESULT 15  
 AAR78283  
 ID AAR78283 standard; peptide; 17 AA.  
 XX  
 AC AAR78283;  
 XX  
 DT 13-MAR-1996 (first entry)  
 XX  
 DE GnRH immunomimetic and spacer (GnRH(1-10)-Ser10).  
 XX  
 KW Immunomimetic; gonadotropin releasing hormone; GnRH; LHRH; vaccine;  
 KW luteinising hormone releasing hormone; GnRH; immunomimetic; uterine;  
 KW diphtheria toxoid; DT; gynaecological; endometriosis; uterine fibroids;  
 KW gonadal steroid hormone associated dependent disease; gonadotropin;  
 KW immunological contraception; mammal; breast; cancer; prostate;  
 KW benign prostatic hypertrophy.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..10  
 FT Modified-site 1 /note= "GnRH"  
 FT /label= OTHER  
 FT /note= "pyroglutamic acid"  
 FT 11..17  
 FT /note= "spacer"  
 XX  
 PN WO9520600-A1.  
 XX  
 PD 03-AUG-1995.  
 XX  
 PF 26-JAN-1995; 95WO-US001225.  
 XX  
 PR 27-JAN-1994; 94US-00188223.  
 XX  
 PA (APHT-) APHTON CORP.  
 XX  
 PI Grimes S, Scibienski R;

XX WPI; 1995-275410/36.  
 XX  
 PT New anti-gonadotropin releasing hormone immunogenic composition(s) - used  
 PT for treating gonadotropin and gonadal steroid hormone dependent  
 PT disease(s) and providing contraception.  
 XX  
 PS Claim 1; Page 29; 39pp; English.  
 XX

CC The sequences given in AAR78282-85 represent immunomimetics to  
 CC gonadotropin releasing hormone (GnRH). These peptides comprise the wild  
 CC type GnRH sequence and a spacer attached to either the N- or C-terminal.  
 CC The spacer molecules serve as a link through which the immunomimetic is  
 CC attached to an immunological carrier such as diphtheria toxoid (DT) and  
 CC also affects the immune response generated by the vaccinated mammal  
 CC against the immunomimetic. Compositions comprising these peptides may be  
 CC used for treating a mammal for gonadotropin and gonadal steroid hormone  
 CC associated dependent disease or for providing immunological contraception  
 CC in mammals. They can also be used for treating breast cancer, uterine and  
 CC other gynaecological cancers, endometriosis, uterine fibroids, prostate  
 CC cancer, or benign prostatic hypertrophy  
 XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 45; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 |||||  
 Db 11 SSPPPPC 17

RESULT 16  
 AAY58140  
 ID AAY58140 standard; peptide; 17 AA.  
 XX  
 AC AAY58140;  
 XX  
 DT 07-MAR-2000 (first entry)  
 XX  
 DE Gonadotropin releasing hormone (GnRH) peptide analogue 4.  
 XX  
 KW Gonadotropin releasing hormone; GnRH; leukotoxin; LKT; fusion protein;  
 KW antibody; immunogenic; chimeric; vaccine; testosterone; androgenic;  
 KW non-androgenic; steroid; reduction; weight gain; muscle distribution;  
 KW fat distribution; male pattern; boar taint; flavour; impairment;  
 KW reliable; immunocastration; meat production.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "Pyroglutamic acid"  
 FT  
 PN WO9956771-A2.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PF 05-MAY-1999; 99WO-CA000360.  
 XX  
 PR 05-MAY-1998; 98US-0084217P.  
 XX  
 PA (BIOS-) BIOSTAR INC.  
 XX  
 PI Manns JG, Acres SD, Harland R;  
 XX  
 DR WPI; 2000-062125/05.  
 XX  
 PT Production of uncastrated male food animals using vaccines.  
 XX  
 PS Disclosure; Page 11; 87pp; English.

CC Sequences AAY58136-Y58141 represent gonadotropin releasing hormone (GnRH) analogues which may be used as an alternative to sequence AAY58135 in embodiments of the present invention. The invention relates to a method of using two GnRH immunogen vaccines to produce uncastrated male animals for meat production, one vaccination prior to or during the fattening period to reduce circulating testosterone levels, and the second vaccination about 2-8 weeks before slaughter to substantially reduce androgenic and/or non-androgenic steroids. The invention is used to produce food animals that exhibit the weight gain and muscle/fat distribution of male animals without the problems associated with male animals. Such problems include "boar taint", a urine-like odour found in cooked meat of uncastrated pigs which is caused by steroids stored in the tissues, and similar flavour impairments in the meat of other intact male animals. The invention is more reliable than prior art immunocastration techniques

SQ Sequence 17 AA;  
 Query Match 100.0%; Score 45; DB 3; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 DB 11 SSPPPPC 17

RESULT 17  
 ID AAB99519  
 ID AAB99519 standard; peptide; 17 AA.  
 AC AAB99519;  
 DT 31-AUG-2001 (first entry)  
 XX Immunomimic peptide C-17 SEQ ID NO:1.

XX Immunomimic; immunisation; immune response; immunogen; antibody.

XX Synthetic.

PH Key Location/Qualifiers  
 FT Modified-site 1 /note= "pyroglutamic acid"

FT WO200134192-A2.

PN 17-MAY-2001.

PD 08-NOV-2000; 2000WO-US030778.

PF 08-NOV-1999; 99US-0164054P.

PR (APHT-) APHTON CORP.

PA Gevas PC, Michaeli D, Grimes S;

PI WPI; 2001-367453/38.

XX Improved method for immunization gives increased antibody titers and reduced irritation by using separate administration of a sustained-release immunogen and adjuvant.

XX Disclosure; Page 9; 20pp; English.

XX The present invention describes a method for immunisation comprising separate administration of an immunogenic sustained-release composition and an immune response enhancing composition. Also described are: (i) an immunisation kit for increasing the immune response to a vaccine target comprising separate sustained release preparations of an immunogenic composition and an immune response stimulating composition; and (ii) an improved composition for parenteral immunisation comprising separately a sustained-release immunogenic composition and an immune response

CC enhancing composition. The method is useful for improving the immune response to an immunogen by eliciting a significant anti-immunogen antibody titre increase. The method is effective in enhancing a high antibody titre allowing a reduction in the amount of the immunomimicking portion of the immunogen and may reduce local irritation at the site of inoculation. The separate administration allows the relative doses to be adjusted to produce the optimum response. The present sequence represents an immunomimic which is given in the exemplification of the present invention

XX Sequence 17 AA;

Query Match 100.0%; Score 45; DB 4; Length 17;

Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 DB 11 SSPPPPC 17

RESULT 18  
 AAG66085  
 ID AAG66085 standard; peptide; 17 AA.

AC AAG66085;

XX 27-FEB-2002 (first entry)

XX GnRH immunogen peptide GnRH(1-10)-Ser10.

XX GnRH; gonadotropin hormone; gonadal steroid hormone; cytostatic; cancer; gonadotropin releasing hormone; endometriosis; prostatic hypertrophy; immunogen.

XX Synthetic.

PH Key Location/Qualifiers  
 FT Region 1..10 /note= "immunomimic"

FT Modified-site 1 /label= pGlu  
 FT Region 11..17 /note= "pyroglutamic acid"

FT US6303123-B1.

PN 16-OCT-2001.

PD 07-JUN-1995; 95US-00478546.

PF 27-JAN-1994; 94US-00188223.

PR (APHT-) APHTON CORP.

PA Grimes S, Scibienski R;

PI WPI; 2002-048293/06.

XX Administering antibodies or immunogenic compositions against gonadotropin releasing hormone is useful to treat gonadotropin hormone-dependent or gonadal steroid hormone-dependent disorders such as breast and prostate cancer.

XX Claim 2; Col 25; 24pp; English.

XX The invention relates to treating a gonadotropin hormone-dependent or gonadal steroid hormone-dependent cancer. The method comprises administering anti-GnRH antibodies which bind and neutralize Gonadotropin Releasing Hormone (GnRH) in vivo. The anti-GnRH immunogenic composition comprises a GnRH immunogenic peptide conjugated through the terminal Cys of the spacer peptide to an immunogenic carrier, preferably diphtheria or

CC tetanus toxoid, with carrier/peptide ratio being in the range of 4.7 to  
 CC 30.1 peptide molecules per carrier molecule. The method is used to treat  
 CC GnRH-dependent cancer, particularly of the breast, uterus or prostate,  
 CC oestrogen-dependent cancer, endometriosis or prostatic hypertrophy. The  
 CC present sequence represents a GnRH immunogen peptide sequence  
 XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 45; DB 5; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 |||||  
 Db 11 SSPPPPC 17

RESULT 19

ADP42680  
 ID ADF42680 standard; peptide; 17 AA.

XX AC ADF42680;

XX DT 12-FEB-2004 (first entry)

XX DE Botaxin epitope and spacer peptide SEQ ID NO:58.

XX KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;  
 XX KW vaccine; asthma; allergy; allergic disease; human; spacer; epitope.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO2003082349-A1.

XX PD 09-OCT-2003.

XX PF 24-MAR-2003; 2003WO-US008970.

XX PR 25-MAR-2002; 2002US-0367591P.

XX PA (MERC-) MERCIA PHARMA LLC.

XX PI Drivas DT;

XX PS WPI; 2003-803977/75.

XX PT Treating a subject for a condition mediated by eotaxin, e.g. asthma, in  
 XX PT allergy or allergic disease by generating an active immune response in  
 XX PT the subject to eotaxin.

XX PS Claim 14; SEQ ID NO 58; 40pp; English.

XX CC The present invention describes a method for treating a subject for a  
 XX CC condition mediated by eotaxin comprising generating an active immune  
 XX CC response in the subject to eotaxin. Also described: (1) an immunogenic  
 XX CC composition (C) comprising eotaxin or its peptide fragment coupled to an  
 XX CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical  
 XX CC formulation for use as a vaccine comprising (C) and an adjuvant and a  
 XX CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be  
 XX CC used in vaccines. The method is useful for treating a subject for a  
 XX CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.  
 XX CC The present sequence represents a human eotaxin epitope and spacer amino  
 XX CC acid sequence, which is used in the exemplification of the present  
 XX CC invention.

SQ Sequence 17 AA;

Query Match 100.0%; Score 45; DB 7; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7

Db |||||  
 11 SSPPPPC 17

RESULT 20

ADP42674  
 ID ADF42674 standard; peptide; 17 AA.

XX AC ADF42674;

XX DT 12-FEB-2004 (first entry)

XX DE Botaxin epitope and spacer peptide SEQ ID NO:52.

XX KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;  
 XX KW vaccine; asthma; allergy; allergic disease; human; spacer; epitope.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO2003082349-A1.

XX PD 09-OCT-2003.

XX PF 24-MAR-2003; 2003WO-US008970.

XX PR 25-MAR-2002; 2002US-0367591P.

XX PA (MERC-) MERCIA PHARMA LLC.

XX PI Drivas DT;

XX PS WPI; 2003-803977/75.

XX PT Treating a subject for a condition mediated by eotaxin, e.g. asthma,  
 XX PT allergy or allergic disease by generating an active immune response in  
 XX PT the subject to eotaxin.

XX PS Claim 14; SEQ ID NO 52; 40pp; English.

XX CC The present invention describes a method for treating a subject for a  
 XX CC condition mediated by eotaxin comprising generating an active immune  
 XX CC response in the subject to eotaxin. Also described: (1) an immunogenic  
 XX CC composition (C) comprising eotaxin or its peptide fragment coupled to an  
 XX CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical  
 XX CC formulation for use as a vaccine comprising (C) and an adjuvant and a  
 XX CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be  
 XX CC used in vaccines. The method is useful for treating a subject for a  
 XX CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.  
 XX CC The present sequence represents a human eotaxin epitope and spacer amino  
 XX CC acid sequence, which is used in the exemplification of the present  
 XX CC invention.

SQ Sequence 17 AA;

Query Match 100.0%; Score 45; DB 7; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7

Db |||||  
 11 SSPPPPC 17

RESULT 21

ADP42672  
 ID ADF42672 standard; peptide; 17 AA.

XX AC ADF42672;

XX DT 12-FEB-2004 (first entry)

XX DE Botaxin epitope and spacer peptide SEQ ID NO:50.

XX eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;  
KW vaccine; asthma; allergy; allergic disease; human; spacer; epitope.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX WO2003082349-A1.  
FN  
PD 09-OCT-2003.  
XX  
XX 24-MAR-2003; 2003WO-US008970.  
XX  
XX 25-MAR-2002; 2002US-0367591P.  
PR  
XX (MERC-) MERCIA PHARMA LLC.  
XX  
XX Drivas DT;  
XX WPI; 2003-803977/75.  
XX  
XX Treating a subject for a condition mediated by eotaxin, e.g. asthma,  
PT allergy or allergic disease by generating an active immune response in  
PT the subject to eotaxin.  
XX  
XX Claim 14; SEQ ID NO 50; 40pp; English.  
XX  
XX The present invention describes a method for treating a subject for a  
CC condition mediated by eotaxin comprising generating an active immune  
CC response in the subject to eotaxin. Also described: (1) an immunogenic  
CC composition (C) comprising eotaxin or its peptide fragment coupled to an  
CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical  
CC formulation for use as a vaccine comprising (C) and an adjuvant and a  
CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be  
CC used in vaccines. The method is useful for treating a subject for a  
CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.  
CC The present sequence represents a human eotaxin epitope and spacer amino  
CC acid sequence, which is used in the exemplification of the present  
CC invention.  
XX  
XX Sequence 17 AA;  
SQ  
Query Match 100.0%; Score 45; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. NO. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSPPPPC 7  
Db |||||  
11 SSPPPPC 17  
RESULT 22  
ADF42678  
ID ADF42678 standard; peptide; 17 AA.  
XX  
AC ADF42678;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Eotaxin epitope and spacer peptide SEQ ID NO:56.  
XX  
KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;  
KW vaccine; asthma; allergy; allergic disease; human; spacer; epitope.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX WO2003082349-A1.  
FN  
PD 09-OCT-2003.  
XX  
XX 24-MAR-2003; 2003WO-US008970.  
XX

PR 25-MAR-2002; 2002US-0367591P.  
XX (MERC-) MERCIA PHARMA LLC.  
XX  
XX Drivas DT;  
XX WPI; 2003-803977/75.  
XX  
XX Treating a subject for a condition mediated by eotaxin, e.g. asthma,  
PT allergy or allergic disease by generating an active immune response in  
PT the subject to eotaxin.  
XX  
XX Claim 14; SEQ ID NO 56; 40pp; English.  
XX  
XX The present invention describes a method for treating a subject for a  
CC condition mediated by eotaxin comprising generating an active immune  
CC response in the subject to eotaxin. Also described: (1) an immunogenic  
CC composition (C) comprising eotaxin or its peptide fragment coupled to an  
CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical  
CC formulation for use as a vaccine comprising (C) and an adjuvant and a  
CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be  
CC used in vaccines. The method is useful for treating a subject for a  
CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.  
CC The present sequence represents a human eotaxin epitope and spacer amino  
CC acid sequence, which is used in the exemplification of the present  
CC invention.  
XX  
XX Sequence 17 AA;  
SQ  
Query Match 100.0%; Score 45; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. NO. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSPPPPC 7  
Db |||||  
11 SSPPPPC 17  
RESULT 23  
ADF42676  
ID ADF42676 standard; peptide; 17 AA.  
XX  
AC ADF42676;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Eotaxin epitope and spacer peptide SEQ ID NO:54.  
XX  
KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;  
KW vaccine; asthma; allergy; allergic disease; human; spacer; epitope.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX WO2003082349-A1.  
FN  
PD 09-OCT-2003.  
XX  
XX 24-MAR-2003; 2003WO-US008970.  
XX  
XX 25-MAR-2002; 2002US-0367591P.  
PR  
XX (MERC-) MERCIA PHARMA LLC.  
XX  
XX Drivas DT;  
XX WPI; 2003-803977/75.  
XX  
XX Treating a subject for a condition mediated by eotaxin, e.g. asthma,  
PT allergy or allergic disease by generating an active immune response in  
PT the subject to eotaxin.  
XX  
XX Claim 14; SEQ ID NO 54; 40pp; English.  
XX  
XX

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XX CC The present invention describes a method for treating a subject for a
XX CC condition mediated by eotaxin comprising generating an active immune
XX CC response in the subject to eotaxin. Also described: (1) an immunogenic
XX CC composition (C) comprising eotaxin or its peptide fragment coupled to an
XX CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical
XX CC formulation for use as a vaccine comprising (C) and an adjuvant and a
XX CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be
XX CC used in vaccines. The method is useful for treating a subject for a
XX CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.
XX CC The present sequence represents a human eotaxin epitope and spacer amino
XX CC acid sequence, which is used in the exemplification of the present
XX CC invention.
XX SQ Sequence 17 AA;

  Query Match      100.0%; Score 45; DB 7; Length 17;
  Best Local Similarity 100.0%; Pred. No. 21;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 11 SSPPPPC 17

RESULT 24
ID ADF42682 standard; peptide; 17 AA.
XX AC ADF42682;
XX DT 12-FEB-2004 (first entry)
XX DE Botaxin epitope and spacer peptide SEQ ID NO:60.
XX KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;
XX KW vaccine; asthma; allergy; allergic disease; human; spacer; epitope.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO2003082349-A1.
XX PD 09-OCT-2003.
XX PF 24-MAR-2003; 2003WO-US008970.
XX PR 25-MAR-2002; 2002US-0367591P.
XX PA (MERC-) MERCIA PHARMA LLC.
XX PI Drivas DT;
XX WPI; 2003-803977/75.
XX DR
XX PT Treating a subject for a condition mediated by eotaxin, e.g. asthma,
XX PT allergy or allergic disease by generating an active immune response in
XX PT the subject to eotaxin.
XX PS Claim 14; SEQ ID NO 60; 40pp; English.
XX CC

The present invention describes a method for treating a subject for a
XX CC condition mediated by eotaxin comprising generating an active immune
XX CC response in the subject to eotaxin. Also described: (1) an immunogenic
XX CC composition (C) comprising eotaxin or its peptide fragment coupled to an
XX CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical
XX CC formulation for use as a vaccine comprising (C) and an adjuvant and a
XX CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be
XX CC used in vaccines. The method is useful for treating a subject for a
XX CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.
XX CC The present sequence represents a human eotaxin epitope and spacer amino
XX CC acid sequence, which is used in the exemplification of the present
XX CC invention.
XX SQ Sequence 17 AA;

  Query Match      100.0%; Score 45; DB 7; Length 17;
  Best Local Similarity 100.0%; Pred. No. 21;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 11 SSPPPPC 17

RESULT 25
ID ADH89223 standard; peptide; 17 AA.
XX AC ADH89223;
XX DT 06-MAY-2004 (first entry)
XX DE Gastrin G-17 peptide GI7DT, SEQ ID 18.
XX KW Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;
XX KW gastrin G-34; gonadotropin releasing hormone; GnRH;
XX KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;
XX KW thyroid cancer; lung cancer; reproductive system cancer.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "Pyroglutamic acid"
XX FT Modified-site 17 /note= "This residue is covalently linked to the carrier
XX FT molecule Diphtheria toxoid (DT) through the sulpharyl
XX FT group on this residue by reacting with heterobifunctional
XX FT linker molecule to the epsilon-amino groups of the lysine
XX FT residues present on the carrier protein"
XX PN WO2004004687-A2.
XX PD 15-JAN-2004.
XX PF 03-JUL-2003; 2003WO-US021176.
XX PR 03-JUL-2002; 2002US-0394179P.
XX PA (APHT-) APHTON CORP.
XX PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX PI Michaeli D, Grimes S, Barenholz Y, Even-Chen S;
XX WPI; 2004-099340/10.
XX DR
XX FT Injectable liposomal composition for delivery of a water-soluble
XX FT substance e.g. vaccine for preventing pregnancy, comprises several
XX FT liposomal vesicles comprising a high weight ratio of lipid to
XX FT encapsulated water-soluble substance.
XX PS Claim 39; SEQ ID NO 18; 73pp; English.
XX CC

The present invention relates to injectable liposomal compositions (I)
XX CC for delivery of a water-soluble substance e.g. immunomimic peptides. (I)
XX CC comprises several liposomal vesicles comprising a high weight ratio of a
XX CC lipid to an encapsulated water-soluble substance so as to achieve a high
XX CC efficiency of encapsulation. the immunomimic peptide is chosen from
XX CC gastrin G-17 (ADH89206 to ADH89213 and ADH89223), gastrin G-34 (ADH89217-
XX CC ADH89219), gonadotropin releasing hormone (GnRH) peptide (ADH89220 and
XX CC ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-
XX CC ADH89222 and ADH89225). (I) comprising vaccines directed against hormone
XX CC or hormone cognate receptors, where the vaccine comprises at least one:
XX CC hormone-immunomimic peptide such as gastrin G-17 or G-34 is useful for
XX CC treating gastrointestinal malignancy, and non-gastrointestinal tumors
XX CC

```

CC such as thyroid and lung cancer; or GnRH or hCG immunomimic peptide is  
 CC useful as contraceptive and for treating cancers in male and female  
 CC reproductive systems. The present sequence comprises a G17 peptide linked  
 CC to a spacer peptide at the C-terminal end.

XX Sequence 17 AA;

Query Match 100.0%; Score 45; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
 |||||  
 Db 11 SSPPPPC 17

## RESULT 26

ADS18227  
 ID ADS18227 standard; peptide; 17 AA.

AC ADS18227;

XX 30-DEC-2004 (first entry)

XX Human eotaxin peptide fragment SeqID50.

XX inflammatory condition; eosinophil accumulation; immune response;  
 KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;  
 KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;  
 KW allergic disease; human.

XX Homo sapiens.

XX WO2004084837-A2.

XX 07-OCT-2004.

XX 24-MAR-2004; 2004WO-US008901.

XX 24-MAR-2003; 2003US-0457137P.

XX (MERC-) MERCIA PHARMA LLC.

XX Drivas DT, Blackburn P;

XX WPI; 2004-710267/69.

XX Treating inflammatory conditions resulting from eosinophil accumulation  
 PT (e.g. asthma, allergy or allergic disease) comprises generating an active  
 PT immune response against eotaxin and interleukin-5.

PS Claim 12; SEQ ID NO 50; 55pp; English.

XX This invention relates to a novel method of treating a subject for an  
 CC inflammatory condition which results from eosinophil accumulation which  
 CC comprises generating an active immune response in the patient comprising  
 CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-  
 CC 13). The invention may be useful for the development of compounds with an  
 CC antiinflammatory, antiasthmatic or antiallergic activity or for the  
 CC production of a vaccine. The composition and methods are useful for  
 CC preventing or treating inflammatory conditions resulting from eosinophil  
 CC accumulation, such as asthma, allergy or allergic diseases. The present  
 CC sequence is that of a peptide fragment derived from human eotaxin which  
 CC may be used within the method of the invention.

XX Sequence 17 AA;

Query Match 100.0%; Score 45; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
 |||||

Db 11 SSPPPPC 17

## RESULT 27

ADS18233  
 ID ADS18233 standard; peptide; 17 AA.

XX ADS18233;

XX 30-DEC-2004 (first entry)

XX Human eotaxin-derived modified peptide fragment SeqID56.

XX inflammatory condition; eosinophil accumulation; immune response;  
 KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;  
 KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;  
 KW allergic disease; human.

XX Homo sapiens.

XX Synthetic.

XX WO2004084837-A2.

XX 07-OCT-2004.

XX 24-MAR-2004; 2004WO-US008901.

XX 24-MAR-2003; 2003US-0457137P.

XX (MERC-) MERCIA PHARMA LLC.

XX Drivas DT, Blackburn P;

XX WPI; 2004-710267/69.

XX Treating inflammatory conditions resulting from eosinophil accumulation  
 PT (e.g. asthma, allergy or allergic disease) comprises generating an active  
 PT immune response against eotaxin and interleukin-5.

PS Claim 12; SEQ ID NO 56; 55pp; English.

XX This invention relates to a novel method of treating a subject for an  
 CC inflammatory condition which results from eosinophil accumulation which  
 CC comprises generating an active immune response in the patient comprising  
 CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-  
 CC 13). The invention may be useful for the development of compounds with an  
 CC antiinflammatory, antiasthmatic or antiallergic activity or for the  
 CC production of a vaccine. The composition and methods are useful for  
 CC preventing or treating inflammatory conditions resulting from eosinophil  
 CC accumulation, such as asthma, allergy or allergic diseases. The present  
 CC sequence is that of a modified (cysteine residues substituted by  
 CC threonine) peptide fragment derived from human eotaxin which may be used  
 CC within the method of the invention.

XX Sequence 17 AA;

Query Match 100.0%; Score 45; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
 |||||  
 Db 11 SSPPPPC 17

## RESULT 28

ADS18237  
 ID ADS18237 standard; peptide; 17 AA.

XX ADS18237;

XX 30-DEC-2004 (first entry)

```

DE Human eotaxin-derived modified peptide fragment SeqID60.
XX inflammatory condition; eosinophil accumulation; immune response;
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;
KW allergic disease; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004084837-A2.
XX
PD 07-OCT-2004.
XX
XX 24-MAR-2004; 2004WO-US008901.
XX
PR 24-MAR-2003; 2003US-0457137P.
XX
XX (MERC-) MERCIA PHARMA LLC.
XX
XX Drivas DT, Blackburn P;
XX
XX WPI; 2004-710267/69.
XX
XX Treating inflammatory conditions resulting from eosinophil accumulation
PT (e.g. asthma, allergy or allergic disease) comprises generating an active
PT immune response against eotaxin and interleukin-5.
XX
XX Claim 12; SEQ ID NO 60; 55pp; English.
XX
XX This invention relates to a novel method of treating a subject for an
CC inflammatory condition which results from eosinophil accumulation which
CC comprises generating an active immune response in the patient comprising
CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-
CC 13). The invention may be useful for the development of compounds with an
CC antiinflammatory, antiasthmatic or antiallergic activity or for the
CC production of a vaccine. The composition and methods are useful for
CC preventing or treating inflammatory conditions resulting from eosinophil
CC accumulation, such as asthma, allergy or allergic diseases. The present
CC sequence is that of a modified (cysteine residues substituted by
CC threonine) peptide fragment derived from human eotaxin which may be used
CC within the method of the invention.
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 45; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db |||||
11 SSPPPPC 17

RESULT 29
ADSI8235
ID ADSI8235 standard; peptide; 17 AA.
XX
XX ADSI8235;
XX
XX 30-DEC-2004 (first entry)
XX
XX Human eotaxin-derived modified peptide fragment SeqID58.
DE inflammatory condition; eosinophil accumulation; immune response;
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;
KW allergic disease; human.
XX
XX Homo sapiens.
OS Synthetic.
XX
PN WO2004084837-A2.

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XX 07-OCT-2004.
XX
XX 24-MAR-2004; 2004WO-US008901.
XX
XX 24-MAR-2003; 2003US-0457137P.
XX
XX (MERC-) MERCIA PHARMA LLC.
XX
XX Drivas DT, Blackburn P;
XX
XX WPI; 2004-710267/69.
XX
XX Treating inflammatory conditions resulting from eosinophil accumulation
PT (e.g. asthma, allergy or allergic disease) comprises generating an active
PT immune response against eotaxin and interleukin-5.
XX
XX Claim 12; SEQ ID NO 58; 55pp; English.
XX
XX This invention relates to a novel method of treating a subject for an
CC inflammatory condition which results from eosinophil accumulation which
CC comprises generating an active immune response in the patient comprising
CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-
CC 13). The invention may be useful for the development of compounds with an
CC antiinflammatory, antiasthmatic or antiallergic activity or for the
CC production of a vaccine. The composition and methods are useful for
CC preventing or treating inflammatory conditions resulting from eosinophil
CC accumulation, such as asthma, allergy or allergic diseases. The present
CC sequence is that of a modified (cysteine residues substituted by
CC threonine) peptide fragment derived from human eotaxin which may be used
CC within the method of the invention.
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 45; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db |||||
11 SSPPPPC 17

RESULT 30
ADSI8229
ID ADSI8229 standard; peptide; 17 AA.
XX
XX ADSI8229;
XX
XX 30-DEC-2004 (first entry)
XX
XX Human eotaxin peptide fragment SeqID52.
DE inflammatory condition; eosinophil accumulation; immune response;
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;
KW allergic disease; human.
XX
XX Homo sapiens.
XX
XX WO2004084837-A2.
XX
XX 07-OCT-2004.
XX
XX 24-MAR-2004; 2004WO-US008901.
XX
XX 24-MAR-2003; 2003US-0457137P.
XX
XX (MERC-) MERCIA PHARMA LLC.
XX
XX Drivas DT, Blackburn P;
XX
XX WPI; 2004-710267/69.

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XX Treating inflammatory conditions resulting from eosinophil accumulation  
PT (e.g. asthma, allergy or allergic disease) comprises generating an active  
PT immune response against eotaxin and interleukin-5.  
XX  
XX Claim 12; SEQ ID NO 52; 55pp; English.  
XX  
XX This invention relates to a novel method of treating a subject for an  
CC inflammatory condition which results from eosinophil accumulation which  
CC comprises generating an active immune response in the patient comprising  
CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-  
CC 13). The invention may be useful for the development of compounds with an  
CC antiinflammatory, antiasthmatic or antiallergic activity or for the  
CC production of a vaccine. The composition and methods are useful for  
CC preventing or treating inflammatory conditions resulting from eosinophil  
CC accumulation, such as asthma, allergy or allergic diseases. The present  
CC sequence is that of a peptide fragment derived from human eotaxin which  
CC may be used within the method of the invention.  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 45; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SSPPPPC 7  
Db 11 SSPPPPC 17  
RESULT 31  
ADS18231  
ID ADS18231 standard; peptide; 17 AA.  
XX  
AC ADS18231;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DB Human eotaxin peptide fragment SeqID54.  
XX  
KW inflammatory condition; eosinophil accumulation; immune response;  
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;  
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;  
KW allergic disease; human.  
OS Homo sapiens.  
XX  
PN WO2004084837-A2.  
XX  
PD 07-OCT-2004.  
XX  
PF 24-MAR-2004; 2004WO-US008901.  
XX  
PR 24-MAR-2003; 2003US-0457137P.  
XX  
PA (MERC-) MERCIA PHARMA LLC.  
XX  
PI Drivas DT, Blackburn P;  
XX  
PS WPI; 2004-710267/69.  
XX  
PT Treating inflammatory conditions resulting from eosinophil accumulation  
PT (e.g. asthma, allergy or allergic disease) comprises generating an active  
PT immune response against eotaxin and interleukin-5.  
XX  
XX Claim 12; SEQ ID NO 54; 55pp; English.  
XX  
XX This invention relates to a novel method of treating a subject for an  
CC inflammatory condition which results from eosinophil accumulation which  
CC comprises generating an active immune response in the patient comprising  
CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-  
CC 13). The invention may be useful for the development of compounds with an  
CC antiinflammatory, antiasthmatic or antiallergic activity or for the

CC production of a vaccine. The composition and methods are useful for  
CC preventing or treating inflammatory conditions resulting from eosinophil  
CC accumulation, such as asthma, allergy or allergic diseases. The present  
CC sequence is that of a peptide fragment derived from human eotaxin which  
CC may be used within the method of the invention.  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 45; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SSPPPPC 7  
Db 11 SSPPPPC 17  
RESULT 32  
ADS18292  
ID ADS18292 standard; peptide; 18 AA.  
XX  
AC ADS18292;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DB Human interleukin (IL)-5-derived modified peptide fragment SeqID15.  
XX  
KW inflammatory condition; eosinophil accumulation; immune response;  
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;  
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;  
KW allergic disease; human.  
OS Homo sapiens.  
XX  
OS Synthetic.  
XX  
PN WO2004084837-A2.  
XX  
PD 07-OCT-2004.  
XX  
PF 24-MAR-2004; 2004WO-US008901.  
XX  
PR 24-MAR-2003; 2003US-0457137P.  
XX  
PA (MERC-) MERCIA PHARMA LLC.  
XX  
PI Drivas DT, Blackburn P;  
XX  
PS WPI; 2004-710267/69.  
XX  
PT Treating inflammatory conditions resulting from eosinophil accumulation  
PT (e.g. asthma, allergy or allergic disease) comprises generating an active  
PT immune response against eotaxin and interleukin-5.  
XX  
XX Claim 12; SEQ ID NO 115; 55pp; English.  
XX  
XX This invention relates to a novel method of treating a subject for an  
CC inflammatory condition which results from eosinophil accumulation which  
CC comprises generating an active immune response in the patient comprising  
CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-  
CC 13). The invention may be useful for the development of compounds with an  
CC antiinflammatory, antiasthmatic or antiallergic activity or for the  
CC production of a vaccine. The composition and methods are useful for  
CC preventing or treating inflammatory conditions resulting from eosinophil  
CC accumulation, such as asthma, allergy or allergic diseases. The present  
CC sequence is that of a modified (cysteine residues substituted by  
CC threonine) peptide fragment derived from human IL-5 which may be used  
CC within the method of the invention.  
XX  
SQ Sequence 18 AA;  
Query Match 100.0%; Score 45; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 Db 12 SSPPPPC 18

RESULT 33  
 ADQ48435  
 ID ADQ48435 standard; peptide; 22 AA.  
 XX ADQ48435;  
 XX 23-SEP-2004 (first entry)  
 XX Human gastrin receptor immunomimic peptide for GRE4 epitope SeqID.  
 XX immunogen; gastrin receptor peptide epitope; GRE; GRP;  
 KW gastrin-dependent tumour; immunostimulator; CCK-B/gastrin receptor;  
 KW biopsy; human.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO2004056862-A2.  
 XX 08-JUL-2004.  
 XX 17-DEC-2003; 2003WO-US040449.  
 XX 19-DEC-2002; 2002US-00323692.  
 XX (APHT-) APHTON CORP.  
 XX Michaeli D, Caplin M, Watson SA, Grimes S;  
 XX WPI; 2004-507696/48.

Novel immunogen comprising gastrin receptor-peptide epitope conjugated at its cysteine end to immunogenic carrier, useful for treating patient suffering from gastrin responsive tumor.

Disclosure; SEQ ID NO 7; 66pp; English.

This invention relates to a novel immunogen that comprises a gastrin receptor peptide epitope (GRE) - formally designated as GRP - conjugated to an immunogenic carrier for the treatment of gastrin-dependent tumours. Specifically, it refers to immunogens (immunostimulators) capable of inducing antibodies in vivo that can bind to gastrin receptors and as such prevent binding of growth stimulating peptide hormones, which in turn can be used to prevent or treat gastrin stimulated malignant or premalignant growth. The present invention describes the active or passive immunisation of a patient with a CCK-B/gastrin receptor immunogen or antibody thereof that are specific to the tumour and can be used to arrest tumour growth. As such, the method is useful for diagnosing the gastrin receptor in a biopsy, which involves obtaining a biopsy specimen from a patient, exposing the specimen to antibodies conjugated to detectable molecules, and hence detecting the amount of bound antibody by colorimetric, chemiluminescent, fluorescent, radiometric or scintigraphic techniques. This peptide sequence is a human CCK-B/ gastrin receptor immunomimic peptide with a synthetic spacer used to project the peptide away from the protein carrier, in order to enhance binding to the lymphocyte receptors, given in an exemplification of the invention.

Sequence 22 AA;  
 Query Match 100.0%; Score 45; DB 8; Length 22;  
 Best Local Similarity 100.0%; Pred. NO. 26;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 Db 16 SSPPPPC 22

RESULT 34  
 ADQ48432  
 ID ADQ48432 standard; peptide; 24 AA.  
 XX ADQ48432;  
 XX 23-SEP-2004 (first entry)  
 XX Human gastrin receptor immunomimic peptide for GRE1 epitope SeqID.  
 XX immunogen; gastrin receptor peptide epitope; GRE; GRP;  
 KW gastrin-dependent tumour; immunostimulator; CCK-B/gastrin receptor;  
 KW biopsy; human.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO2004056862-A2.  
 XX 08-JUL-2004.  
 XX 17-DEC-2003; 2003WO-US040449.  
 XX 19-DEC-2002; 2002US-00323692.  
 XX (APHT-) APHTON CORP.  
 XX Michaeli D, Caplin M, Watson SA, Grimes S;  
 XX WPI; 2004-507696/48.

Novel immunogen comprising gastrin receptor-peptide epitope conjugated at its cysteine end to immunogenic carrier, useful for treating patient suffering from gastrin responsive tumor.

Disclosure; SEQ ID NO 4; 66pp; English.

This invention relates to a novel immunogen that comprises a gastrin receptor peptide epitope (GRE) - formally designated as GRP - conjugated to an immunogenic carrier for the treatment of gastrin-dependent tumours. Specifically, it refers to immunogens (immunostimulators) capable of inducing antibodies in vivo that can bind to gastrin receptors and as such prevent binding of growth stimulating peptide hormones, which in turn can be used to prevent or treat gastrin stimulated malignant or premalignant growth. The present invention describes the active or passive immunisation of a patient with a CCK-B/gastrin receptor immunogen or antibody thereof that are specific to the tumour and can be used to arrest tumour growth. As such, the method is useful for diagnosing the gastrin receptor in a biopsy, which involves obtaining a biopsy specimen from a patient, exposing the specimen to antibodies conjugated to detectable molecules, and hence detecting the amount of bound antibody by colorimetric, chemiluminescent, fluorescent, radiometric or scintigraphic techniques. This peptide sequence is a human CCK-B/ gastrin receptor immunomimic peptide with a synthetic spacer used to project the peptide away from the protein carrier, in order to enhance binding to the lymphocyte receptors, given in an exemplification of the invention.

Sequence 24 AA;  
 Query Match 100.0%; Score 45; DB 8; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7  
 Db 18 SSPPPPC 24

RESULT 35  
 ADF42668  
 ID ADF42668 standard; peptide; 27 AA.  
 XX

AC ADF42668;  
XX  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Eotaxin epitope and spacer peptide SEQ ID NO:46.  
XX  
KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;  
KW vaccine; asthma; allergy; allergic disease; human; spacer; epitope.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX WO2003082349-A1.  
XX  
PD 09-OCT-2003.  
XX  
XX 24-MAR-2003; 2003WO-US008970.  
XX  
PR 25-MAR-2002; 2002US-0367591P.  
XX  
PA (MERC-) MERCIA PHARMA LLC.  
XX  
PI Drivas DT;  
XX  
XX WPI; 2003-803977/75.  
XX  
XX The present invention describes a method for treating a subject for a  
CC condition mediated by eotaxin comprising generating an active immune  
CC response in the subject to eotaxin. Also described: (1) an immunogenic  
CC composition (C) comprising eotaxin or its peptide fragment coupled to an  
CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical  
CC formulation for use as a vaccine comprising (C) and an adjuvant and a  
CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be  
CC used in vaccines. The method is useful for treating a subject for a  
CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.  
CC The present sequence represents a human eotaxin epitope and spacer amino  
CC acid sequence, which is used in the exemplification of the present  
CC invention.  
XX  
XX Claim 14; SEQ ID NO 46; 40pp; English.  
XX  
XX The present invention describes a method for treating a subject for a  
CC condition mediated by eotaxin comprising generating an active immune  
CC response in the subject to eotaxin. Also described: (1) an immunogenic  
CC composition (C) comprising eotaxin or its peptide fragment coupled to an  
CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical  
CC formulation for use as a vaccine comprising (C) and an adjuvant and a  
CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be  
CC used in vaccines. The method is useful for treating a subject for a  
CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.  
CC The present sequence represents a human eotaxin epitope and spacer amino  
CC acid sequence, which is used in the exemplification of the present  
CC invention.  
XX  
XX Query Match 100.0%; Score 45; DB 7; Length 27;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SSPPPPC 7  
Db 21 SSPPPPC 27  
|||||  
RESULT 36  
ADF42671  
ID ADF42671 standard; peptide; 27 AA.  
XX  
AC ADF42671;  
XX  
XX 12-FEB-2004 (first entry)  
XX  
DE Eotaxin epitope and spacer peptide SEQ ID NO:49.  
XX  
KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;  
KW vaccine; asthma; allergy; allergic disease; human; spacer; epitope.  
XX  
XX Synthetic.  
XX OS Homo sapiens.  
XX  
XX WO2003082349-A1.  
XX  
FN

XX  
PD 09-OCT-2003.  
XX  
XX 24-MAR-2003; 2003WO-US008970.  
XX  
PR 25-MAR-2002; 2002US-0367591P.  
XX  
PA (MERC-) MERCIA PHARMA LLC.  
XX  
PI Drivas DT;  
XX  
XX WPI; 2003-803977/75.  
XX  
XX Treating a subject for a condition mediated by eotaxin, e.g. asthma,  
PT allergy or allergic disease by generating an active immune response in  
PT the subject to eotaxin.  
XX  
XX Claim 14; SEQ ID NO 49; 40pp; English.  
XX  
XX The present invention describes a method for treating a subject for a  
CC condition mediated by eotaxin comprising generating an active immune  
CC response in the subject to eotaxin. Also described: (1) an immunogenic  
CC composition (C) comprising eotaxin or its peptide fragment coupled to an  
CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical  
CC formulation for use as a vaccine comprising (C) and an adjuvant and a  
CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be  
CC used in vaccines. The method is useful for treating a subject for a  
CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.  
CC The present sequence represents a human eotaxin epitope and spacer amino  
CC acid sequence, which is used in the exemplification of the present  
CC invention.  
XX  
XX Query Match 100.0%; Score 45; DB 7; Length 27;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SSPPPPC 7  
Db 21 SSPPPPC 27  
|||||  
RESULT 37  
ADF42669  
ID ADF42669 standard; peptide; 27 AA.  
XX  
AC ADF42669;  
XX  
XX 12-FEB-2004 (first entry)  
XX  
DE Eotaxin epitope and spacer peptide SEQ ID NO:47.  
XX  
KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;  
KW vaccine; asthma; allergy; allergic disease; human; spacer; epitope.  
XX  
XX Synthetic.  
XX OS Homo sapiens.  
XX  
XX WO2003082349-A1.  
XX  
PD 09-OCT-2003.  
XX  
XX 24-MAR-2003; 2003WO-US008970.  
XX  
PR 25-MAR-2002; 2002US-0367591P.  
XX  
PA (MERC-) MERCIA PHARMA LLC.  
XX  
PI Drivas DT;  
XX  
XX WPI; 2003-803977/75.  
XX

PT Treating a subject for a condition mediated by eotaxin, e.g. asthma,  
PT allergy or allergic disease by generating an active immune response in  
PT the subject to eotaxin.  
XX  
PS Claim 14; SEQ ID NO 47; 40pp; English.  
XX  
CC The present invention describes a method for treating a subject for a  
CC condition mediated by eotaxin comprising generating an active immune  
CC response in the subject to eotaxin. Also described: (1) an immunogenic  
CC composition (C) comprising eotaxin or its peptide fragment coupled to an  
CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical  
CC formulation for use as a vaccine comprising (C) and an adjuvant and a  
CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be  
CC used in vaccines. The method is useful for treating a subject for a  
CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.  
CC The present sequence represents a human eotaxin epitope and spacer amino  
CC acid sequence, which is used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 27 AA;  
Query Match 100.0%; Score 45; DB 7; Length 27;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSPPPPC 7  
Db 1 SSPPPPC 7  
|||||  
RESULT 38  
ADS18223  
ID ADS18223 standard; peptide; 27 AA.  
XX  
AC ADS18223;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE Inflammatory condition-related human eotaxin/spacer peptide SeqID46.  
XX  
KW inflammatory condition; eosinophil accumulation; immune response;  
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;  
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;  
KW allergic disease; human; spacer peptide.  
XX  
OS Homo sapiens.  
OS Unidentified.  
OS Synthetic.  
XX  
PN WO2004084837-A2.  
XX  
PD 07-OCT-2004.  
XX  
PF 24-MAR-2004; 2004WO-US008901.  
XX  
PR 24-MAR-2003; 2003US-0457137P.  
XX  
PA (MERC-) MERCIA PHARMA LLC.  
XX  
PI Drivas DT, Blackburn P;  
XX  
DR WPI; 2004-710267/69.  
XX  
PT Treating inflammatory conditions resulting from eosinophil accumulation  
PT (e.g. asthma, allergy or allergic disease) comprises generating an active  
PT immune response against eotaxin and interleukin-5.  
XX  
PS Claim 12; SEQ ID NO 46; 55pp; English.  
XX  
CC This invention relates to a novel method of treating a subject for an  
CC inflammatory condition which results from eosinophil accumulation which  
CC comprises generating an active immune response in the patient comprising  
CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-  
CC 13). The invention may be useful for the development of compounds with an  
CC antinflammatory, antiasthmatic or antiallergic activity or for the  
CC production of a vaccine. The composition and methods are useful for  
CC preventing or treating inflammatory conditions resulting from eosinophil  
CC accumulation, such as asthma, allergy or allergic diseases. The present  
CC sequence is that of a peptide, derived from human eotaxin linked to a  
CC spacer peptide, which may be used within the method of the invention.  
XX  
SQ Sequence 27 AA;  
Query Match 100.0%; Score 45; DB 8; Length 27;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSPPPPC 7  
Db 21 SSPPPPC 27  
|||||

CC 13). The invention may be useful for the development of compounds with an  
CC antinflammatory, antiasthmatic or antiallergic activity or for the  
CC production of a vaccine. The composition and methods are useful for  
CC preventing or treating inflammatory conditions resulting from eosinophil  
CC accumulation, such as asthma, allergy or allergic diseases. The present  
CC sequence is that of a peptide, derived from human eotaxin linked to a  
CC spacer peptide, which may be used within the method of the invention.  
XX  
SQ Sequence 27 AA;  
Query Match 100.0%; Score 45; DB 8; Length 27;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSPPPPC 7  
Db 21 SSPPPPC 27  
|||||  
RESULT 39  
ADS18224  
ID ADS18224 standard; peptide; 27 AA.  
XX  
AC ADS18224;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE Inflammatory condition-related human eotaxin/spacer peptide SeqID47.  
XX  
KW inflammatory condition; eosinophil accumulation; immune response;  
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;  
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;  
KW allergic disease; human; spacer peptide.  
XX  
OS Homo sapiens.  
OS Unidentified.  
OS Synthetic.  
XX  
PN WO2004084837-A2.  
XX  
PD 07-OCT-2004.  
XX  
PF 24-MAR-2004; 2004WO-US008901.  
XX  
PR 24-MAR-2003; 2003US-0457137P.  
XX  
PA (MERC-) MERCIA PHARMA LLC.  
XX  
PI Drivas DT, Blackburn P;  
XX  
DR WPI; 2004-710267/69.  
XX  
PT Treating inflammatory conditions resulting from eosinophil accumulation  
PT (e.g. asthma, allergy or allergic disease) comprises generating an active  
PT immune response against eotaxin and interleukin-5.  
XX  
PS Claim 12; SEQ ID NO 47; 55pp; English.  
XX  
CC This invention relates to a novel method of treating a subject for an  
CC inflammatory condition which results from eosinophil accumulation which  
CC comprises generating an active immune response in the patient comprising  
CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-  
CC 13). The invention may be useful for the development of compounds with an  
CC antinflammatory, antiasthmatic or antiallergic activity or for the  
CC production of a vaccine. The composition and methods are useful for  
CC preventing or treating inflammatory conditions resulting from eosinophil  
CC accumulation, such as asthma, allergy or allergic diseases. The present  
CC sequence is that of a peptide, derived from human eotaxin linked to a  
CC spacer peptide, which may be used within the method of the invention.  
XX  
SQ Sequence 27 AA;  
Query Match 100.0%; Score 45; DB 8; Length 27;

Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
|||||  
Db 1 SSPPPPC 7

RESULT 40  
ADS18226  
ID ADS18226 standard; peptide; 27 AA.  
XX  
AC ADS18226;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE Inflammatory condition-related human eotaxin/spacer peptide SeqID49.  
XX  
KW inflammatory condition; eosinophil accumulation; immune response;  
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;  
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;  
KW allergic disease; human; spacer peptide.  
XX  
OS Homo sapiens.  
OS Unidentified.  
OS Synthetic.  
XX  
PN WO2004084837-A2.  
XX  
PD 07-OCT-2004.  
XX  
PF 24-MAR-2004; 2004WO-US008901.  
XX  
PR 24-MAR-2003; 2003US-0457137P.  
XX  
PA (MERC-) MERCIA PHARMA LLC.  
XX  
PI Drivas DT, Blackburn P;  
XX  
DR WPI; 2004-710267/69.  
XX  
PT Treating inflammatory conditions resulting from eosinophil accumulation  
PT (e.g. asthma, allergy or allergic disease) comprises generating an active  
PT immune response against eotaxin and interleukin-5.  
XX  
PS Claim 12; SEQ ID NO 49; 55pp; English.  
XX  
CC This invention relates to a novel method of treating a subject for an  
CC inflammatory condition which results from eosinophil accumulation which  
CC comprises generating an active immune response in the patient comprising  
CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-  
CC 13). The invention may be useful for the development of compounds with an  
CC antiinflammatory, antiasthmatic or antiallergic activity or for the  
CC production of a vaccine. The composition and methods are useful for  
CC preventing or treating inflammatory conditions resulting from eosinophil  
CC accumulation, such as asthma, allergy or allergic diseases. The present  
CC sequence is that of a peptide, derived from human eotaxin linked to a  
CC spacer peptide, which may be used within the method of the invention.  
XX  
SQ Sequence 27 AA;

Query Match 100.0%; Score 45; DB 8; Length 27;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
|||||  
Db 21 SSPPPPC 27

RESULT 41  
ADP42665  
ID ADP42665 standard; peptide; 28 AA.

Best Local Similarity 100.0%; Score 45; DB 7; Length 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
|||||  
Db 22 SSPPPPC 28

RESULT 42  
ADP42664  
ID ADP42664 standard; peptide; 28 AA.  
XX  
AC ADP42664;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Botaxin epitope and spacer peptide SEQ ID NO:42.  
XX  
KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;  
KW vaccine; asthma; allergy; allergic disease; human; spacer; epitope.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX

XX  
AC ADF42665;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Botaxin epitope and spacer peptide SEQ ID NO:43.  
XX  
KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;  
KW vaccine; asthma; allergy; allergic disease; human; spacer; epitope.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO2003082349-A1.  
XX  
PD 09-OCT-2003.  
XX  
PF 24-MAR-2003; 2003WO-US008970.  
XX  
PR 25-MAR-2002; 2002US-0367591P.  
XX  
PA (MERC-) MERCIA PHARMA LLC.  
XX  
PI Drivas DT;  
XX  
DR WPI; 2003-803977/75.  
XX  
PT Treating a subject for a condition mediated by eotaxin, e.g. asthma,  
PT allergy or allergic disease by generating an active immune response in  
PT the subject to eotaxin.  
XX  
PS Claim 14; SEQ ID NO 43; 40pp; English.  
XX  
CC The present invention describes a method for treating a subject for a  
CC condition mediated by eotaxin comprising generating an active immune  
CC response in the subject to eotaxin. Also described: (1) an immunogenic  
CC composition (C) comprising eotaxin or its peptide fragment coupled to an  
CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical  
CC formulation for use as a vaccine comprising (C) and an adjuvant and a  
CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be  
CC used in vaccines. The method is useful for treating a subject for a  
CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.  
CC The present sequence represents a human eotaxin epitope and spacer amino  
CC acid sequence, which is used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 28 AA;

Query Match 100.0%; Score 45; DB 7; Length 28;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
|||||  
Db 22 SSPPPPC 28

RESULT 42  
ADP42664  
ID ADP42664 standard; peptide; 28 AA.  
XX  
AC ADP42664;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Botaxin epitope and spacer peptide SEQ ID NO:42.  
XX  
KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;  
KW vaccine; asthma; allergy; allergic disease; human; spacer; epitope.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX

PN WO2003082349-A1.  
XX 09-OCT-2003.  
XX 24-MAR-2003; 2003WO-US008970.  
XX 25-MAR-2002; 2002US-0367591P.  
XX (MERC-) MERCIA PHARMA LLC.  
XX Drivas DT;  
XX WPI; 2003-803977/75.  
XX Treating a subject for a condition mediated by eotaxin, e.g. asthma,  
PT allergy or allergic disease by generating an active immune response in  
PT the subject to eotaxin.  
XX Claim 14; SEQ ID NO 42; 40pp; English.  
XX The present invention describes a method for treating a subject for a  
CC condition mediated by eotaxin comprising generating an active immune  
CC response in the subject to eotaxin. Also described: (1) an immunogenic  
CC composition (C) comprising eotaxin or its peptide fragment coupled to an  
CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical  
CC formulation for use as a vaccine comprising (C) and an adjuvant and a  
CC vehicle. (C) has antiallergic and antiallergic activities, and can be  
CC used in vaccines. The method is useful for treating a subject for a  
CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.  
CC The present sequence represents a human eotaxin epitope and spacer amino  
CC acid sequence, which is used in the exemplification of the present  
CC invention.  
XX Sequence 28 AA;  
SQ Query Match 100.0%; Score 45; DB 7; Length 28;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSPPPPC 7  
DB 1 SSPPPPC 7  
RESULT 43  
ADQ48440  
ID ADQ48440 standard; peptide; 28 AA.  
XX ADQ48440;  
XX 23-SEP-2004 (first entry)  
XX Human gastrin receptor immunomimic peptide for GRE11S epitope SeqID.  
XX immunogen; gastrin receptor peptide epitope; GRE; GRP;  
XX gastrin-dependent tumour; immunostimulator; CCK-B/gastrin receptor;  
XX biopsy; human.  
XX Homo sapiens.  
XX Synthetic.  
XX WO2004056862-A2.  
XX 08-JUL-2004.  
XX 17-DEC-2003; 2003WO-US040449.  
XX 19-DEC-2002; 2002US-00323692.  
XX (APHT-) APHTON CORP.  
XX Michaeli D, Caplin M, Watson SA, Grimes S;  
XX

DR WPI; 2004-507696/48.  
XX Novel immunogen comprising gastrin receptor-peptide epitope conjugated at  
PT its cysteine end to immunogenic carrier, useful for treating patient  
PT suffering from gastrin responsive tumor.  
XX Claim 1; SEQ ID NO 12; 66pp; English.  
XX This invention relates to a novel immunogen that comprises a gastrin  
CC receptor peptide epitope (GRE) - formally designated as GRP - conjugated  
CC to an immunogenic carrier for the treatment of gastrin-dependent tumours.  
CC Specifically, it refers to immunogens (immunostimulators) capable of  
CC inducing antibodies in vivo that can bind to gastrin receptors and as  
CC such prevent binding of growth stimulating peptide hormones, which in  
CC turn can be used to prevent or treat gastrin stimulated malignant or  
CC premalignant growth. The present invention describes the active or  
CC passive immunisation of a patient with a CCK-B/gastrin receptor immunogen  
CC or antibody thereof that are specific to the tumour and can be used to  
CC arrest tumour growth. As such, the method is useful for diagnosing the  
CC gastrin receptor in a biopsy, which involves obtaining a biopsy specimen  
CC from a patient, exposing the specimen to antibodies conjugated to  
CC detectable molecules, and hence detecting the amount of bound antibody by  
CC colorimetric, chemiluminescent, fluorescent, radiometric or scintigraphic  
CC techniques. This peptide sequence is a human CCK-B/ gastrin receptor  
CC immunomimic peptide with a synthetic spacer used to project the peptide  
CC away from the protein carrier, in order to enhance binding to the  
CC lymphocyte receptors, given in an exemplification of the invention.  
XX Sequence 28 AA;  
SQ Query Match 100.0%; Score 45; DB 8; Length 28;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSPPPPC 7  
DB 22 SSPPPPC 28  
RESULT 44  
ADS18220  
ID ADS18220 standard; peptide; 28 AA.  
XX ADS18220;  
XX 30-DEC-2004 (first entry)  
XX Inflammatory condition-related human eotaxin/spacer peptide SeqID43.  
XX inflammatory condition; eosinophil accumulation; immune response;  
XX autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;  
XX antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;  
XX allergic disease; human; spacer peptide.  
XX Homo sapiens.  
XX Unidentified.  
XX Synthetic.  
XX WO2004084837-A2.  
XX PD 07-OCT-2004.  
XX 24-MAR-2004; 2004WO-US008901.  
XX 24-MAR-2003; 2003US-0457137P.  
XX (MERC-) MERCIA PHARMA LLC.  
XX Drivas DT, Blackburn P;  
XX WPI; 2004-710267/69.  
XX Treating inflammatory conditions resulting from eosinophil accumulation  
PT

PT (e.g. asthma, allergy or allergic disease) comprises generating an active  
 PT immune response against eotaxin and interleukin-5.

PS Claim 12; SEQ ID NO 43; 55pp; English.

XX This invention relates to a novel method of treating a subject for an  
 CC inflammatory condition which results from eosinophil accumulation which  
 CC comprises generating an active immune response in the patient comprising  
 CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-  
 CC 13). The invention may be useful for the development of compounds with an  
 CC antiinflammatory, antialsthmatic or antiallergic activity or for the  
 CC production of a vaccine. The composition and methods are useful for  
 CC preventing or treating inflammatory conditions resulting from eosinophil  
 CC accumulation, such as asthma, allergy or allergic diseases. The present  
 CC sequence is that of a peptide, derived from human eotaxin linked to a  
 CC spacer peptide, which may be used within the method of the invention.

XX Sequence 28 AA;

Query Match 100.0%; Score 45; DB 8; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7

Db 22 SSPPPPC 28

RESULT 45

ADS18219  
 ID ADS18219 standard; peptide; 28 AA.

XX AC ADS18219;

XX 30-DEC-2004 (first entry)

XX Inflammatory condition-related human eotaxin/spacer peptide SeqID42.

XX inflammatory condition; eosinophil accumulation; immune response;  
 KW autoantibody; eotaxin; interleukin; IL-5; IL-4, IL-9, IL-13;  
 KW antiinflammatory; antialsthmatic; antiallergic; vaccine; asthma; allergy;  
 KW allergic disease; human; spacer peptide.

XX Homo sapiens.

OS Unidentified.

OS Synthetic..

XX WO2004084837-A2.

XX 07-OCT-2004.

XX 24-MAR-2004; 2004WO-US008901.

XX 24-MAR-2003; 2003US-0457137P.

XX (MERC-) MERCIA PHARMA LLC.

XX Drivas DT, Blackburn P;

XX WPI; 2004-710267/69.

XX Treating inflammatory conditions resulting from eosinophil accumulation  
 PT (e.g. asthma, allergy or allergic disease) comprises generating an active  
 PT immune response against eotaxin and interleukin-5.

PS Claim 12; SEQ ID NO 42; 55pp; English.

XX This invention relates to a novel method of treating a subject for an  
 CC inflammatory condition which results from eosinophil accumulation which  
 CC comprises generating an active immune response in the patient comprising  
 CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-  
 CC 13). The invention may be useful for the development of compounds with an  
 CC antiinflammatory, antialsthmatic or antiallergic activity or for the

CC production of a vaccine. The composition and methods are useful for  
 CC preventing or treating inflammatory conditions resulting from eosinophil  
 CC accumulation, such as asthma, allergy or allergic diseases. The present  
 CC sequence is that of a peptide, derived from human eotaxin linked to a  
 CC spacer peptide, which may be used within the method of the invention.

XX Sequence 28 AA;

Query Match 100.0%; Score 45; DB 8; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7

Db 1 SSPPPPC 7

RESULT 46

ADG79465

ID ADG79465 standard; protein; 83 AA.

XX AC ADG79465;

XX 11-MAR-2004 (first entry)

XX Human secreted protein of the invention SEQ ID NO:271.

XX ss; cytostatic; vasotropic; haemostatic; cardiovascular;  
 KW gastrointestinal; immunomodulator; inotropic; cerebroprotective;  
 KW neuroprotective; nephrotropic; antiinflammatory; antibacterial; virucide;  
 KW gynaecological; antidiabetic; gene therapy; vaccine; cancer;  
 KW blood disorder; immune disorder; infection; inflammatory disorder;  
 KW type II diabetes; gene; human; secreted protein.

XX Homo sapiens.

XX WO200268638-A1.

XX 06-SEP-2002.

XX 21-FEB-2002; 2002WO-US0005064.

XX 23-FEB-2001; 2001US-0270658P.

XX 12-JUL-2001; 2001US-0304444P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Komatsoulis GA, Birse CE, Choi GH, Olsen HS, Ni J;  
 PI Bell A;

XX WPI; 2002-750418/81.

XX N-PSDB; ADG79278.

XX New isolated polypeptide and encoding polynucleotide useful for  
 PT diagnosing, preventing, treating and/or ameliorating diseases such as  
 PT cancer, blood disorders, infections, inflammatory and immune disorders  
 PT and type II diabetes.

XX Disclosure; SEQ ID NO 271; 936pp; English.

XX The invention relates to a novel isolated polypeptide. A protein of the  
 CC invention has cytostatic, vasotropic, haemostatic, cardiovascular,  
 CC gastrointestinal, immunomodulator, inotropic, cerebroprotective,  
 CC neuroprotective, nephrotropic, antiinflammatory, antibacterial, virucide,  
 CC gynaecological, and antidiabetic activity. A polynucleotide of the  
 CC invention may have a use in gene therapy, and as a vaccine. The methods  
 CC and compositions of the invention are useful for diagnosing, preventing,  
 CC treating and/or ameliorating diseases such as cancer (neural,  
 CC reproductive, gastrointestinal, endocrine, renal, CNS and respiratory  
 CC neoplasms), blood disorders, immune disorders, infections, inflammatory  
 CC disorders and type II diabetes. They can also be used in chromosome  
 CC identification, screening assays and molecular weight markers. The  
 CC present sequence is used in the exemplification of the invention.

```

XX SQ Sequence 83 AA;
Query Match 100.0%; Score 45; DB 5; Length 83;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 52 SSPPPPC 58

RESULT 47
ADG79566
ID ADG79566 standard; protein; 83 AA.
XX AC ADG79566;
XX DT 11-MAR-2004 (first entry)
XX DE Human secreted protein of the invention SEQ ID NO:372.
XX KW ss; cytostatic; vasotropic; haemostatic; cardiovascular;
KW gastrointestinal; immunomodulator; inotropic; cerebroprotective;
KW neuroprotective; nephrotropic; antiinflammatory; antibacterial; virucide;
KW gynaecological; antidiabetic; gene therapy; vaccine; cancer;
KW blood disorder; immune disorder; infection; inflammatory disorder;
KW type II diabetes; gene; human; secreted protein.
XX OS Homo sapiens.
XX PN WO200268638-A1.
XX PD 06-SEP-2002.
XX PF 21-FEB-2002; 2002WO-US005064.
XX PR 23-FEB-2001; 2001US-0270658P.
XX PR 12-JUL-2001; 2001US-030444P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Komatsoulis GA, Birse CE, Choi GH, Olsen HS, Ni J;
PI Bell A;
XX WPI; 2002-750418/81.
XX DR N-PSDB; ADG79380.
XX KW New isolated polypeptide and encoding polynucleotide useful for
PT diagnosing, preventing, treating and/or ameliorating diseases such as
PT cancer, blood disorders, infections, inflammation and immune disorders
PT and type II diabetes.
XX PS Disclosure; SEQ ID NO 373; 936pp; English.
XX CC The invention relates to a novel isolated polypeptide. A protein of the
CC invention has cytostatic, vasotropic, haemostatic, cardiovascular,
CC gastrointestinal, immunomodulator, inotropic, cerebroprotective,
CC neuroprotective, nephrotropic, antiinflammatory, antibacterial, virucide,
CC gynaecological, and antidiabetic activity. A polynucleotide of the
CC invention may have a use in gene therapy, and as a vaccine. The methods
CC and compositions of the invention are useful for diagnosing, preventing,
CC treating and/or ameliorating diseases such as cancer (neural,
CC reproductive, gastrointestinal, endocrine, renal, CNS and respiratory
CC neoplasias), blood disorders, immune disorders, infections, inflammatory
CC disorders and type II diabetes. They can also be used in chromosome
CC identification, screening assays and molecular weight markers. The
CC present sequence is used in the exemplification of the invention.
XX SQ Sequence 83 AA;
Query Match 100.0%; Score 45; DB 5; Length 83;
Best Local Similarity 100.0%; Pred. No. 73;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 52 SSPPPPC 58

RESULT 48
ADI42793
ID ADI42793 standard; protein; 223 AA.
XX AC ADI42793;
XX DT 22-APR-2004 (first entry)
XX DE Plant transcription factor #456.
XX KW transgenic; plant; enhanced tolerance to abiotic stress;
KW glyphosphate tolerance; hormone sensitivity; disease resistance;
KW sugar sensing; flowering; flower structure; stem bifurcation;
KW branching pattern; apical dominance; trichome; stem morphology;
KW root growth; root hair; seed development; cell proliferation;
KW cell differentiation; premature senescence; necrosis; plant size;
KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
KW plant anthocyanin; light response; shade avoidance; bioinformatic;
KW transcription factor; gene; ds.
XX OS Oryza sativa.
XX PN US2004019927-A1.
XX PD 29-JAN-2004.
XX PF 25-FEB-2003; 2003US-00374780.
XX PR 18-APR-2001; 2001US-00837944.
XX PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAKE/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
XX PI Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V;
PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE;
PI Pilgrim ML, Dubell AN, Pineda O, Yu G;
XX WPI; 2004-132245/13.
XX CC New transgenic plant comprising a recombinant polynucleotide of any one
CC of more than 500 nucleotide sequences, useful in bioinformatic search
CC methods.
XX PS Claim 1; SEQ ID NO 1256; 435pp; English.
XX CC The invention describes a transgenic plant comprising a recombinant
CC polynucleotide of any one of more than 500 nucleotide sequences fully
CC defined in the specification or its complement. The method of the
CC invention can be used to produce a plant having altered traits such as:
CC enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone
CC sensitivity; disease resistance; sugar sensing; early or late flowering;
CC altered flower structure, change in stem bifurcations, altered branching
CC pattern, reduced apical dominance, reduced trichome density; lack of

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CC trichomes; reduced ectopic trichome development; altered trichome  
 CC development; increase in trichome number; altered stem morphology;  
 CC increased root growth; increased root hairs; altered seed development;  
 CC altered cell proliferation or cell differentiation; rapid development;  
 CC premature senescence; increased necrosis; increase in seedling or plant  
 CC size; decreased plant size; leaf morphology; seed morphology; seed  
 CC biochemistry; increase in root anthocyanins; increase in plant  
 CC anthocyanins, or alteration in light response or shade avoidance. The  
 CC transgenic plant, polynucleotides and polypeptides are useful in  
 CC bioinformatic search methods. This is the amino acid sequence of a plant  
 CC transcription factor, and an orthologue of Arabidopsis thaliana  
 CC transcription factors isolated in the invention, that can be used in the  
 CC creation of a transgenic plant with altered traits.

XX SQ Sequence 223 AA;

Query Match 100.0%; Score 45; DB 8; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
 Db 194 SSPPPPC 200  
 |||||

# RESULT 49

AEA27327  
 ID AEA27327 standard; protein; 422 AA.

XX AC AEA27327;

XX DT 28-JUL-2005 (first entry)

XX DE Stress tolerant plant-related transcription factor protein #1168.

XX KW transcription factor; transgenic plant; agriculture; drought resistance;  
 XX stress tolerance.

XX OS Oryza sativa.

XX PN WO2005047516-A2.

XX PD 26-MAY-2005.

XX PF 12-NOV-2004; 2004WO-US037584.

XX PR 13-NOV-2003; 2003US-00714887.

XX PR 05-DEC-2003; 2003US-0527658P.

XX PR 05-FEB-2004; 2004US-0542928P.

XX PA (MEND-) MENDEL BIOTECHNOLOGY INC.

XX PI Heard JE, Riechmann JL, Creelman RA, Ratcliffe OJ, Canales RD;

XX PI Repetti P, Kumimoto RW, Gutterman NI, Reuber TL, Pineda O;

XX PI Sherman BK, Morrison TA, Keddle JS, Jiang C, Century KS, Adam L;

XX PI Zhang JZ, Hempel PD, Libby JM;

XX DR WPI; 2005-372386/38.

XX PT New transgenic plants for producing commercially or agriculturally useful  
 PT plants having improved tolerance to drought, shade and low nitrogen  
 PT conditions.

XX PS Disclosure; Fig 14; 407pp; English.

XX CC This invention relates to a novel plant transcription factor  
 CC polypeptides, the DNA sequences which encode them and their use in  
 CC creating transgenic plants. The transgenic plant and methods are useful  
 CC for producing commercially or agriculturally useful plants having  
 CC improved tolerance to drought, shade and low nitrogen conditions when  
 CC compared to wild-type reference plants. The present sequence is that of a  
 CC plant transcription factor protein which was used during the development  
 CC of the transgenic plants of the invention.

XX SQ Sequence 422 AA;

Query Match 100.0%; Score 45; DB 9; Length 422;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
 Db 393 SSPPPPC 399  
 |||||

# RESULT 50

AEA26381  
 ID AEA26381 standard; protein; 422 AA.

XX AC AEA26381;

XX DT 28-JUL-2005 (first entry)

XX DE Stress tolerant plant-related transcription factor protein SeqID222.

XX KW transcription factor; transgenic plant; agriculture; drought resistance;  
 XX stress tolerance.

XX OS Oryza sativa.

XX PN WO2005047516-A2.

XX PD 26-MAY-2005.

XX PF 12-NOV-2004; 2004WO-US037584.

XX PR 13-NOV-2003; 2003US-00714887.

XX PR 05-DEC-2003; 2003US-0527658P.

XX PR 05-FEB-2004; 2004US-0542928P.

XX PA (MEND-) MENDEL BIOTECHNOLOGY INC.

XX PI Heard JE, Riechmann JL, Creelman RA, Ratcliffe OJ, Canales RD;

XX PI Repetti P, Kumimoto RW, Gutterman NI, Reuber TL, Pineda O;

XX PI Sherman BK, Morrison TA, Keddle JS, Jiang C, Century KS, Adam L;

XX PI Zhang JZ, Hempel PD, Libby JM;

XX DR WPI; 2005-372386/38.

XX DR N-PSDB; AEA26380.

XX PT New transgenic plants for producing commercially or agriculturally useful  
 PT plants having improved tolerance to drought, shade and low nitrogen  
 PT conditions.

XX PS Example 8; SEQ ID NO 222; 407pp; English.

XX CC This invention relates to a novel plant transcription factor  
 CC polypeptides, the DNA sequences which encode them and their use in  
 CC creating transgenic plants. The transgenic plant and methods are useful  
 CC for producing commercially or agriculturally useful plants having  
 CC improved tolerance to drought, shade and low nitrogen conditions when  
 CC compared to wild-type reference plants. The present sequence is that of a  
 CC plant transcription factor protein which was used during the development  
 CC of the transgenic plants of the invention.

XX SQ Sequence 422 AA;

Query Match 100.0%; Score 45; DB 9; Length 422;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
 Db 393 SSPPPPC 399  
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Search completed: January 3, 2006, 09:19:40  
Job time : 101.667 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:20:09 ; Search time 72.8571 Seconds  
(without alignments)  
51.614 Million cell updates/sec

Title: US-10-759-832-7  
Perfect score: 53  
Sequence: 1 EGPWLEEE 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published Applications AA\_Main:\*

- 1: /cgm2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgm2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgm2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgm2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgm2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgm2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	9	4	US-10-314-057-7
2	53	100.0	9	4	US-10-613-377A-7
3	53	100.0	9	5	US-10-759-832-7
4	53	100.0	9	5	US-10-762-226-7
5	53	100.0	9	5	US-10-829-137-1
6	53	100.0	9	6	US-11-036-690-7
7	53	100.0	10	4	US-10-613-377A-8
8	53	100.0	10	5	US-10-759-832-8
9	53	100.0	10	6	US-11-036-690-8
10	53	100.0	12	5	US-10-762-226-6
11	53	100.0	16	5	US-10-762-226-1
12	53	100.0	17	4	US-10-197-954-60
13	53	100.0	17	4	US-10-613-377A-1
14	53	100.0	17	4	US-10-613-377A-18
15	53	100.0	17	5	US-10-372-917-13
16	53	100.0	17	5	US-10-759-832-1
17	53	100.0	17	5	US-10-759-832-18
18	53	100.0	17	5	US-10-760-085-60
19	53	100.0	17	5	US-10-813-336-1
20	53	100.0	17	5	US-10-206-081-2
21	53	100.0	17	5	US-10-770-712-61
22	53	100.0	17	6	US-11-036-690-1
23	53	100.0	17	6	US-11-036-690-18
24	53	100.0	17	6	US-11-066-697-422
25	53	100.0	18	4	US-10-613-377A-2
26	53	100.0	18	5	US-10-759-832-2
27	53	100.0	18	5	US-10-813-336-2

28	53	100.0	18	6	US-11-036-690-2	Sequence 2, Appli
29	53	100.0	34	5	US-10-813-336-3	Sequence 3, Appli
30	53	100.0	35	5	US-10-813-336-4	Sequence 4, Appli
31	50	94.3	17	5	US-10-839-017-3	Sequence 3, Appli
32	50	94.3	33	4	US-10-360-101-170	Sequence 170, App
33	50	94.3	33	5	US-10-728-082-1	Sequence 1, Appli
34	50	94.3	33	5	US-10-728-082-2	Sequence 2, Appli
35	50	94.3	33	5	US-10-719-450-1	Sequence 1, Appli
36	50	94.3	33	5	US-10-719-450-2	Sequence 2, Appli
37	50	94.3	33	5	US-10-505-239-5	Sequence 5, Appli
38	50	94.3	34	4	US-10-104-607B-5	Sequence 5, Appli
39	50	94.3	34	5	US-10-408-765A-196	Sequence 196, App
40	50	94.3	34	5	US-10-770-712-62	Sequence 62, Appl
41	50	94.3	34	6	US-11-066-697-423	Sequence 423, App
42	49	92.5	19	4	US-10-244-324A-1	Sequence 1, Appli
43	49	92.5	19	4	US-10-394-322A-70	Sequence 70, Appl
44	49	92.5	19	5	US-10-931-348-3	Sequence 3, Appli
45	48	90.6	8	4	US-10-613-377A-6	Sequence 6, Appli
46	48	90.6	8	5	US-10-759-832-6	Sequence 6, Appli
47	48	90.6	8	6	US-11-036-690-6	Sequence 6, Appli
48	48	90.6	16	4	US-10-192-257-4	Sequence 4, Appli
49	48	90.6	16	5	US-10-728-082-3	Sequence 3, Appli
50	48	90.6	16	5	US-10-728-082-4	Sequence 4, Appli
51	48	90.6	16	5	US-10-719-450-3	Sequence 3, Appli
52	48	90.6	16	5	US-10-719-450-4	Sequence 4, Appli
53	48	90.6	17	4	US-10-104-607B-4	Sequence 4, Appli
54	46	86.8	18	4	US-10-227-012-2	Sequence 2, Appli
55	45	84.9	238	3	US-09-934-455-198	Sequence 198, App
56	45	84.9	238	4	US-10-225-066A-60	Sequence 60, Appl
57	45	84.9	238	4	US-10-302-267-140	Sequence 140, App
58	45	84.9	238	4	US-10-374-780A-2568	Sequence 2568, AD
59	45	84.9	238	4	US-10-412-699B-828	Sequence 828, App
60	45	84.9	238	5	US-10-225-066A-60	Sequence 60, Appl
61	44	83.0	14	5	US-10-762-226-2	Sequence 2, Appli
62	43	81.1	7	4	US-10-613-377A-5	Sequence 5, Appli
63	43	81.1	7	5	US-10-759-832-5	Sequence 5, Appli
64	43	81.1	7	6	US-11-036-690-5	Sequence 5, Appli
65	43	81.1	335	5	US-10-732-923-3821	Sequence 3821, Ap
66	42	79.2	113	4	US-10-424-599-188431	Sequence 188431, Ap
67	42	79.2	330	5	US-10-732-923-3807	Sequence 3807, Ap
68	42	79.2	370	5	US-10-732-923-3808	Sequence 3808, Ap
69	41	77.4	68	4	US-10-767-701-55510	Sequence 55510, A
70	41	77.4	91	4	US-10-424-599-159478	Sequence 159478, A
71	41	77.4	243	4	US-10-425-115-306189	Sequence 306189, A
72	41	77.4	260	4	US-10-424-599-164163	Sequence 164163, A
73	41	77.4	260	4	US-10-424-599-231485	Sequence 231485, A
74	41	77.4	262	4	US-10-425-114-54675	Sequence 54675, A
75	41	77.4	273	3	US-09-533-029-40	Sequence 40, Appl
76	41	77.4	273	4	US-10-412-699B-162	Sequence 162, App
77	41	77.4	340	4	US-10-437-963-150943	Sequence 150943, A
78	41	77.4	368	4	US-10-425-114-73060	Sequence 73060, A
79	40	75.5	182	3	US-09-764-864-1205	Sequence 1205, Ap
80	40	75.5	310	4	US-10-389-566-1005	Sequence 1005, Ap
81	40	75.5	349	4	US-10-278-173-138	Sequence 138, App
82	40	75.5	349	4	US-10-278-536-114	Sequence 114, App
83	40	75.5	349	4	US-10-412-699B-134	Sequence 134, App
84	40	75.5	612	4	US-10-087-192-312	Sequence 312, App
85	39	73.6	98	4	US-10-425-115-210995	Sequence 210995, A
86	39	73.6	336	4	US-10-264-049-2878	Sequence 2878, Ap
87	39	73.6	381	4	US-10-437-963-105149	Sequence 105149, A
88	39	73.6	392	4	US-10-437-963-150925	Sequence 150925, A
89	39	73.6	496	4	US-10-050-200-9	Sequence 9, Appli
90	39	73.6	492	6	US-11-012-797A-27	Sequence 27, Appl
91	39	73.6	525	4	US-10-411-010-28	Sequence 28, Appl
92	39	73.6	525	5	US-10-411-010-28	Sequence 28, Appl
93	39	73.6	525	5	US-10-723-860-604	Sequence 604, App
94	39	73.6	525	5	US-10-953-264-27	Sequence 27, Appl
95	39	73.6	525	5	US-10-953-264-28	Sequence 28, Appl
96	39	73.6	525	5	US-10-370-715B-80	Sequence 80, Appl
97	39	73.6	551	4	US-10-159-257A-202	Sequence 202, App
98	39	73.6	567	4	US-10-358-283-10	Sequence 10, Appl
99	39	73.6	619	4	US-10-282-122A-73477	Sequence 73477, A
100	39	73.6	628	4	US-10-358-283-8	Sequence 8, Appli

101	39	73.6	718	4	US-10-437-963-179902	Sequence 179902,	174	38	71.7	325	4	US-10-225-066A-276	Sequence 276, App
102	39	73.6	752	4	US-10-358-283-6	Sequence 6, Appli	175	38	71.7	325	4	US-10-374-780A-2564	Sequence 2564, Ap
103	39	73.6	753	4	US-10-358-283-4	Sequence 4, Appli	176	38	71.7	325	4	US-10-389-596B-1251	Sequence 1251, Ap
104	39	73.6	763	4	US-10-358-283-15	Sequence 15, Appli	177	38	71.7	325	4	US-10-412-699B-818	Sequence 818, App
105	39	73.6	880	6	US-11-097-143-11949	Sequence 41949, A	178	38	71.7	325	5	US-10-225-066A-276	Sequence 276, App
106	39	73.6	909	4	US-10-437-963-105153	Sequence 105153,	179	38	71.7	329	4	US-10-282-122A-49060	Sequence 49060, A
107	39	73.6	930	4	US-10-247-685-15	Sequence 15, Appli	180	38	71.7	340	4	US-10-425-114-66503	Sequence 66503, A
108	39	73.6	930	4	US-10-358-283-2	Sequence 2, Appli	181	38	71.7	368	4	US-10-425-115-189929	Sequence 189929,
109	39	73.6	930	4	US-10-358-283-30	Sequence 30, Appli	182	38	71.7	369	3	US-09-838-561-8	Sequence 8, Appli
110	39	73.6	930	4	US-10-788-792-246	Sequence 246, App	183	38	71.7	369	3	US-09-816-760-8	Sequence 8, Appli
111	39	73.6	930	5	US-10-723-860-417	Sequence 417, App	184	38	71.7	369	3	US-09-356-993-4	Sequence 4, Appli
112	39	73.6	960	4	US-10-389-566-2373	Sequence 2373, Ap	185	38	71.7	369	4	US-10-303-664A-42	Sequence 42, Appli
113	39	73.6	1108	4	US-10-389-566-1377	Sequence 1377, Ap	186	38	71.7	369	4	US-10-172-585-8	Sequence 8, Appli
114	39	73.6	1108	4	US-10-389-566-1650	Sequence 1650, Ap	187	38	71.7	369	4	US-10-291-261-398	Sequence 398, App
115	39	73.6	1413	4	US-10-288-798-24	Sequence 24, Appli	188	38	71.7	369	4	US-10-606-366-4	Sequence 4, Appli
116	39	73.6	1413	4	US-10-362-892-24	Sequence 24, Appli	189	38	71.7	369	4	US-10-664-506-8	Sequence 8, Appli
117	38	71.7	6	4	US-10-613-377A-4	Sequence 4, Appli	190	38	71.7	369	5	US-10-737-450-126	Sequence 126, App
118	38	71.7	6	5	US-10-759-832-4	Sequence 4, Appli	191	38	71.7	373	4	US-10-243-552-398	Sequence 398, App
119	38	71.7	6	5	US-10-813-836-5	Sequence 5, Appli	192	38	71.7	374	4	US-10-425-114-42001	Sequence 42001, A
120	38	71.7	6	6	US-11-036-690-4	Sequence 4, Appli	193	38	71.7	414	5	US-10-732-923-2967	Sequence 2967, Ap
121	38	71.7	12	4	US-10-314-057-1	Sequence 1, Appli	194	38	71.7	501	4	US-10-124-498-2	Sequence 2, Appli
122	38	71.7	12	5	US-10-762-226-3	Sequence 3, Appli	195	38	71.7	501	4	US-10-066-521-2	Sequence 2, Appli
123	38	71.7	12	5	US-10-829-137-5	Sequence 5, Appli	196	38	71.7	560	4	US-10-424-599-160400	Sequence 160400, A
124	38	71.7	44	5	US-10-856-499-2298	Sequence 2298, Ap	197	38	71.7	581	4	US-10-425-114-71817	Sequence 171817, A
125	38	71.7	49	5	US-10-856-499-2131	Sequence 2131, Ap	198	38	71.7	587	4	US-10-437-963-135215	Sequence 135215,
126	38	71.7	62	4	US-10-021-811-16	Sequence 16, Appli	199	38	71.7	593	4	US-10-437-963-193037	Sequence 193037,
127	38	71.7	62	4	US-10-659-869-16	Sequence 16, Appli	200	38	71.7	894	4	US-10-369-493-6531	Sequence 6531, Ap
128	38	71.7	76	5	US-10-856-499-2123	Sequence 2123, Ap	201	38	71.7	920	4	US-10-369-493-6532	Sequence 6532, Ap
129	38	71.7	85	4	US-10-437-963-157514	Sequence 157514, A	202	38	71.7	931	5	US-10-794-342-14	Sequence 14, Appli
130	38	71.7	90	4	US-10-767-701-45826	Sequence 45826, A	203	38	71.7	1291	4	US-10-156-761-14161	Sequence 14161, A
131	38	71.7	94	4	US-10-425-115-349437	Sequence 349437, A	204	38	71.7	1336	4	US-10-437-963-173565	Sequence 173565,
132	38	71.7	94	5	US-10-814-492-28	Sequence 28, Appli	205	37	69.8	50	3	US-09-757-049A-4	Sequence 4, Appli
133	38	71.7	99	4	US-10-424-599-145051	Sequence 145051, A	206	37	69.8	50	3	US-09-757-049A-5	Sequence 5, Appli
134	38	71.7	105	4	US-10-767-701-58026	Sequence 58026, A	207	37	69.8	50	3	US-09-757-049A-6	Sequence 6, Appli
135	38	71.7	108	4	US-10-425-115-321444	Sequence 321444, A	208	37	69.8	52	3	US-09-912-962-13	Sequence 13, Appli
136	38	71.7	146	4	US-10-158-057-277	Sequence 277, App	209	37	69.8	52	3	US-09-912-962-14	Sequence 14, Appli
137	38	71.7	152	4	US-10-424-599-160367	Sequence 160367, A	210	37	69.8	111	4	US-10-437-963-107958	Sequence 107958,
138	38	71.7	179	4	US-10-021-811-4	Sequence 4, Appli	211	37	69.8	122	4	US-10-425-115-207784	Sequence 207784,
139	38	71.7	179	4	US-10-659-869-4	Sequence 4, Appli	212	37	69.8	146	4	US-10-156-761-10707	Sequence 10707, A
140	38	71.7	190	4	US-10-437-963-194999	Sequence 194999, A	213	37	69.8	146	4	US-10-767-701-35665	Sequence 35665, A
141	38	71.7	196	4	US-10-094-749-3146	Sequence 3146, Ap	214	37	69.8	151	4	US-10-767-701-34938	Sequence 34938, A
142	38	71.7	203	4	US-10-425-114-53773	Sequence 53773, A	215	37	69.8	156	3	US-09-892-398-4	Sequence 4, Appli
143	38	71.7	205	4	US-10-389-566-5071	Sequence 5071, App	216	37	69.8	167	4	US-10-892-398-46	Sequence 46, Appli
144	38	71.7	205	4	US-10-425-115-336396	Sequence 336396, A	217	37	69.8	169	4	US-10-156-761-182268	Sequence 182268,
145	38	71.7	217	4	US-10-425-115-217492	Sequence 217492, A	218	37	69.8	206	4	US-10-021-811-34	Sequence 34, Appli
146	38	71.7	219	4	US-10-437-963-167370	Sequence 167370, A	219	37	69.8	206	4	US-10-659-869-34	Sequence 34, Appli
147	38	71.7	221	4	US-10-021-811-14	Sequence 14, Appli	220	37	69.8	227	4	US-10-437-963-150058	Sequence 150058,
148	38	71.7	221	4	US-10-659-869-14	Sequence 14, Appli	221	37	69.8	246	4	US-10-424-599-162351	Sequence 162351,
149	38	71.7	223	4	US-10-425-115-318215	Sequence 318215, A	222	37	69.8	265	5	US-10-450-763-46754	Sequence 46754, A
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151	38	71.7	232	4	US-10-425-114-48181	Sequence 48181, A	224	37	69.8	274	5	US-10-450-763-52713	Sequence 52713, A
152	38	71.7	232	4	US-10-425-114-50622	Sequence 50622, A	225	37	69.8	278	5	US-10-450-763-51810	Sequence 51810, A
153	38	71.7	234	4	US-10-412-699B-176	Sequence 176, App	226	37	69.8	292	4	US-10-424-599-205655	Sequence 205655,
154	38	71.7	237	4	US-10-424-599-279181	Sequence 279181, A	227	37	69.8	301	5	US-10-732-923-2785	Sequence 2785, A
155	38	71.7	237	4	US-10-425-115-246868	Sequence 246868, A	228	37	69.8	303	4	US-10-156-761-12125	Sequence 12125, A
156	38	71.7	242	4	US-10-425-115-318204	Sequence 318204, A	229	37	69.8	304	3	US-09-934-455-64	Sequence 64, Appli
157	38	71.7	247	4	US-10-424-599-272398	Sequence 272398, A	230	37	69.8	304	4	US-10-225-068-188	Sequence 188, App
158	38	71.7	258	4	US-10-425-114-39775	Sequence 39775, A	231	37	69.8	304	4	US-10-225-068A-772	Sequence 772, App
159	38	71.7	256	5	US-10-732-923-23334	Sequence 23334, A	232	37	69.8	304	4	US-10-374-780A-2256	Sequence 2256, Ap
160	38	71.7	258	4	US-10-225-066A-344	Sequence 344, App	233	37	69.8	304	4	US-10-412-699B-118	Sequence 118, App
161	38	71.7	258	4	US-10-374-780A-2696	Sequence 2696, Ap	234	37	69.8	304	5	US-10-225-068A-188	Sequence 188, App
162	38	71.7	258	5	US-10-225-066A-344	Sequence 344, App	235	37	69.8	304	5	US-10-225-068A-772	Sequence 772, App
163	38	71.7	263	4	US-10-424-599-279183	Sequence 279183, A	236	37	69.8	329	5	US-10-732-923-3798	Sequence 3798, Ap
164	38	71.7	264	4	US-10-425-114-44078	Sequence 44078, A	237	37	69.8	336	5	US-10-278-536-206	Sequence 3616, Ap
165	38	71.7	278	4	US-10-437-963-142633	Sequence 142633, A	238	37	69.8	367	4	US-10-374-780A-1968	Sequence 1968, Ap
166	38	71.7	280	4	US-10-437-963-194997	Sequence 194997, A	239	37	69.8	367	4	US-10-412-699B-132	Sequence 132, App
167	38	71.7	285	4	US-10-425-115-318282	Sequence 318282, A	240	37	69.8	367	4	US-10-412-699B-132	Sequence 132, App
168	38	71.7	300	4	US-10-424-599-272400	Sequence 272400, A	241	37	69.8	398	4	US-10-369-493-21605	Sequence 21605, A
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170	38	71.7	317	4	US-10-168-274-20	Sequence 20, Appli	243	37	69.8	691	6	US-11-097-143-5805	Sequence 5805, Ap
171	38	71.7	317	4	US-10-606-366-2	Sequence 2, Appli	244	37	69.8	700	4	US-10-171-311-160	Sequence 160, App
172	38	71.7	318	4	US-10-052-201B-284	Sequence 284, App	245	37	69.8	700	4	US-10-301-822-141	Sequence 141, App
173	38	71.7	318	4	US-10-425-115-321447	Sequence 321447, A	246	37	69.8	700	5	US-10-751-736-103	Sequence 103, App

247	37	69.8	700	5	US-10-645-756-36	Sequence 36, Appl	320	67.9	853	4	US-10-257-904-3	Sequence 3, Appl
248	37	69.8	729	4	US-10-123-731-2	Sequence 2, Appl	321	67.9	869	4	US-10-104-047-2532	Sequence 2532, Ap
249	37	69.8	729	4	US-10-232-759A-20	Sequence 20, Appl	322	67.9	884	4	US-10-250-889-79	Sequence 79, Appl
250	37	69.8	761	5	US-10-756-149-5087	Sequence 5087, Ap	323	67.9	993	4	US-10-004-551-14	Sequence 14, Appl
251	37	69.8	769	5	US-10-450-763-51813	Sequence 51813, A	324	67.9	993	5	US-10-618-281-9	Sequence 9, Appl
252	37	69.8	1431	5	US-10-840-512-218	Sequence 218, App	325	67.9	993	6	US-11-045-029-14	Sequence 14, Appl
253	36	67.9	99	3	US-09-828-648-7	Sequence 7, Appl	326	67.9	994	4	US-10-004-551-16	Sequence 16, Appl
254	36	67.9	99	5	US-10-732-706-7	Sequence 7, Appl	327	67.9	994	4	US-10-312-354-2	Sequence 2, Appl
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262	36	67.9	193	4	US-10-282-122A-77500	Sequence 77500, A	335	67.9	1421	4	US-10-437-963-149400	Sequence 149400,
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267	36	67.9	261	4	US-10-236-392-158	Sequence 158, App	340	67.9	53	5	US-10-856-499-2353	Sequence 2353, Ap
268	36	67.9	261	4	US-10-236-392-170	Sequence 170, App	341	67.9	45	5	US-10-424-599-224553	Sequence 224553,
269	36	67.9	261	4	US-10-236-392-172	Sequence 172, App	342	67.9	61	5	US-10-856-499-2308	Sequence 2308, Ap
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271	36	67.9	266	4	US-10-424-599-201840	Sequence 201840,	344	67.9	61	5	US-10-856-499-2324	Sequence 2324, Ap
272	36	67.9	271	5	US-10-481-032A-318	Sequence 318, App	345	67.9	66	5	US-10-856-499-2359	Sequence 2359, Ap
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275	36	67.9	286	5	US-10-450-763-38273	Sequence 38273, A	348	67.9	67	4	US-10-425-115-278099	Sequence 278099,
276	36	67.9	307	4	US-10-156-761-11788	Sequence 11788, A	349	67.9	73	4	US-10-425-115-236892	Sequence 236892,
277	36	67.9	326	4	US-10-437-963-139417	Sequence 139417,	350	67.9	74	4	US-10-425-115-304051	Sequence 304051,
278	36	67.9	358	4	US-10-322-281-397	Sequence 397, App	351	67.9	75	5	US-10-450-763-47498	Sequence 47498, A
279	36	67.9	361	4	US-10-166-225A-108	Sequence 108, App	352	67.9	76	5	US-10-856-499-845	Sequence 845, App
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285	36	67.9	393	4	US-10-225-066A-774	Sequence 774, App	358	67.9	86	4	US-10-029-386-28547	Sequence 28547, A
286	36	67.9	393	4	US-10-374-780A-2262	Sequence 2262, Ap	359	67.9	87	4	US-10-424-599-253567	Sequence 253567,
287	36	67.9	393	5	US-10-225-066A-774	Sequence 774, App	360	67.9	88	4	US-10-424-599-269558	Sequence 269558,
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289	36	67.9	525	4	US-10-004-551-18	Sequence 18, Appl	362	67.9	90	4	US-10-021-811-52	Sequence 52, Appl
290	36	67.9	525	4	US-10-004-551-20	Sequence 20, Appl	363	67.9	90	4	US-10-659-869-52	Sequence 52, Appl
291	36	67.9	525	4	US-10-004-551-22	Sequence 22, Appl	364	67.9	94	4	US-10-424-599-208344	Sequence 208344,
292	36	67.9	525	4	US-10-236-392-160	Sequence 160, App	365	67.9	95	4	US-10-425-115-366945	Sequence 366945,
293	36	67.9	525	4	US-10-236-392-162	Sequence 162, App	366	67.9	102	4	US-10-437-963-110146	Sequence 110146,
294	36	67.9	525	4	US-10-236-392-164	Sequence 164, App	367	67.9	102	5	US-10-856-499-872	Sequence 872, App
295	36	67.9	525	6	US-11-045-029-18	Sequence 18, Appl	368	67.9	103	4	US-10-437-963-133135	Sequence 133135,
296	36	67.9	525	6	US-11-045-029-20	Sequence 20, Appl	369	67.9	103	4	US-10-425-115-233889	Sequence 233889,
297	36	67.9	525	6	US-11-045-029-22	Sequence 22, Appl	370	67.9	106	4	US-10-424-599-152188	Sequence 152188,
298	36	67.9	526	4	US-10-004-551-24	Sequence 24, Appl	371	67.9	107	4	US-10-424-599-269270	Sequence 269270,
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303	36	67.9	543	4	US-10-236-392-168	Sequence 168, App	376	67.9	117	4	US-10-437-963-195413	Sequence 195413,
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307	36	67.9	776	4	US-10-225-066A-1060	Sequence 1060, Ap	380	67.9	124	4	US-10-659-869-62	Sequence 62, Appl
308	36	67.9	776	4	US-10-374-780A-2392	Sequence 2392, Ap	381	67.9	124	4	US-10-424-599-160573	Sequence 160573,
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312	36	67.9	811	4	US-10-144-194A-26	Sequence 26, Appl	385	67.9	127	5	US-10-856-499-2109	Sequence 2109, Ap
313	36	67.9	811	4	US-10-144-194A-98	Sequence 98, Appl	386	67.9	130	5	US-10-856-499-2109	Sequence 2109, Ap
314	36	67.9	811	5	US-10-491-566-28	Sequence 28, Appl	387	67.9	131	4	US-10-425-115-305358	Sequence 305358,
315	36	67.9	815	5	US-10-491-566-98	Sequence 98, Appl	388	67.9	131	4	US-10-278-173-134	Sequence 134, App
316	36	67.9	816	5	US-10-450-763-34394	Sequence 34394, A	389	67.9	136	4	US-10-412-699B-126	Sequence 126, App
317	36	67.9	829	5	US-10-450-763-56142	Sequence 56142, A	390	67.9	145	4	US-10-767-701-35225	Sequence 35225, A
318	36	67.9	829	4	US-10-257-904-4	Sequence 4, Appl	391	67.9	146	5	US-10-856-499-2110	Sequence 2110, Ap
319	36	67.9	839	4	US-10-437-963-165045	Sequence 165045,	392	67.9	149	3	US-09-764-864-1171	Sequence 1171, Ap
									149	4	US-10-437-963-177630	Sequence 177630,

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394	35	66.0	154	4	US-10-424-599-260171	Sequence 260171, A	467	35	66.0	310	4	US-10-437-963-120855	Sequence 120855, A
395	35	66.0	156	4	US-10-437-963-133682	Sequence 133682, A	468	35	66.0	311	4	US-10-437-963-158770	Sequence 158770, A
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399	35	66.0	164	4	US-10-424-599-187123	Sequence 187123, A	472	35	66.0	317	4	US-10-425-115-303455	Sequence 303455, A
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401	35	66.0	171	4	US-10-425-115-276102	Sequence 276102, A	474	35	66.0	319	4	US-10-425-114-40269	Sequence 40269, A
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403	35	66.0	190	4	US-10-424-599-152186	Sequence 152186, A	476	35	66.0	320	4	US-10-437-963-104877	Sequence 104877, A
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405	35	66.0	196	4	US-10-425-114-40172	Sequence 40172, A	478	35	66.0	321	4	US-10-389-566-1243	Sequence 1243, App
406	35	66.0	196	4	US-10-437-963-185304	Sequence 185304, A	479	35	66.0	321	4	US-10-412-699B-1074	Sequence 1074, App
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419	35	66.0	257	4	US-10-437-963-122749	Sequence 122749, A	492	35	66.0	324	4	US-10-032-201B-273	Sequence 30, Appl
420	35	66.0	261	4	US-10-225-066A-232	Sequence 232, App	493	35	66.0	324	4	US-10-225-067-30	Sequence 273, App
421	35	66.0	261	4	US-10-374-780A-264	Sequence 264, App	494	35	66.0	324	4	US-10-374-780A-2582	Sequence 2582, App
422	35	66.0	261	5	US-10-225-066A-232	Sequence 232, App	495	35	66.0	324	4	US-10-412-699B-854	Sequence 854, App
423	35	66.0	264	3	US-09-443-704-16	Sequence 16, Appl	496	35	66.0	324	5	US-10-495-918-132	Sequence 132, App
424	35	66.0	264	4	US-10-008-118A-16	Sequence 16, Appl	497	35	66.0	326	5	US-09-934-455-364	Sequence 364, App
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426	35	66.0	268	4	US-10-425-114-71542	Sequence 71542, A	499	35	66.0	328	4	US-10-296-115-1181	Sequence 1181, App
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430	35	66.0	275	4	US-10-424-599-211312	Sequence 211312, A	503	35	66.0	332	4	US-10-325-068-6	Sequence 6, Appl
431	35	66.0	276	4	US-10-250-889-71	Sequence 71, Appl	504	35	66.0	332	4	US-10-374-780A-46	Sequence 46, Appl
432	35	66.0	276	4	US-10-425-115-287376	Sequence 287376, A	505	35	66.0	332	4	US-10-659-869-54	Sequence 54, Appl
433	35	66.0	277	4	US-10-374-780A-569	Sequence 569, App	506	35	66.0	332	4	US-10-412-699B-184	Sequence 184, App
434	35	66.0	279	4	US-10-425-114-43132	Sequence 43132, A	507	35	66.0	332	4	US-10-425-115-205557	Sequence 205557, A
435	35	66.0	279	4	US-10-437-963-148430	Sequence 148430, A	508	35	66.0	332	5	US-10-225-068-6	Sequence 6, Appl
436	35	66.0	280	4	US-10-437-963-131634	Sequence 131634, A	509	35	66.0	334	5	US-10-424-599-185737	Sequence 185737, A
437	35	66.0	282	4	US-10-295-403-54	Sequence 54, Appl	510	35	66.0	334	5	US-10-739-930-8712	Sequence 8712, App
438	35	66.0	282	4	US-10-225-066A-636	Sequence 636, App	511	35	66.0	335	4	US-10-295-403-58	Sequence 58, Appl
439	35	66.0	282	4	US-10-302-867-148	Sequence 148, App	512	35	66.0	335	4	US-10-225-066A-222	Sequence 222, App
440	35	66.0	282	4	US-10-374-780A-2572	Sequence 2572, App	513	35	66.0	335	4	US-10-374-780A-2066	Sequence 2066, App
441	35	66.0	282	4	US-10-412-699B-460	Sequence 460, App	514	35	66.0	335	4	US-10-412-699B-628	Sequence 628, App
442	35	66.0	282	4	US-10-412-699B-838	Sequence 838, App	515	35	66.0	335	4	US-10-412-699B-1820	Sequence 1820, App
443	35	66.0	282	5	US-10-225-066A-636	Sequence 636, App	516	35	66.0	335	5	US-10-225-066A-222	Sequence 222, App
444	35	66.0	284	4	US-10-437-963-141701	Sequence 141701, A	517	35	66.0	336	4	US-10-424-599-162163	Sequence 162163, A
445	35	66.0	286	3	US-09-934-455-510	Sequence 510, App	518	35	66.0	336	4	US-10-424-599-233789	Sequence 233789, A
446	35	66.0	286	4	US-10-225-066A-1094	Sequence 1094, App	519	35	66.0	337	4	US-10-424-599-253566	Sequence 253566, A
447	35	66.0	286	4	US-10-374-780A-386	Sequence 386, App	520	35	66.0	337	4	US-10-425-114-39945	Sequence 39945, A
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449	35	66.0	287	4	US-10-437-963-172274	Sequence 172274, A	522	35	66.0	341	4	US-10-374-780A-598	Sequence 598, App
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453	35	66.0	299	4	US-10-302-267-138	Sequence 138, App	526	35	66.0	341	4	US-10-437-963-106646	Sequence 106646, A
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457	35	66.0	302	4	US-10-008-118A-18	Sequence 18, Appl	530	35	66.0	343	4	US-10-225-066A-1040	Sequence 1040, App
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459	35	66.0	304	4	US-10-425-114-46944	Sequence 46944, A	532	35	66.0	345	4	US-10-739-930-6196	Sequence 6196, App
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462	35	66.0	307	4	US-10-412-699B-1071	Sequence 1071, App	535	35	66.0	347	4	US-10-437-963-192936	Sequence 192936, A
463	35	66.0	307	4	US-10-425-115-33125	Sequence 33125, A	536	35	66.0	348	5	US-10-739-930-8660	Sequence 8660, App
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542	35	66.0	351	4	US-10-413-699B-1804	Sequence 1804, Ap	615	35	66.0	1276	5	US-10-450-763-42165	Sequence 42165, A
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547	35	66.0	365	4	US-10-389-566-1932	Sequence 1932, App	620	35	66.0	41	4	US-10-029-386-30505	Sequence 30505, A
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557	35	66.0	380	4	US-10-424-599-177103	Sequence 177103, A	630	34	64.2	61	5	US-10-856-499-2361	Sequence 2361, Ap
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562	35	66.0	401	4	US-10-369-493-20360	Sequence 20360, Ap	635	34	64.2	77	4	US-10-425-115-305173	Sequence 305173, A
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574	35	66.0	529	3	US-09-712-363-175	Sequence 175, App	647	34	64.2	106	4	US-10-425-114-48446	Sequence 48446, A
575	35	66.0	529	4	US-10-080-170-407	Sequence 407, App	648	34	64.2	109	3	US-09-751-100B-96	Sequence 96, Appl
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580	35	66.0	559	4	US-10-114-270-66	Sequence 66, Appl	653	34	64.2	116	5	US-10-450-763-59940	Sequence 59940, A
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687	34	64.2	184	5	US-10-450-763-57469	Sequence 57469, A	760	34	64.2	249	4	US-10-374-780A-1540	Sequence 1540, Ap
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689	34	64.2	191	4	US-10-425-114-53452	Sequence 53452, A	762	34	64.2	249	4	US-10-412-699B-1634	Sequence 1634, Ap
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695	34	64.2	195	5	US-10-450-763-47734	Sequence 47734, A	768	34	64.2	258	4	US-10-008-186A-4	Sequence 4, Appli
696	34	64.2	204	4	US-10-021-811-32	Sequence 32, Appl	769	34	64.2	258	4	US-10-437-963-192931	Sequence 192931, A
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702	34	64.2	206	4	US-10-021-811-36	Sequence 36, Appl	775	34	64.2	262	4	US-10-437-963-162141	Sequence 162141, A
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706	34	64.2	206	4	US-10-302-267-130	Sequence 130, App	779	34	64.2	266	4	US-10-412-699B-152	Sequence 152, App
707	34	64.2	206	4	US-10-225-067-98	Sequence 98, Appl	780	34	64.2	268	4	US-10-424-599-153045	Sequence 153045, A
708	34	64.2	206	4	US-10-374-780A-258	Sequence 258, App	781	34	64.2	273	3	US-09-533-029-62	Sequence 62, Appl
709	34	64.2	206	4	US-10-424-599-269054	Sequence 269054, A	782	34	64.2	273	4	US-10-278-173-140	Sequence 140, App
710	34	64.2	206	4	US-10-659-869-36	Sequence 36, Appl	783	34	64.2	273	4	US-10-278-536-58	Sequence 58, Appl
711	34	64.2	206	4	US-10-412-699B-842	Sequence 842, App	784	34	64.2	273	4	US-10-225-066A-776	Sequence 776, App
712	34	64.2	206	5	US-10-225-068-2	Sequence 2, Appli	785	34	64.2	273	4	US-10-374-780A-40	Sequence 40, Appl
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## ALIGNMENTS

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US-10-314-057-7  
; Sequence 7, Application US/10314057  
; Publication No. US20030068326A1  
; GENERAL INFORMATION:  
; APPLICANT: Gevas, Philip  
; APPLICANT: Stephen, Grimes  
; APPLICANT: Karr, Stephen  
; APPLICANT: Michaeli, Dov  
; TITLE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux Disease  
; FILE REFERENCE: ACGIUSA  
; CURRENT APPLICATION NUMBER: US/10/314,057  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: US/09/700,378  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: PCT/US99/10734  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 60/085,610  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: human  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: pyroglutamic acid  
US-10-314-057-7

Query Match 100.0%; Score 53; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9  
Db 1 EGPWLEEE 9

RESULT 2  
US-10-613-377A-7  
; Sequence 7, Application US/10613377A  
; Publication No. US20040208920A1

; GENERAL INFORMATION:  
; APPLICANT: Apton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059  
; CURRENT APPLICATION NUMBER: US/10/613,377A  
; CURRENT FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-613-377A-7

Query Match 100.0%; Score 53; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9  
Db 1 EGPWLEEE 9

RESULT 3  
US-10-759-832-7  
; Sequence 7, Application US/10759832  
; Publication No. US20040247661A1  
; GENERAL INFORMATION:  
; APPLICANT: Apton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059CIP  
; CURRENT APPLICATION NUMBER: US/10/759,832  
; CURRENT FILING DATE: 2004-01-15  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 10/613,377  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-759-832-7

Query Match 100.0%; Score 53; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9  
Db 1 EGPWLEEE 9

RESULT 4  
US-10-762-226-7  
; Sequence 7, Application US/10762226  
; Publication No. US20050025770A1  
; GENERAL INFORMATION:

APPLICANT: Gevas, Philip C.  
APPLICANT: Karr, Stephen L.  
APPLICANT: Grimes, Stephen  
APPLICANT: Michaeli, Dov  
APPLICANT: Watson, Susan A.  
TITLE OF INVENTION: Immunological Methods for the Treatment of  
TITLE OF INVENTION: Gastrointestinal Cancer  
FILE REFERENCE: 1102865-0031  
CURRENT APPLICATION NUMBER: US/10/762,226  
CURRENT FILING DATE: 2004-01-20  
PRIOR APPLICATION NUMBER: 60/011,411  
PRIOR FILING DATE: 1996-02-08  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: Pyroglutamic acid residue  
US-10-762-226-7

Query Match 100.0%; Score 53; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
Db 1 EGPWLEEEE 9

RESULT 5  
US-10-829-137-1  
Sequence 1, Application US/10829137  
Publication No. US20050187152A1  
GENERAL INFORMATION:  
APPLICANT: Gevas, Philip  
APPLICANT: Grimes, Stephen  
APPLICANT: Karr, Stephen  
APPLICANT: Michaeli, Dov  
APPLICANT: Watson, Susan  
TITLE OF INVENTION: Prevention and Treatment of Hypergastrinemia  
FILE REFERENCE: AC2USA  
CURRENT APPLICATION NUMBER: US/10/829,137  
CURRENT FILING DATE: 2004-04-21  
PRIOR APPLICATION NUMBER: US/09/700,329  
PRIOR FILING DATE: 2001-02-08  
PRIOR APPLICATION NUMBER: PCT/US99/10751  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/085,714  
PRIOR FILING DATE: 1998-05-15  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 9  
TYPE: PRT  
ORGANISM: human gastrin peptide  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)..(1)  
OTHER INFORMATION: pyroglutamic acid  
US-10-829-137-1

Query Match 100.0%; Score 53; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
Db 1 EGPWLEEEE 9

RESULT 6  
US-11-036-690-7  
Sequence 7, Application US/11036690  
Publication No. US20050169979A1  
GENERAL INFORMATION:  
APPLICANT: Aphton Corporation  
TITLE OF INVENTION: Liposomal Vaccine  
FILE REFERENCE: 1102865-0059CIP  
CURRENT APPLICATION NUMBER: US/11/036,690  
CURRENT FILING DATE: 2005-01-14  
PRIOR APPLICATION NUMBER: 60/394,179  
PRIOR FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: 10/613,377  
PRIOR FILING DATE: 2003-07-03  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 7  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: synthetic  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)..(1)  
OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-11-036-690-7

Query Match 100.0%; Score 53; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
Db 1 EGPWLEEEE 9

RESULT 7  
US-10-613-377A-8  
Sequence 8, Application US/10613377A  
Publication No. US20040208920A1  
GENERAL INFORMATION:  
APPLICANT: Aphton Corporation  
TITLE OF INVENTION: Liposomal Vaccine  
FILE REFERENCE: 1102865-0059  
CURRENT APPLICATION NUMBER: US/10/613,377A  
CURRENT FILING DATE: 2003-07-03  
PRIOR APPLICATION NUMBER: 60/394,179  
PRIOR FILING DATE: 2002-07-03  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 8  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: synthetic  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)..(1)  
OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-613-377A-8

Query Match 100.0%; Score 53; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
Db 1 EGPWLEEEE 9

## RESULT 8

US-10-759-832-8  
; Sequence 8, Application US/10759832  
; Publication No. US20040247661A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059CIP  
; CURRENT APPLICATION NUMBER: US/10/759,832  
; CURRENT FILING DATE: 2004-01-15  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 10/613,377  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-759-832-8

Query Match 100.0%; Score 53; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
Db 1 EGPWLEEEE 9  
|||||

## RESULT 9

US-11-036-690-8  
; Sequence 8, Application US/11036690  
; Publication No. US20050169979A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059CIP  
; CURRENT APPLICATION NUMBER: US/11/036,690  
; CURRENT FILING DATE: 2005-01-14  
; PRIOR FILING DATE: 2005-01-14  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 10/613,377  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-11-036-690-8

Query Match 100.0%; Score 53; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
Db 1 EGPWLEEEE 9  
|||||

## RESULT 10

US-10-762-226-1  
; Sequence 1, Application US/10762226  
; Publication No. US20050025770A1  
; GENERAL INFORMATION:  
; APPLICANT: Gevas, Philip C.  
; APPLICANT: Karr, Stephen L.  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Watson, Susan A.  
; TITLE OF INVENTION: Immunological Methods for the Treatment of  
; FILE REFERENCE: 1102865-0031  
; CURRENT APPLICATION NUMBER: US/10/762,226  
; CURRENT FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: 60/011,411  
; PRIOR FILING DATE: 1996-02-08  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Pyroglutamic acid residue  
US-10-762-226-1

Query Match 100.0%; Score 53; DB 5; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
Db 1 EGPWLEEEE 9  
|||||

## RESULT 11

US-10-762-226-6  
; Sequence 6, Application US/10762226  
; Publication No. US20050025770A1  
; GENERAL INFORMATION:  
; APPLICANT: Gevas, Philip C.  
; APPLICANT: Karr, Stephen L.  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Watson, Susan A.  
; TITLE OF INVENTION: Immunological Methods for the Treatment of  
; FILE REFERENCE: 1102865-0031  
; CURRENT APPLICATION NUMBER: US/10/762,226  
; CURRENT FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: 60/011,411  
; PRIOR FILING DATE: 1996-02-08  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Pyroglutamic acid residue  
US-10-762-226-6

Query Match 100.0%; Score 53; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9

Db 1 EGPWLEEEE 9  
|||||

## RESULT 12

US-10-197-954-60  
; Sequence 60, Application US/10197954  
; Publication No. US20030119021A1  
; GENERAL INFORMATION:  
; APPLICANT: K'ster, Hubert  
; APPLICANT: Siddiqi, Suhaib  
; APPLICANT: Little, Daniel  
; TITLE OF INVENTION: Capture Compounds, Collections Thereof  
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex  
; TITLE OF INVENTION: Compositions  
; FILE REFERENCE: 24743-2305  
; CURRENT APPLICATION NUMBER: US/10/197,954  
; CURRENT FILING DATE: 2002-07-16  
; PRIOR APPLICATION NUMBER: 60/306,019  
; PRIOR FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: 60/314,123  
; PRIOR FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: 60/363,433  
; PRIOR FILING DATE: 2002-03-11  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 60  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-197-954-60

Query Match 100.0%; Score 53; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
|||||

Db 1 EGPWLEEEE 9

## RESULT 13

US-10-613-377A-1  
; Sequence 1, Application US/10613377A  
; Publication No. US20040208920A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059  
; CURRENT APPLICATION NUMBER: US/10/613,377A  
; CURRENT FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-613-377A-1

Query Match 100.0%; Score 53; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
|||||

Db 1 EGPWLEEEE 9

## RESULT 14

US-10-613-377A-18  
; Sequence 18, Application US/10613377A  
; Publication No. US20040208920A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059  
; CURRENT APPLICATION NUMBER: US/10/613,377A  
; CURRENT FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide of Gnrh amino acid sequence linked to a spacer  
; OTHER INFORMATION: peptide  
US-10-613-377A-18

Query Match 100.0%; Score 53; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
|||||

Db 1 EGPWLEEEE 9

## RESULT 15

US-10-372-917-13  
; Sequence 13, Application US/10372917  
; Publication No. US20040209799A1  
; GENERAL INFORMATION:  
; APPLICANT: VASIOS, GEORGE  
; TITLE OF INVENTION: JAK/STAT PATHWAY INHIBITORS AND THE USES THEREOF  
; FILE REFERENCE: 5004C  
; CURRENT APPLICATION NUMBER: US/10/372,917  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: 60/177,872  
; PRIOR FILING DATE: 2000-01-24  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn ver. 3.2  
; SEQ ID NO 13  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-372-917-13

Query Match 100.0%; Score 53; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
|||||

Db 1 EGPWLEEEE 9

## RESULT 16

US-10-759-832-1  
; Sequence 1, Application US/10759832  
; Publication No. US20040247661A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059CIP

; CURRENT APPLICATION NUMBER: US/10/759,832  
; CURRENT FILING DATE: 2004-01-15  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 10/613,377  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD.RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-759-832-1

Query Match 100.0%; Score 53; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
| | | | |  
Db 1 EGPWLEEEE 9

RESULT 17  
US-10-759-832-18  
; Sequence 18, Application US/10759832  
; Publication No. US20040247661A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059CIP  
; CURRENT APPLICATION NUMBER: US/10/759,832  
; CURRENT FILING DATE: 2004-01-15  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 10/613,377  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide of Gnrh amino acid sequence linked to a spacer  
US-10-759-832-18

Query Match 100.0%; Score 53; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
| | | | |  
Db 1 EGPWLEEEE 9

RESULT 18  
US-10-760-085-60  
; Sequence 60, Application US/10760085  
; Publication No. US20050042771A1  
; GENERAL INFORMATION:  
; APPLICANT: Hubert K'ster  
; APPLICANT: Daniel Paul Little  
; APPLICANT: Suhaib Mahmood Siddiqi  
; APPLICANT: Matthew Peter Grallish  
; APPLICANT: Subramaniam Marappan  
; APPLICANT: Chester Frederick Haseman III  
; APPLICANT: Ping Yip

; TITLE OF INVENTION: Capture Compounds, Collections Thereof  
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex  
; TITLE OF INVENTION: Compositions  
; FILE REFERENCE: 24743-2309  
; CURRENT APPLICATION NUMBER: US/10/760,085  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: 60/441,398  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 60  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-760-085-60

Query Match 100.0%; Score 53; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
| | | | |  
Db 1 EGPWLEEEE 9

RESULT 19  
US-10-813-336-1  
; Sequence 1, Application US/10813336  
; Publication No. US20050069966A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Gastrin Hormone Immunoassays  
; FILE REFERENCE: 1102865-0046  
; CURRENT APPLICATION NUMBER: US/10/813,336  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US 60/458,244  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD.RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
; FEATURE:  
; NAME/KEY: MOD.RES  
; LOCATION: (17)..(17)  
; OTHER INFORMATION: AMIDATION  
US-10-813-336-1

Query Match 100.0%; Score 53; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
| | | | |  
Db 1 EGPWLEEEE 9

RESULT 20  
US-10-206-081-2  
; Sequence 2, Application US/10206081  
; Publication No. US20050100974A1  
; GENERAL INFORMATION:  
; APPLICANT: SURFACE LOGIX, INC.  
; TITLE OF INVENTION: METHODS OF DETECTING IMMOBILIZED BIOMOLECULES  
; FILE REFERENCE: 11641/126  
; CURRENT APPLICATION NUMBER: US/10/206,081  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US 60/307,839

;; PRIOR FILING DATE: 2001-07-27  
;; NUMBER OF SEQ ID NOS: 4  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 2  
;; LENGTH: 17  
;; TYPE: PRT  
;; ORGANISM: Artificial  
;; FEATURE:  
;; OTHER INFORMATION: kinase substrate  
US-10-206-081-2

Query Match 100.0%; Score 53; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
| | | | |  
Db 1 EGPWLEEEE 9

## RESULT 21

US-10-770-712-61  
;; Sequence 61, Application US/10770712  
;; Publication No. US2005017033A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Vojdani, Aristo  
;; TITLE OF INVENTION: IDENTIFICATION OF ETIOLOGY OF AUTISM  
;; FILE REFERENCE: IMSC12.008A  
;; CURRENT APPLICATION NUMBER: US/10/770,712  
;; CURRENT FILING DATE: 2004-02-03  
;; NUMBER OF SEQ ID NOS: 133  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 61  
;; LENGTH: 17  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: synthetically prepared peptide sequence  
US-10-770-712-61

Query Match 100.0%; Score 53; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
| | | | |  
Db 1 EGPWLEEEE 9

## RESULT 22

US-11-036-690-1  
;; Sequence 1, Application US/11036690  
;; Publication No. US2005016997A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Aptcon Corporation  
;; TITLE OF INVENTION: Liposomal Vaccine  
;; FILE REFERENCE: 1102865-0059CIP  
;; CURRENT APPLICATION NUMBER: US/11/036,690  
;; CURRENT FILING DATE: 2005-01-14  
;; PRIOR APPLICATION NUMBER: 60/394,179  
;; PRIOR FILING DATE: 2002-07-03  
;; PRIOR APPLICATION NUMBER: 10/613,377  
;; PRIOR FILING DATE: 2003-07-03  
;; NUMBER OF SEQ ID NOS: 20  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 1  
;; LENGTH: 17  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: MOD RES  
;; LOCATION: (1)-(1)  
;; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID

## US-11-036-690-1

Query Match 100.0%; Score 53; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
| | | | |  
Db 1 EGPWLEEEE 9

## RESULT 23

US-11-036-690-18  
;; Sequence 18, Application US/11036690  
;; Publication No. US2005016997A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Aptcon Corporation  
;; TITLE OF INVENTION: Liposomal Vaccine  
;; FILE REFERENCE: 1102865-0059CIP  
;; CURRENT APPLICATION NUMBER: US/11/036,690  
;; CURRENT FILING DATE: 2005-01-14  
;; PRIOR APPLICATION NUMBER: 60/394,179  
;; PRIOR FILING DATE: 2002-07-03  
;; PRIOR APPLICATION NUMBER: 10/613,377  
;; PRIOR FILING DATE: 2003-07-03  
;; NUMBER OF SEQ ID NOS: 20  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 18  
;; LENGTH: 17  
;; TYPE: PRT  
;; ORGANISM: Artificial  
;; FEATURE:  
;; OTHER INFORMATION: synthetic peptide of GnRH amino acid sequence linked to a spacer  
US-11-036-690-18

Query Match 100.0%; Score 53; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
| | | | |  
Db 1 EGPWLEEEE 9

## RESULT 24

US-11-066-697-422  
;; Sequence 422, Application US/11066697  
;; Publication No. US20050187159A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bridon, Dominique P.  
;; APPLICANT: Ezrin, Alan M.  
;; APPLICANT: Milner, Peter G.  
;; APPLICANT: Holmes, Darren L.  
;; APPLICANT: Thibaudau, Karen  
;; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
;; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
;; TITLE OF INVENTION: COMPONENTS  
;; FILE REFERENCE: 500862002301  
;; CURRENT APPLICATION NUMBER: US/11/066,697  
;; CURRENT FILING DATE: 2005-02-25  
;; PRIOR APPLICATION NUMBER: 09/657,276  
;; PRIOR FILING DATE: 2000-09-07  
;; PRIOR APPLICATION NUMBER: 60/153,406  
;; PRIOR FILING DATE: 1999-09-10  
;; PRIOR APPLICATION NUMBER: 60/159,783  
;; PRIOR FILING DATE: 1999-10-15  
;; NUMBER OF SEQ ID NOS: 1617  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 422  
;; LENGTH: 17  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-11-066-697-422

Query Match 100.0%; Score 53; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
Db 1 EGPWLEEEE 9

## RESULT 25

US-10-613-377A-2  
; Sequence 2, Application US/10613377A  
; Publication No. US20040208920A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059  
; CURRENT APPLICATION NUMBER: US/10/613,377A  
; CURRENT FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-613-377A-2

Query Match 100.0%; Score 53; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
Db 1 EGPWLEEEE 9

## RESULT 26

US-10-759-832-2  
; Sequence 2, Application US/10759832  
; Publication No. US20040247661A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059CIP  
; CURRENT APPLICATION NUMBER: US/10/759,832  
; CURRENT FILING DATE: 2004-01-15  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 10/613,377  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-759-832-2

Query Match 100.0%; Score 53; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
Db 1 EGPWLEEEE 9

## RESULT 27

US-10-813-336-2  
; Sequence 2, Application US/10813336  
; Publication No. US20050069966A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Gastrin Hormone Immunoassays  
; FILE REFERENCE: 1102865-0046  
; CURRENT APPLICATION NUMBER: US/10/813,336  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US 60/458,244  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-813-336-2

Query Match 100.0%; Score 53; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
Db 1 EGPWLEEEE 9

## RESULT 28

US-11-036-690-2  
; Sequence 2, Application US/11036690  
; Publication No. US20050169979A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059CIP  
; CURRENT APPLICATION NUMBER: US/11/036,690  
; CURRENT FILING DATE: 2005-01-14  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 10/613,377  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-11-036-690-2

Query Match 100.0%; Score 53; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9

Db 1 EGPWLEEEE 9  
|||||

## RESULT 29

US-10-813-336-3  
; Sequence 3, Application US/10813336  
; Publication No. US20050069966A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Gastrin Hormone Immunoassays  
; FILE REFERENCE: 1102865-0046  
; CURRENT APPLICATION NUMBER: US/10/813,336  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US 60/458,244  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
; NAME/KEY: MOD\_RES  
; LOCATION: (34)..(34)  
; OTHER INFORMATION: AMIDATION  
US-10-813-336-3

Query Match 100.0%; Score 53; DB 5; Length 34;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
|||||

Db 18 EGPWLEEEE 26

## RESULT 30

US-10-813-336-4  
; Sequence 4, Application US/10813336  
; Publication No. US20050069966A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Gastrin Hormone Immunoassays  
; FILE REFERENCE: 1102865-0046  
; CURRENT APPLICATION NUMBER: US/10/813,336  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US 60/458,244  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-813-336-4

Query Match 100.0%; Score 53; DB 5; Length 35;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
|||||

Db 18 EGPWLEEEE 26

## RESULT 31

US-10-839-017-3  
; Sequence 3, Application US/10839017  
; Publication No. US20050058635A1  
; GENERAL INFORMATION:  
; APPLICANT: DEMUTH, HANS-ULRICH  
; APPLICANT: HOFFMANN, TORSTEN  
; APPLICANT: NIESTROJ, ANDRE J.  
; APPLICANT: SCHILLING, STEPHAN  
; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL CYCLASE  
; FILE REFERENCE: 20488-53  
; CURRENT APPLICATION NUMBER: US/10/839,017  
; CURRENT FILING DATE: 2004-05-05  
; PRIOR APPLICATION NUMBER: 60/468,043  
; PRIOR FILING DATE: 2003-05-05  
; PRIOR APPLICATION NUMBER: 60/512,038  
; PRIOR FILING DATE: 2003-10-15  
; PRIOR APPLICATION NUMBER: 60/468,014  
; PRIOR FILING DATE: 2003-05-05  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 3  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: C-term amidated  
US-10-839-017-3

Query Match 94.3%; Score 50; DB 5; Length 17;  
Best Local Similarity 88.9%; Pred. No. 0.59;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
:|||||

Db 1 QGPWLEEEE 9

## RESULT 32

US-10-360-101-170  
; Sequence 170, Application US/10360101  
; Publication No. US20040009550A1  
; GENERAL INFORMATION:  
; APPLICANT: Moll, Gert N.  
; APPLICANT: Leenhouts, Cornelis J.  
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way  
; FILE REFERENCE: 2183-5673  
; CURRENT APPLICATION NUMBER: US/10/360,101  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: EP 02077060.8  
; PRIOR FILING DATE: 2002-05-24  
; NUMBER OF SEQ ID NOS: 309  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 170  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: S8,C11-sequence of Big Gastrin-1  
US-10-360-101-170

Query Match 94.3%; Score 50; DB 4; Length 33;  
Best Local Similarity 88.9%; Pred. No. 1.1;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
:|||||

Db 17 QGPWLEEEE 25

## RESULT 33

US-10-728-082-1

```
/ Sequence 1, Application US/10728082
/ Publication No. US20040229810A1
/ GENERAL INFORMATION:
/ APPLICANT: Cruz, Antonio
/ TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
/ FILE REFERENCE: 24492-013CIP
/ CURRENT APPLICATION NUMBER: US/10/728,082
/ CURRENT FILING DATE: 2003-12-03
/ PRIOR APPLICATION NUMBER: USSN 60/428,100
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: USSN 10/719,450
/ PRIOR FILING DATE: 2003-11-21
/ PRIOR APPLICATION NUMBER: USSN 60/428,562
/ PRIOR FILING DATE: 2002-11-22
/ PRIOR APPLICATION NUMBER: USSN 60/430,590
/ PRIOR FILING DATE: 2002-12-03
/ PRIOR APPLICATION NUMBER: USSN 60/519,933
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: USSN 60/420,187
/ PRIOR FILING DATE: 2002-10-22
/ PRIOR APPLICATION NUMBER: USSN 60/420,399
/ PRIOR FILING DATE: 2002-10-22
/ PRIOR APPLICATION NUMBER: USSN 10/691,123
/ PRIOR FILING DATE: 2003-10-22
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1
/ LENGTH: 33
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-728-082-1

Query Match          94.3%; Score 50; DB 5; Length 33;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EGPWLEEEE 9
        :|||||
Db      17 QGPWLEEEE 25

RESULT 34
US-10-728-082-2
/ Sequence 2, Application US/10728082
/ Publication No. US20040229810A1
/ GENERAL INFORMATION:
/ APPLICANT: Cruz, Antonio
/ TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
/ FILE REFERENCE: 24492-013CIP
/ CURRENT APPLICATION NUMBER: US/10/728,082
/ CURRENT FILING DATE: 2003-12-03
/ PRIOR APPLICATION NUMBER: USSN 60/428,100
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: USSN 10/719,450
/ PRIOR FILING DATE: 2003-11-21
/ PRIOR APPLICATION NUMBER: USSN 60/428,562
/ PRIOR FILING DATE: 2002-11-22
/ PRIOR APPLICATION NUMBER: USSN 60/430,590
/ PRIOR FILING DATE: 2002-12-03
/ PRIOR APPLICATION NUMBER: USSN 60/519,933
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: USSN 60/420,187
/ PRIOR FILING DATE: 2002-10-22
/ PRIOR APPLICATION NUMBER: USSN 60/420,399
/ PRIOR FILING DATE: 2002-10-22
/ PRIOR APPLICATION NUMBER: USSN 10/691,123
/ PRIOR FILING DATE: 2003-10-22
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2
/ LENGTH: 33
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-719-450-1

Query Match          94.3%; Score 50; DB 5; Length 33;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EGPWLEEEE 9
        :|||||
Db      17 QGPWLEEEE 25

RESULT 35
US-10-719-450-1
/ Sequence 1, Application US/10719450
/ Publication No. US20040266682A1
/ GENERAL INFORMATION:
/ APPLICANT: Cruz, Antonio
/ TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
/ FILE REFERENCE: 24492-013
/ CURRENT APPLICATION NUMBER: US/10/719,450
/ CURRENT FILING DATE: 2003-11-21
/ PRIOR APPLICATION NUMBER: USSN 60/428,100
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: USSN 60/428,562
/ PRIOR FILING DATE: 2002-11-22
/ PRIOR APPLICATION NUMBER: USSN 60/430,590
/ PRIOR FILING DATE: 2002-12-03
/ PRIOR APPLICATION NUMBER: USSN 60/519,933
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: USSN 60/420,187
/ PRIOR FILING DATE: 2002-10-22
/ PRIOR APPLICATION NUMBER: USSN 60/420,399
/ PRIOR FILING DATE: 2002-10-22
/ PRIOR APPLICATION NUMBER: USSN 10/691,123
/ PRIOR FILING DATE: 2003-10-22
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1
/ LENGTH: 33
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-719-450-1

Query Match          94.3%; Score 50; DB 5; Length 33;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EGPWLEEEE 9
        :|||||
Db      17 QGPWLEEEE 25

RESULT 36
US-10-719-450-2
/ Sequence 2, Application US/10719450
/ Publication No. US20040266682A1
/ GENERAL INFORMATION:
/ APPLICANT: Cruz, Antonio
/ TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
/ FILE REFERENCE: 24492-013
/ CURRENT APPLICATION NUMBER: US/10/719,450
/ CURRENT FILING DATE: 2003-11-21
/ PRIOR APPLICATION NUMBER: USSN 60/428,100
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: USSN 60/428,562
/ PRIOR FILING DATE: 2002-11-22
/ PRIOR APPLICATION NUMBER: USSN 60/430,590
```

```
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: variant gastrin peptide M31L as compared to SEQ ID NO:1
US-10-719-450-2

Query Match          94.3%; Score 50; DB 5; Length 33;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 17 QGPWLEEEE 25

RESULT 37
US-10-505-239-5
; Sequence 5, Application US/10505239
; Publication No. US20050171014A1
; GENERAL INFORMATION:
; APPLICANT: TARASOVA, Nadya I
; APPLICANT: MICHEJDA, Christopher J
; APPLICANT: DYBA, Marcin
; APPLICANT: COHRAN, Carolyn
; TITLE OF INVENTION: CONJUGATES OF LIGAND, LINKER AND CYTOTOXIC AGENT AND RELATED
; FILE REFERENCE: 229694
; CURRENT APPLICATION NUMBER: US/10/505,239
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: PCT/US03/06344
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/360,543
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/370,189
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-505-239-5

Query Match          94.3%; Score 50; DB 5; Length 33;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 17 QGPWLEEEE 25

RESULT 38
US-10-104-607B-5
; Sequence 5, Application US/10104607B
; Publication No. US20030091574A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation

; TITLE OF INVENTION: Combination Treatment of Pancreatic Cancer
; FILE REFERENCE: 1102865-0052
; CURRENT APPLICATION NUMBER: US/10/104,607B
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/278,294
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 34
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(1)
; OTHER INFORMATION: XAA = Pyroglutamine
; NAME/KEY: PEPTIDE
; LOCATION: (34)..(34)
; OTHER INFORMATION: XAA= Amidated phenylalanine
US-10-104-607B-5

Query Match          94.3%; Score 50; DB 4; Length 34;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 18 QGPWLEEEE 26

RESULT 39
US-10-408-765A-196
; Sequence 196, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-196

Query Match          94.3%; Score 50; DB 4; Length 34;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 18 QGPWLEEEE 26

RESULT 40
US-10-770-712-62
; Sequence 62, Application US/10770712
; Publication No. US20050170333A1
; GENERAL INFORMATION:
; APPLICANT: Vojdani, Aristo
; TITLE OF INVENTION: IDENTIFICATION OF ETIOLOGY OF AUTISM
; FILE REFERENCE: IMSCI2.008A
```

```
; CURRENT APPLICATION NUMBER: US/10/770,712
; CURRENT FILING DATE: 2004-02-03
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically prepared peptide sequence
US-10-770-712-62

Query Match          94.3%; Score 50; DB 5; Length 34;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
    :|||||||
Db 18 QGPWLEEEE 26

RESULT 41
US-11-066-697-423
; Sequence 423, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibadeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 423
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-423

Query Match          94.3%; Score 50; DB 6; Length 34;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
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Db 18 QGPWLEEEE 26

RESULT 42
US-10-244-324A-1
; Sequence 1, Application US/10244324A
; Publication No. US20030162795A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Product Inc.
; TITLE OF INVENTION: THIENOPYRIDINE AND THIENOPYRIDINE DERIVATIVES
; TITLE OF INVENTION: USEFUL AS ANTICANCER AGENTS
; FILE REFERENCE: PC9882C
; CURRENT APPLICATION NUMBER: US/10/244,324A

; CURRENT APPLICATION NUMBER: US/10/770,712
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Description of
US-10-244-324A-1

Query Match          92.5%; Score 49; DB 4; Length 19;
Best Local Similarity 88.9%; Pred. No. 0.94;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
    :|||||||
Db 3 KGPWLEEEE 11

RESULT 43
US-10-394-322A-70
; Sequence 70, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-70

Query Match          92.5%; Score 49; DB 4; Length 19;
Best Local Similarity 88.9%; Pred. No. 0.94;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
    :|||||||
Db 3 KGPWLEEEE 11

RESULT 44
US-10-931-348-3
; Sequence 3, Application US/10931348
; Publication No. US20050026219A1
; GENERAL INFORMATION:
; APPLICANT: Birk, Gerald
; APPLICANT: Hadarnovsky, Steffen
; TITLE OF INVENTION: Process for Label-Free Measurement of Modified Substrate
; FILE REFERENCE: 1/1200-2-CIP-1
; CURRENT APPLICATION NUMBER: US/10/931,348
; CURRENT FILING DATE: 2004-09-01
; PRIOR APPLICATION NUMBER: US 09/823,150
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 10/716,125
; PRIOR FILING DATE: 2003-11-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: phosphorylated modified substrate  
US-10-931-348-3

Query Match 92.5%; Score 49; DB 5; Length 19;  
Best Local Similarity 88.9%; Pred. No. 0.94;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
:|||||  
Db 3 KGPWLEEE 11

## RESULT 45

US-10-613-377A-6  
; Sequence 6, Application US/10613377A  
; Publication No. US20040208920A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059  
; CURRENT APPLICATION NUMBER: US/10/613,377A  
; CURRENT FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide of amino acid sequence 1-8 of human gastrin 17  
; OTHER INFORMATION: linked to spacer peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)-(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-613-377A-6

Query Match 90.6%; Score 48; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8  
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Db 1 EGPWLEEE 8

## RESULT 46

US-10-759-832-6  
; Sequence 6, Application US/10759832  
; Publication No. US20040247661A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059CIP  
; CURRENT APPLICATION NUMBER: US/10/759,832  
; CURRENT FILING DATE: 2004-01-15  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 10/613,377  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide of amino acid sequence 1-8 of human gastrin 17  
; OTHER INFORMATION: linked to spacer peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES

; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-759-832-6

Query Match 90.6%; Score 48; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8  
:|||||  
Db 1 EGPWLEEE 8

## RESULT 47

US-11-036-690-6  
; Sequence 6, Application US/11036690  
; Publication No. US20050169979A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059CIP  
; CURRENT APPLICATION NUMBER: US/11/036,690  
; CURRENT FILING DATE: 2005-01-14  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 10/613,377  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide of amino acid sequence 1-8 of human gastrin 17  
; OTHER INFORMATION: linked to spacer peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)-(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-11-036-690-6

Query Match 90.6%; Score 48; DB 6; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8  
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Db 1 EGPWLEEE 8

## RESULT 48

US-10-192-257-4  
; Sequence 4, Application US/10192257  
; Publication No. US20030021786A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Conditions  
; FILE REFERENCE: 1102865-0057  
; CURRENT APPLICATION NUMBER: US/10/192,257  
; CURRENT FILING DATE: 2002-07-09  
; PRIOR APPLICATION NUMBER: US 60/303,868  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(1)

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; OTHER INFORMATION: Xaa=pyroglutamic acid
US-10-192-257-4

Query Match          90.6%; Score 48; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEEEE 9
Db 2 GPWLEEEE 9

RESULT 49
US-10-728-082-3
; Sequence 3, Application US/10728082
; Publication No. US20040229810A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013CIP
; CURRENT APPLICATION NUMBER: US/10/728,082
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: USN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USN 10/719,450
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-728-082-3

Query Match          90.6%; Score 48; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEEEE 9
Db 1 GPWLEEEE 8

RESULT 50
US-10-728-082-4
; Sequence 4, Application US/10728082
; Publication No. US20040229810A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013CIP
; CURRENT APPLICATION NUMBER: US/10/728,082
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: USN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USN 10/719,450
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USN 60/428,562
; PRIOR FILING DATE: 2002-11-22

; OTHER INFORMATION: variant gastrin peptide - M14L as compared to SEQ ID NO:3
US-10-728-082-4

Query Match          90.6%; Score 48; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEEEE 9
Db 1 GPWLEEEE 8

Search completed: January 3, 2006, 09:55:33
Job time : 81.8571 secs
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:20:09 ; Search time 6.42857 Seconds  
(without alignments)  
10.484 Million cell updates/sec

Title: US-10-759-832-7

Perfect score: 53

Sequence: 1 EGPWLEEE 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications AA New:

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- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep.\*
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- 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	49	92.5	17	US-10-997-066-31
2	49	92.5	19	US-11-145-566-38
3	38	71.7	369	US-11-000-463-398
4	37	69.8	700	US-11-186-284-141
5	36	67.9	241	US-10-467-657-1330
6	36	67.9	361	US-11-129-143-108
7	34	64.2	432	US-11-194-246-308
8	34	64.2	485	US-10-204-029-7
9	33	62.3	376	US-11-082-389-58
10	33	62.3	281	US-11-055-822-152
11	33	62.3	397	US-11-060-008-8
12	33	62.3	413	US-11-060-008-9
13	33	62.3	575	US-11-131-212-24
14	32	60.4	251	US-11-135-855-38
15	32	60.4	254	US-11-067-323-578
16	32	60.4	271	US-10-667-295-98
17	32	60.4	277	US-10-667-295-97
18	32	60.4	296	US-10-667-295-96
19	32	60.4	358	US-10-821-234-1563
20	32	60.4	365	US-10-821-234-1575
21	32	60.4	434	US-10-793-626-1456
22	32	60.4	557	US-10-793-626-1486
23	32	60.4	575	US-11-131-212-23
24	32	60.4	690	US-10-613-744-19
25	31.5	59.4	130	US-10-507-275-1
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99	29	54.7	322	6	US-10-878-556A-59	Sequence 59, Appl	172	28	52.8	924	6	US-10-857-780-20	Sequence 20, Appl
100	29	54.7	350	6	US-10-131-826A-518	Sequence 518, App	173	28	52.8	924	7	US-11-107-028-26	Sequence 26, Appl
101	29	54.7	358	6	US-10-821-234-878	Sequence 878, App	174	28	52.8	1072	7	US-11-109-157A-13	Sequence 13, Appl
102	29	54.7	399	6	US-11-094-519A-37	Sequence 37, Appl	175	28	52.8	1122	6	US-10-821-234-1657	Sequence 1657, Ap
103	29	54.7	402	6	US-10-821-234-1581	Sequence 1581, Ap	176	28	52.8	1177	7	US-11-115-639-22	Sequence 22, Appl
104	29	54.7	428	6	US-10-689-742-50	Sequence 50, Appl	177	28	52.8	1177	7	US-11-115-639-23	Sequence 23, Appl
105	29	54.7	497	6	US-10-454-437-182	Sequence 182, App	178	28	52.8	1177	7	US-11-115-639-24	Sequence 24, Appl
106	29	54.7	514	7	US-11-186-284-228	Sequence 228, App	179	28	52.8	1177	7	US-11-115-639-25	Sequence 25, Appl
107	29	54.7	534	7	US-11-167-856-24	Sequence 24, Appl	180	28	52.8	1177	7	US-11-115-639-26	Sequence 26, Appl
108	29	54.7	538	7	US-11-167-856-20	Sequence 20, Appl	181	28	52.8	1177	7	US-11-115-639-27	Sequence 27, Appl
109	29	54.7	644	6	US-10-821-234-1107	Sequence 1107, Ap	182	28	52.8	1177	7	US-11-115-639-28	Sequence 28, Appl
110	29	54.7	739	7	US-11-057-047-2	Sequence 2, Appl	183	28	52.8	1177	7	US-11-115-639-29	Sequence 29, Appl
111	29	54.7	739	7	US-11-057-047-1	Sequence 1, Appl	184	28	52.8	1177	7	US-11-115-639-30	Sequence 30, Appl
112	29	54.7	780	6	US-10-878-556A-197	Sequence 197, App	185	28	52.8	1183	7	US-11-115-639-13	Sequence 13, Appl
113	29	54.7	793	7	US-11-060-914-2	Sequence 2, Appl	186	28	52.8	1183	7	US-11-115-639-14	Sequence 14, Appl
114	29	54.7	793	6	US-10-821-234-1034	Sequence 1034, Ap	187	28	52.8	1183	7	US-11-115-639-15	Sequence 15, Appl
115	29	54.7	814	6	US-10-878-556A-161	Sequence 161, App	188	28	52.8	1183	7	US-11-115-639-16	Sequence 16, Appl
116	29	54.7	919	6	US-10-821-234-951	Sequence 951, App	189	28	52.8	1183	7	US-11-115-639-17	Sequence 17, Appl
117	29	54.7	943	6	US-10-821-234-1012	Sequence 1012, Ap	190	28	52.8	1183	7	US-11-115-639-18	Sequence 18, Appl
118	29	54.7	964	7	US-11-137-455-58	Sequence 58, Appl	191	28	52.8	1184	7	US-11-115-639-49	Sequence 49, Appl
119	29	54.7	965	7	US-11-133-424-2	Sequence 2, Appl	192	28	52.8	1184	7	US-11-115-639-50	Sequence 50, Appl
120	29	54.7	965	7	US-11-147-047-51	Sequence 51, Appl	193	28	52.8	1184	7	US-11-115-639-51	Sequence 51, Appl
121	29	54.7	1049	7	US-11-137-465-42	Sequence 42, Appl	194	28	52.8	1193	7	US-11-115-639-19	Sequence 19, Appl
122	29	54.7	1234	6	US-10-995-561-870	Sequence 870, App	195	28	52.8	1193	7	US-11-115-639-20	Sequence 20, Appl
123	29	54.7	1365	6	US-10-995-561-867	Sequence 867, App	196	28	52.8	1193	7	US-11-115-639-21	Sequence 21, Appl
124	29	54.7	1366	6	US-10-995-561-868	Sequence 868, App	197	28	52.8	1208	7	US-11-115-639-46	Sequence 46, Appl
125	29	54.7	1411	6	US-10-995-561-869	Sequence 869, App	198	28	52.8	1208	7	US-11-115-639-47	Sequence 47, Appl
126	29	54.7	2101	6	US-10-857-780-23	Sequence 23, Appl	199	28	52.8	1208	7	US-11-115-639-48	Sequence 48, Appl
127	29	54.7	3144	7	US-11-055-035-1	Sequence 1, Appl	200	28	52.8	1213	6	US-11-074-176-256	Sequence 256, App
128	29	54.7	3655	7	US-11-075-185-5	Sequence 5, Appl	201	28	52.8	1274	6	US-10-454-437-360	Sequence 360, App
129	28	52.8	108	6	US-10-925-366A-159	Sequence 159, App	202	28	52.8	1881	7	US-11-040-472-8	Sequence 8, Appl
130	28	52.8	108	6	US-10-925-366A-174	Sequence 174, App	203	28	52.8	2280	7	US-11-022-562-211	Sequence 211, App
131	28	52.8	108	6	US-10-925-366A-188	Sequence 188, App	204	28	52.8	2516	6	US-10-847-956A-2	Sequence 2, Appl
132	28	52.8	108	6	US-10-925-366A-190	Sequence 190, App	205	28	52.8	2516	6	US-10-821-234-1262	Sequence 1262, Ap
133	28	52.8	125	6	US-10-467-657-7284	Sequence 7284, Ap	206	28	52.8	3433	6	US-10-714-781A-67	Sequence 67, Appl
134	28	52.8	179	6	US-10-467-657-306	Sequence 306, App	207	27	50.9	68	6	US-10-467-657-3150	Sequence 3150, Ap
135	28	52.8	179	6	US-10-467-657-6422	Sequence 6422, Ap	208	27	50.9	79	6	US-10-986-501-281	Sequence 281, App
136	28	52.8	210	6	US-10-467-657-698	Sequence 698, App	209	27	50.9	101	6	US-10-793-626-1672	Sequence 1672, Ap
137	28	52.8	223	6	US-10-793-626-2824	Sequence 2824, Ap	210	27	50.9	113	6	US-10-995-561-690	Sequence 690, App
138	28	52.8	231	6	US-10-454-437-414	Sequence 414, App	211	27	50.9	120	6	US-10-793-626-958	Sequence 958, App
139	28	52.8	250	7	US-11-135-855-41	Sequence 41, Appl	212	27	50.9	120	6	US-10-793-626-1444	Sequence 1444, Ap
140	28	52.8	260	7	US-11-055-822-906	Sequence 906, App	213	27	50.9	145	6	US-10-793-626-2378	Sequence 2378, Ap
141	28	52.8	279	6	US-10-467-657-1310	Sequence 1310, Ap	214	27	50.9	170	6	US-10-980-388-107	Sequence 107, App
142	28	52.8	280	6	US-10-467-657-1326	Sequence 1326, Ap	215	27	50.9	176	6	US-10-131-826A-98	Sequence 98, Appl
143	28	52.8	280	7	US-11-102-497-6	Sequence 6, Appl	216	27	50.9	184	6	US-10-881-873-44	Sequence 44, Appl
144	28	52.8	295	7	US-11-055-822-62	Sequence 62, Appl	217	27	50.9	202	6	US-10-858-730-96	Sequence 96, Appl
145	28	52.8	308	6	US-10-131-826A-100	Sequence 100, App	218	27	50.9	206	6	US-10-873-528-78	Sequence 78, Appl
146	28	52.8	368	7	US-11-055-822-662	Sequence 662, App	219	27	50.9	232	7	US-11-067-323-504	Sequence 504, App
147	28	52.8	368	7	US-11-060-008-13	Sequence 13, Appl	220	27	50.9	232	7	US-11-067-323-656	Sequence 656, App
148	28	52.8	370	7	US-11-055-822-796	Sequence 796, App	221	27	50.9	232	7	US-11-067-323-658	Sequence 658, App
149	28	52.8	390	7	US-10-821-234-1053	Sequence 1053, Ap	222	27	50.9	232	7	US-11-067-323-660	Sequence 660, App
150	28	52.8	391	7	US-11-082-389-172	Sequence 172, App	223	27	50.9	234	6	US-10-485-517-333	Sequence 333, App
151	28	52.8	391	7	US-11-082-389-174	Sequence 174, App	224	27	50.9	240	6	US-10-878-556A-37	Sequence 37, Appl
152	28	52.8	406	7	US-11-107-028-7	Sequence 7, Appl	225	27	50.9	252	7	US-11-067-323-18	Sequence 18, Appl
153	28	52.8	421	7	US-11-055-822-902	Sequence 902, App	226	27	50.9	252	7	US-11-067-323-28	Sequence 28, Appl
154	28	52.8	423	7	US-11-187-856-8	Sequence 8, Appl	227	27	50.9	253	6	US-10-467-657-8346	Sequence 8346, Ap
155	28	52.8	434	7	US-11-059-867-16	Sequence 16, Appl	228	27	50.9	253	6	US-11-067-323-2	Sequence 2, Appl
156	28	52.8	447	6	US-10-467-657-364	Sequence 364, App	229	27	50.9	254	7	US-11-067-323-4	Sequence 4, Appl
157	28	52.8	447	6	US-10-467-657-4406	Sequence 4406, Ap	230	27	50.9	254	7	US-11-067-323-6	Sequence 6, Appl
158	28	52.8	455	7	US-11-059-867-17	Sequence 17, Appl	231	27	50.9	254	7	US-11-067-323-8	Sequence 8, Appl
159	28	52.8	465	7	US-11-059-867-15	Sequence 15, Appl	232	27	50.9	254	7	US-11-067-323-10	Sequence 10, Appl
160	28	52.8	565	6	US-10-467-657-8046	Sequence 8046, Ap	233	27	50.9	254	7	US-11-067-323-12	Sequence 12, Appl
161	28	52.8	605	6	US-10-131-826A-160	Sequence 160, App	234	27	50.9	254	7	US-11-067-323-14	Sequence 14, Appl
162	28	52.8	617	6	US-11-143-980-35	Sequence 35, Appl	235	27	50.9	254	7	US-11-067-323-16	Sequence 16, Appl
163	28	52.8	643	6	US-10-467-657-5900	Sequence 5900, Ap	236	27	50.9	254	7	US-11-067-323-20	Sequence 20, Appl
164	28	52.8	643	6	US-10-873-427A-4	Sequence 4, Appl	237	27	50.9	254	7	US-11-067-323-22	Sequence 22, Appl
165	28	52.8	648	6	US-10-793-626-568	Sequence 568, App	238	27	50.9	254	7	US-11-067-323-24	Sequence 24, Appl
166	28	52.8	734	6	US-10-652-893-2	Sequence 2, Appl	239	27	50.9	254	7	US-11-067-323-26	Sequence 26, Appl
167	28	52.8	734	6	US-11-137-465-65	Sequence 65, Appl	240	27	50.9	254	7	US-11-067-323-30	Sequence 30, Appl
168	28	52.8	782	6	US-10-995-561-861	Sequence 861, App	241	27	50.9	254	7	US-11-067-323-32	Sequence 32, Appl
169	28	52.8	795	7	US-11-109-157A-14	Sequence 14, Appl	242	27	50.9	254	7	US-11-067-323-34	Sequence 34, Appl
170	28	52.8	847	6	US-10-995-561-863	Sequence 863, App	243	27	50.9	254	7	US-11-067-323-36	Sequence 36, Appl
171	28	52.8	847	6	US-10-995-561-865	Sequence 865, App	244	27	50.9	254	7		



391	27	50.9	254	7	US-11-067-323-330	Sequence 330, App	Sequence 330, App	464	27	50.9	254	7	US-11-067-323-480	Sequence 480, App
392	27	50.9	254	7	US-11-067-323-332	Sequence 332, App	Sequence 332, App	465	27	50.9	254	7	US-11-067-323-482	Sequence 482, App
393	27	50.9	254	7	US-11-067-323-334	Sequence 334, App	Sequence 334, App	466	27	50.9	254	7	US-11-067-323-484	Sequence 484, App
394	27	50.9	254	7	US-11-067-323-336	Sequence 336, App	Sequence 336, App	467	27	50.9	254	7	US-11-067-323-486	Sequence 486, App
395	27	50.9	254	7	US-11-067-323-338	Sequence 338, App	Sequence 338, App	468	27	50.9	254	7	US-11-067-323-488	Sequence 488, App
396	27	50.9	254	7	US-11-067-323-340	Sequence 340, App	Sequence 340, App	469	27	50.9	254	7	US-11-067-323-490	Sequence 490, App
397	27	50.9	254	7	US-11-067-323-342	Sequence 342, App	Sequence 342, App	470	27	50.9	254	7	US-11-067-323-492	Sequence 492, App
398	27	50.9	254	7	US-11-067-323-344	Sequence 344, App	Sequence 344, App	471	27	50.9	254	7	US-11-067-323-494	Sequence 494, App
399	27	50.9	254	7	US-11-067-323-346	Sequence 346, App	Sequence 346, App	472	27	50.9	254	7	US-11-067-323-496	Sequence 496, App
400	27	50.9	254	7	US-11-067-323-348	Sequence 348, App	Sequence 348, App	473	27	50.9	254	7	US-11-067-323-498	Sequence 498, App
401	27	50.9	254	7	US-11-067-323-350	Sequence 350, App	Sequence 350, App	474	27	50.9	254	7	US-11-067-323-500	Sequence 500, App
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403	27	50.9	254	7	US-11-067-323-354	Sequence 354, App	Sequence 354, App	476	27	50.9	254	7	US-11-067-323-506	Sequence 506, App
404	27	50.9	254	7	US-11-067-323-356	Sequence 356, App	Sequence 356, App	477	27	50.9	254	7	US-11-067-323-508	Sequence 508, App
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406	27	50.9	254	7	US-11-067-323-360	Sequence 360, App	Sequence 360, App	479	27	50.9	254	7	US-11-067-323-512	Sequence 512, App
407	27	50.9	254	7	US-11-067-323-362	Sequence 362, App	Sequence 362, App	480	27	50.9	254	7	US-11-067-323-514	Sequence 514, App
408	27	50.9	254	7	US-11-067-323-364	Sequence 364, App	Sequence 364, App	481	27	50.9	254	7	US-11-067-323-516	Sequence 516, App
409	27	50.9	254	7	US-11-067-323-366	Sequence 366, App	Sequence 366, App	482	27	50.9	254	7	US-11-067-323-518	Sequence 518, App
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413	27	50.9	254	7	US-11-067-323-374	Sequence 374, App	Sequence 374, App	486	27	50.9	254	7	US-11-067-323-528	Sequence 528, App
414	27	50.9	254	7	US-11-067-323-376	Sequence 376, App	Sequence 376, App	487	27	50.9	254	7	US-11-067-323-530	Sequence 530, App
415	27	50.9	254	7	US-11-067-323-378	Sequence 378, App	Sequence 378, App	488	27	50.9	254	7	US-11-067-323-532	Sequence 532, App
416	27	50.9	254	7	US-11-067-323-380	Sequence 380, App	Sequence 380, App	489	27	50.9	254	7	US-11-067-323-534	Sequence 534, App
417	27	50.9	254	7	US-11-067-323-382	Sequence 382, App	Sequence 382, App	490	27	50.9	254	7	US-11-067-323-536	Sequence 536, App
418	27	50.9	254	7	US-11-067-323-384	Sequence 384, App	Sequence 384, App	491	27	50.9	254	7	US-11-067-323-538	Sequence 538, App
419	27	50.9	254	7	US-11-067-323-386	Sequence 386, App	Sequence 386, App	492	27	50.9	254	7	US-11-067-323-540	Sequence 540, App
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422	27	50.9	254	7	US-11-067-323-392	Sequence 392, App	Sequence 392, App	495	27	50.9	254	7	US-11-067-323-546	Sequence 546, App
423	27	50.9	254	7	US-11-067-323-394	Sequence 394, App	Sequence 394, App	496	27	50.9	254	7	US-11-067-323-548	Sequence 548, App
424	27	50.9	254	7	US-11-067-323-396	Sequence 396, App	Sequence 396, App	497	27	50.9	254	7	US-11-067-323-550	Sequence 550, App
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426	27	50.9	254	7	US-11-067-323-400	Sequence 400, App	Sequence 400, App	499	27	50.9	254	7	US-11-067-323-556	Sequence 556, App
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461	27	50.9	254	7	US-11-067-323-474	Sequence 474, App	Sequence 474, App	534	27	50.9	254	7	US-11-067-323-642	Sequence 642, App
462	27	50.9	254	7	US-11-067-323-476	Sequence 476, App	Sequence 476, App	535	27	50.9	254	7	US-11-067-323-644	Sequence 644, App
463	27	50.9	254	7	US-11-067-323-478	Sequence 478, App	Sequence 478, App	536	27	50.9	254	7	US-11-067-323-646	Sequence 646, App



683	27	50.9	254	7	US-11-067-323-961	Sequence 961, App	756	27	50.9	254	7	US-11-067-323-1115	Sequence 1115, App
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689	27	50.9	254	7	US-11-067-323-977	Sequence 977, App	762	27	50.9	254	7	US-11-067-323-1127	Sequence 1127, App
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692	27	50.9	254	7	US-11-067-323-983	Sequence 983, App	765	27	50.9	254	7	US-11-067-323-1133	Sequence 1133, App
693	27	50.9	254	7	US-11-067-323-985	Sequence 985, App	766	27	50.9	254	7	US-11-067-323-1135	Sequence 1135, App
694	27	50.9	254	7	US-11-067-323-987	Sequence 987, App	767	27	50.9	254	7	US-11-067-323-1137	Sequence 1137, App
695	27	50.9	254	7	US-11-067-323-989	Sequence 989, App	768	27	50.9	254	7	US-11-067-323-1139	Sequence 1139, App
696	27	50.9	254	7	US-11-067-323-991	Sequence 991, App	769	27	50.9	254	7	US-11-067-323-1141	Sequence 1141, App
697	27	50.9	254	7	US-11-067-323-993	Sequence 993, App	770	27	50.9	254	7	US-11-067-323-1143	Sequence 1143, App
698	27	50.9	254	7	US-11-067-323-995	Sequence 995, App	771	27	50.9	255	7	US-11-067-323-1019	Sequence 1019, App
699	27	50.9	254	7	US-11-067-323-997	Sequence 997, App	772	27	50.9	256	7	US-11-055-822-1140	Sequence 1140, App
700	27	50.9	254	7	US-11-067-323-999	Sequence 999, App	773	27	50.9	256	7	US-11-124-291-2	Sequence 2, Appli
701	27	50.9	254	7	US-11-067-323-1001	Sequence 1001, Ap	774	27	50.9	256	6	US-10-131-826A-546	Sequence 546, App
702	27	50.9	254	7	US-11-067-323-1003	Sequence 1003, Ap	775	27	50.9	261	6	US-11-102-240-138	Sequence 138, App
703	27	50.9	254	7	US-11-067-323-1005	Sequence 1005, Ap	776	27	50.9	273	6	US-10-995-561-689	Sequence 689, App
704	27	50.9	254	7	US-11-067-323-1007	Sequence 1007, Ap	777	27	50.9	279	6	US-10-878-556A-120	Sequence 120, App
705	27	50.9	254	7	US-11-067-323-1009	Sequence 1009, Ap	778	27	50.9	281	6	US-10-967-648A-12	Sequence 12, Appl
706	27	50.9	254	7	US-11-067-323-1011	Sequence 1011, Ap	779	27	50.9	288	6	US-10-821-234-1617	Sequence 1617, Ap
707	27	50.9	254	7	US-11-067-323-1013	Sequence 1013, Ap	780	27	50.9	296	6	US-10-965-972-8	Sequence 8, Appli
708	27	50.9	254	7	US-11-067-323-1015	Sequence 1015, Ap	781	27	50.9	301	6	US-10-995-793-75	Sequence 75, Appl
709	27	50.9	254	7	US-11-067-323-1017	Sequence 1017, Ap	782	27	50.9	301	7	US-11-147-047-37	Sequence 37, Appl
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## ALIGNMENTS

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; Publication No. US20050244891A1
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, RONALD J.
; APPLICANT: LEE, LINDA G.
; APPLICANT: SUN, HONGYE
; TITLE OF INVENTION: LIGAND-CONTAINING MICELLES AND USES THEREOF
; FILE REFERENCE: 375461-011US
; CURRENT APPLICATION NUMBER: US/10/997,066
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/525,492
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/628,509
; PRIOR FILING DATE: 2004-11-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 3.3
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; LENGTH: 17
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Query Match      92.5%; Score 49; DB 6; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.014;
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; Publication No. US20050272083A1
; GENERAL INFORMATION:
; APPLICANT: SOWASEKAR SESHAGIRI

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; TITLE OF INVENTION: EGFR Mutations
; FILE REFERENCE: 39766-0153
; CURRENT APPLICATION NUMBER: US/11/145,566
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,425
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/635,344
; PRIOR FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US 60/666,068
; PRIOR FILING DATE: 2005-03-28
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 38
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-145-566-38

```

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Query Match      92.5%; Score 49; DB 7; Length 19;
Best Local Similarity 88.9%; Pred. No. 0.015;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 EGPWLEEEE 9
      :|||||
Db      3 KGPWLEEEE 11

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RESULT 3
US-11-000-463-398
; Sequence 398, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 398
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-398

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Query Match      71.7%; Score 38; DB 7; Length 369;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY      2 GPWLEE 7

```

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Db          47 GPWLEE 52
|||||
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
||| | | | | | | |
Db 194 EGGWTEQEE 202

RESULT 6
US-11-129-143-108
; Sequence 108, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-11-129-143-108

Query Match 67.9%; Score 36; DB 7; Length 361;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PWLEEEE 9
||| | | | | |
Db 181 PWLQEQE 187

RESULT 7
US-11-194-246-308
; Sequence 308, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
; TITLE OF INVENTION: USE
; FILE REFERENCE: 00592 US1 (M&R 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 308
; LENGTH: 432
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-308

Query Match 64.2%; Score 34; DB 7; Length 432;
Best Local Similarity 62.5%; Pred. No. 63;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPWLEEEE 9
| | | | | | | |
Db 128 GQWLEDE 135

US-10-467-657-1330
; Sequence 1330, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1330
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1330

Query Match 67.9%; Score 36; DB 6; Length 241;

US-11-186-284-141
; Sequence 141, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPW01-029F2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 700
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-141

Query Match 69.8%; Score 37; DB 7; Length 700;
Best Local Similarity 55.6%; Pred. No. 32;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
: | | | | : | | :
Db 83 KGPWTKED 91

RESULT 5
US-10-467-657-1330
; Sequence 1330, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1330
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1330

Query Match 67.9%; Score 36; DB 6; Length 241;
```

```
RESULT 8
US-10-204-029-7
; Sequence 7, Application US/10204029
; Publication No. US20050261487A1
; GENERAL INFORMATION:
; APPLICANT: Cully, Doris F.
; APPLICANT: Priest, Birgit
; APPLICANT: Yuan, Jeffrey
; APPLICANT: Zheng, Yingcong
; TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND-GATED ION
; CHANNELS FROM DROSOPHILA MELANOGASTER
; FILE REFERENCE: 20615P
; CURRENT APPLICATION NUMBER: US/10/204,029
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/US01/06096
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/186645
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Drosophila Melanogaster
US-10-204-029-7

Query Match 64.2%; Score 34; DB 6; Length 485;
Best Local Similarity 44.4%; Pred. No. 70;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 407 DGPWIPRQE 415

RESULT 9
US-11-082-389-58
; Sequence 58, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; PRIOR FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.

US-10-759-832-7.rapbn

; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 58
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-58

Query Match 62.3%; Score 33; DB 7; Length 281;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEE 7
Db 44 GPWIED 49

RESULT 10
US-11-055-822-152
; Sequence 152, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 152
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-152

Query Match 62.3%; Score 33; DB 7; Length 376;
Best Local Similarity 71.4%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWELEE 9
Db 116 PWLDEPE 122

RESULT 11
US-11-060-008-8
; Sequence 8, Application US/11060008
; Publication No. US20050257290A1
; GENERAL INFORMATION:
```

; APPLICANT: Klock, Andrew P.  
; APPLICANT: Williams, Deryck J.  
; APPLICANT: McLeird, Merry B.  
; APPLICANT: Bradley, John D.  
; APPLICANT: Davila-Aponte, Jennifer A.  
; APPLICANT: Xu, Siqun  
; APPLICANT: Prevett, Anita M.  
; TITLE OF INVENTION: NEMATODE FATTY ACID DESATURASE-LIKE  
; FILE REFERENCE: 12557-007001  
; CURRENT APPLICATION NUMBER: US/11/060,008  
; CURRENT FILING DATE: 2005-02-17  
; PRIOR APPLICATION NUMBER: US/10/243,468  
; PRIOR FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: US 60/322,003  
; PRIOR FILING DATE: 2001-09-13  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 397  
; TYPE: PRT  
; ORGANISM: Meloidogyne incognita  
US-11-060-008-8

Query Match 62.3%; Score 33; DB 7; Length 397;  
Best Local Similarity 71.4%; Pred. No. 84;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEE 9  
Db 167 PWTTEE 173

RESULT 12  
US-11-060-008-9  
; Sequence 9, Application US/11060008  
; Publication No. US20050257290A1  
; GENERAL INFORMATION:  
; APPLICANT: Klock, Andrew P.  
; APPLICANT: Williams, Deryck J.  
; APPLICANT: McLeird, Merry B.  
; APPLICANT: Bradley, John D.  
; APPLICANT: Davila-Aponte, Jennifer A.  
; APPLICANT: Xu, Siqun  
; APPLICANT: Prevett, Anita M.  
; TITLE OF INVENTION: NEMATODE FATTY ACID DESATURASE-LIKE  
; FILE REFERENCE: 12557-007001  
; CURRENT APPLICATION NUMBER: US/11/060,008  
; CURRENT FILING DATE: 2005-02-17  
; PRIOR APPLICATION NUMBER: US/10/243,468  
; PRIOR FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: US 60/322,003  
; PRIOR FILING DATE: 2001-09-13  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 413  
; TYPE: PRT  
; ORGANISM: Meloidogyne incognita  
US-11-060-008-9

Query Match 62.3%; Score 33; DB 7; Length 413;  
Best Local Similarity 71.4%; Pred. No. 87;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEE 9  
Db 183 PWTTEE 189

RESULT 13  
US-11-131-212-24

; Sequence 24, Application US/11131212  
; Publication No. US20050262593A1  
; GENERAL INFORMATION:  
; APPLICANT: Yutaka KANDA  
; APPLICANT: Mitsuo SATOH  
; APPLICANT: Kazuyasu NAKAMURA  
; APPLICANT: Kazuhisa UCHIDA  
; APPLICANT: Toyohide SHINKAWA  
; APPLICANT: Naoko YAMANE  
; APPLICANT: Motoo YANASAKI  
; APPLICANT: Nobuo HANAI  
; TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL  
; FILE REFERENCE: 249-202  
; CURRENT APPLICATION NUMBER: US/11/131,212  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US/09/971,773  
; PRIOR FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: JP 2000-308526  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: US 60/268,926  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 575  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-131-212-24

Query Match 62.3%; Score 33; DB 7; Length 575;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEE 8  
Db 340 PWLEKE 345

RESULT 14  
US-11-135-855-38  
; Sequence 38, Application US/11135855  
; Publication No. US2005025557A1  
; GENERAL INFORMATION:  
; APPLICANT: SMITHKLINE BEECHAM CORPORATION  
; APPLICANT: SMITHKLINE BEECHAM P.L.C.  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50013  
; CURRENT APPLICATION NUMBER: US/11/135,855  
; CURRENT FILING DATE: 2005-05-24  
; PRIOR APPLICATION NUMBER: US/10/203,708  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: PCT/US01/04703  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 60/182,172  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 60/186,084  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 38  
; LENGTH: 251  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-135-855-38

Query Match 60.4%; Score 32; DB 7; Length 251;  
Best Local Similarity 62.5%; Pred. No. 81;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 8  
Db 103 DGPWPEPE 110

RESULT 15  
US-11-067-323-578  
; Sequence 578, Application US/11067323  
; Publication No. US20050272064A1  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Christopher S.  
; APPLICANT: Fox, Richard J  
; APPLICANT: Gavrilovic, Vesna  
; APPLICANT: Huismann, Gjaalt W  
; APPLICANT: Newman, Lisa M  
; TITLE OF INVENTION: Improved Halohydrin Dehalogenases and Related Polynucleotides  
; FILE REFERENCE: 16028US04 0353 410US  
; CURRENT APPLICATION NUMBER: US/11/067,323  
; CURRENT FILING DATE: 2005-02-23  
; PRIOR APPLICATION NUMBER: 60/546,033  
; PRIOR FILING DATE: 2004-02-18  
; PRIOR APPLICATION NUMBER: 60/494,382  
; PRIOR FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: 10/917,179  
; PRIOR FILING DATE: 2004-08-11  
; NUMBER OF SEQ ID NOS: 1143  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 578  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HHDH variant  
US-11-067-323-578

Query Match 60.4%; Score 32; DB 7; Length 254;  
Best Local Similarity 83.3%; Pred. No. 81;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 EGPWLE 6  
Db 136 EGPWKE 141  
|||||

RESULT 16  
US-10-667-295-98  
; Sequence 98, Application US/10667295  
; Publication No. US20050257293A1  
; GENERAL INFORMATION:  
; APPLICANT: Mascia, Peter  
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM  
; FILE REFERENCE: 11696-047001  
; CURRENT APPLICATION NUMBER: US/10/667,295  
; CURRENT FILING DATE: 2003-09-17  
; PRIOR APPLICATION NUMBER: US 60/411,823  
; PRIOR FILING DATE: 2002-09-17  
; NUMBER OF SEQ ID NOS: 263  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 98  
; LENGTH: 271  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(271)  
; OTHER INFORMATION: Ceres Seq. ID no. 12333222  
US-10-667-295-98

Query Match 60.4%; Score 32; DB 6; Length 271;  
Best Local Similarity 71.4%; Pred. No. 86;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 3 PWLEEEE 9  
Db 210 PWNEQEE 216  
|||

RESULT 17  
US-10-667-295-97  
; Sequence 97, Application US/10667295  
; Publication No. US20050257293A1  
; GENERAL INFORMATION:  
; APPLICANT: Mascia, Peter  
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM  
; FILE REFERENCE: 11696-047001  
; CURRENT APPLICATION NUMBER: US/10/667,295  
; CURRENT FILING DATE: 2003-09-17  
; PRIOR APPLICATION NUMBER: US 60/411,823  
; PRIOR FILING DATE: 2002-09-17  
; NUMBER OF SEQ ID NOS: 263  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 97  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(277)  
; OTHER INFORMATION: Ceres Seq. ID no. 12333221  
US-10-667-295-97

Query Match 60.4%; Score 32; DB 6; Length 277;  
Best Local Similarity 71.4%; Pred. No. 88;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 3 PWLEEEE 9  
Db 216 PWNEQEE 222  
|||

RESULT 18  
US-10-667-295-96  
; Sequence 96, Application US/10667295  
; Publication No. US20050257293A1  
; GENERAL INFORMATION:  
; APPLICANT: Mascia, Peter  
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM  
; FILE REFERENCE: 11696-047001  
; CURRENT APPLICATION NUMBER: US/10/667,295  
; CURRENT FILING DATE: 2003-09-17  
; PRIOR APPLICATION NUMBER: US 60/411,823  
; PRIOR FILING DATE: 2002-09-17  
; NUMBER OF SEQ ID NOS: 263  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 96  
; LENGTH: 296  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(296)  
; OTHER INFORMATION: Ceres Seq. ID no. 12333220  
US-10-667-295-96

Query Match 60.4%; Score 32; DB 6; Length 296;  
Best Local Similarity 71.4%; Pred. No. 93;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 3 PWLEEEE 9  
Db 235 PWNEQEE 241  
|||

RESULT 19  
US-10-821-234-1563  
; Sequence 1563, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit

```
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1563
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1563

Query Match 60.4%; Score 32; DB 6; Length 358;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEE 8
Db 71 PWMEQE 76

RESULT 20
US-10-821-234-1575
; Sequence 1575, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1575
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1575

Query Match 60.4%; Score 32; DB 6; Length 365;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEE 8
Db 74 PWIEQE 79

RESULT 21
US-10-793-626-1456
; Sequence 1456, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1456
; LENGTH: 434
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1456

Query Match 60.4%; Score 32; DB 6; Length 434;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEE 7
Db 108 GPWVDE 113

RESULT 22
US-10-793-626-1486
; Sequence 1486, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1486
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1486

Query Match 60.4%; Score 32; DB 6; Length 557;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEE 7
Db 231 GPWVDE 236

RESULT 23
US-11-131-212-23
; Sequence 23, Application US/11131212
; Publication No. US20050262593A1
; GENERAL INFORMATION:
; APPLICANT: Yutaka KANDA
; APPLICANT: Mitsuao SATOH
; APPLICANT: Kazuyasu NAKAMURA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohide SHINKAWA
; APPLICANT: Naoko YAMANE
; APPLICANT: Motoo YAMASAKI
; APPLICANT: Nobuo HANAI
; TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL
; FILE REFERENCE: 249-202
; CURRENT APPLICATION NUMBER: US/11/131,212
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US/09/971,773
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-308526
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/268,926
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
```

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; SEQ ID NO 23
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Cricetulus griseus
US-11-131-212-23

Query Match      60.4%; Score 32; DB 7; Length 575;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PwLEEE 8
    |||||
Db 340 PwLEEE 345

RESULT 24
US-10-613-744-19
; Sequence 19, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613.744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-613-744-19

Query Match      60.4%; Score 32; DB 6; Length 690;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLE 6
    |||||
Db 678 EGPWSE 683

RESULT 25
US-10-507-275-1
; Sequence 1, Application US/10507275
; Publication No. US20050250166A1
; GENERAL INFORMATION:
; APPLICANT: Masai, Hisao
; APPLICANT: Tamai, Katsuyuki
; APPLICANT: Medical and Biological Laboratories Co., Ltd.
; APPLICANT: Japan Science and Technology Agency
; APPLICANT: Ginkgo Biomedical Research Institute Co., Ltd.
; TITLE OF INVENTION: Cdc7-ASK Kinase Complex, Substrates of the Kinase Complex,
; TITLE OF INVENTION: Specific Antibodies to the Substrates, and Screening Methods
; TITLE OF INVENTION: Using the Same to Screen for Compounds Comprising Cdc7-ASK
; TITLE OF INVENTION: Kinase Inhibitory Ability
; FILE REFERENCE: 082368-001100US
; CURRENT APPLICATION NUMBER: US/10/507,275
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: JP 2002-067702
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: WO PCT/JP03/02918
; PRIOR FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 892
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-275-3

Query Match      59.4%; Score 31.5; DB 6; Length 892;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 EGPWLEEEE 9
    |||||
Db 51 EGP-LEEEE 58

RESULT 26
US-10-507-275-3
; Sequence 3, Application US/10507275
; Publication No. US20050250166A1
; GENERAL INFORMATION:
; APPLICANT: Masai, Hisao
; APPLICANT: Tamai, Katsuyuki
; APPLICANT: Medical and Biological Laboratories Co., Ltd.
; APPLICANT: Japan Science and Technology Agency Co., Ltd.
; APPLICANT: Ginkgo Biomedical Research Institute Co., Ltd.
; TITLE OF INVENTION: Cdc7-ASK Kinase Complex, Substrates of the Kinase Complex,
; TITLE OF INVENTION: Specific Antibodies to the Substrates, and Screening Methods
; TITLE OF INVENTION: Using the Same to Screen for Compounds Comprising Cdc7-ASK
; TITLE OF INVENTION: Kinase Inhibitory Ability
; FILE REFERENCE: 082368-001100US
; CURRENT APPLICATION NUMBER: US/10/507,275
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: JP 2002-067702
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: WO PCT/JP03/02918
; PRIOR FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 892
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-275-3

Query Match      59.4%; Score 31.5; DB 6; Length 892;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 EGPWLEEEE 9
    |||||
Db 51 EGP-LEEEE 58

RESULT 27
US-11-087-227-12
; Sequence 12, Application US/11087227
; Publication No. US20050260566A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Timothy J.
; APPLICANT: Malinowski, Douglas P.
; APPLICANT: Taylor, Adriann J.
; APPLICANT: Parker, Margaret R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: DETECTION OF CERVICAL DISEASE
; FILE REFERENCE: 046143/287139
; CURRENT APPLICATION NUMBER: US/11/087,227
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 60/556,495
; PRIOR FILING DATE: 2004-03-24
; NUMBER OF SEQ ID NOS: 90
```

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 904
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-087-227-12

Query Match      59.4%; Score 31.5; DB 7; Length 904;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1 EGPWLEEE 9
      ||| |||||
Db      60 EGP-LEEE 67

RESULT 28
US-11-055-822-700
; Sequence 700, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 700
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-786

Query Match      58.5%; Score 31; DB 7; Length 159;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 PWLEEE 8
      |||||
Db      126 PWLEAE 131

RESULT 30
US-10-793-626-1756
; Sequence 1756, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1756
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1756

Query Match      58.5%; Score 31; DB 6; Length 338;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 GPWLEE 7  
Db 302 GPWLKD 307

## RESULT 31

US-10-821-234-1565  
; Sequence 1565, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821.234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 1565  
; LENGTH: 338  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1565

Query Match 58.5%; Score 31; DB 6; Length 338;  
Best Local Similarity 66.7%; Pred. No. 1.5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEE 8  
Db 74 PWVEQE 79

## RESULT 32

US-10-770-726-78  
; Sequence 78, Application US/10770726  
; Publication No. US20050266409A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Brown, Eugene  
; APPLICANT: Liu, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING  
; FILE REFERENCE: AM101079 (031896-010000)  
; CURRENT APPLICATION NUMBER: US/10/770.726  
; CURRENT FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 48640  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 78  
; LENGTH: 879  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-770-726-78

Query Match 58.5%; Score 31; DB 6; Length 879;  
Best Local Similarity 83.3%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WLEEEE 9  
Db 673 WLEKEE 678

## RESULT 33

US-10-507-275-5  
; Sequence 5, Application US/10507275  
; Publication No. US20050250166A1  
; GENERAL INFORMATION:

; APPLICANT: Masai, Hisao  
; APPLICANT: Tamai, Katsuyuki  
; APPLICANT: Medical and Biological Laboratories Co., Ltd.  
; APPLICANT: Japan Science and Technology Agency  
; APPLICANT: Ginkgo Biomedical Research Institute Co., Ltd.  
; TITLE OF INVENTION: Cdc7-ASK Kinase Complex, Substrates of the Kinase Complex,  
; TITLE OF INVENTION: Specific Antibodies to the Substrates, and Screening Methods  
; TITLE OF INVENTION: Using the Same to Screen for Compounds Comprising Cdc7-ASK  
; TITLE OF INVENTION: Kinase Inhibitory Ability  
; FILE REFERENCE: 082368-0011000S  
; CURRENT APPLICATION NUMBER: US/10/507.275  
; CURRENT FILING DATE: 2004-09-09  
; PRIOR APPLICATION NUMBER: JP 2002-067702  
; PRIOR FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: WO PCT/JP03/02918  
; PRIOR FILING DATE: 2003-03-12  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 904  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-507-275-5

Query Match 58.5%; Score 31; DB 6; Length 904;  
Best Local Similarity 66.7%; Pred. No. 3.7e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
Db 60 EGPMESEED 68

## RESULT 34

US-11-064-246-10  
; Sequence 10, Application US/11064246  
; Publication No. US20050266431A1  
; GENERAL INFORMATION:  
; APPLICANT: Grosse, William M.,  
; APPLICANT: Alsobrook, John P.,  
; APPLICANT: Lepley, Denise M.,  
; APPLICANT: Burgess, Catherine E.,  
; APPLICANT: Bader, Joel S.,  
; APPLICANT: Bansal, Aruna,  
; APPLICANT: Pena, Carol E.A.,  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Anderson, David  
; APPLICANT: Zhong, Mei  
; APPLICANT: Miller, Charles  
; APPLICANT: Vernet, Corine  
; APPLICANT: Hjal, Tord  
; TITLE OF INVENTION: NUCLEIC ACIDS, POLYPEPTIDES, SINGLE NUCLEOTIDE POLYMORPHISMS AND  
; TITLE OF INVENTION: OF USE THEREOF  
; FILE REFERENCE: Cura 690 CON  
; CURRENT APPLICATION NUMBER: US/11/064.246  
; CURRENT FILING DATE: 2005-02-22  
; PRIOR APPLICATION NUMBER: 10/177.809  
; PRIOR FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: 60/311.285  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 60/299.949  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/300.290  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 60/327.345  
; PRIOR FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 60/327.892  
; PRIOR FILING DATE: 2001-10-09  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Custom

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; SEQ ID NO 10
; LENGTH: 980
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-064-246-10

Query Match      58.5%; Score 31; DB 7; Length 980;
Best Local Similarity 71.4%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 PwLEEEE 9
Db      420 PwLPSEE 426

RESULT 35
US-10-793-626-2052
; Sequence 2052, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2052
; LENGTH: 1442
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2052

Query Match      58.5%; Score 31; DB 6; Length 1442;
Best Local Similarity 55.6%; Pred. No. 5.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 EGPWLEEEE 9
Db      1399 EGPFLSKED 1407

RESULT 36
US-11-113-424-53
; Sequence 53, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29

; SEQ ID NO 53
; LENGTH: 2515
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-11-113-424-53

Query Match      58.5%; Score 31; DB 7; Length 2515;
Best Local Similarity 62.5%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GPWLEEEE 9
Db      2442 GDMTEEEK 2449

RESULT 37
US-11-186-731-2
; Sequence 2, Application US/11186731
; Publication No. US20050255521A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Thereof
; FILE REFERENCE: MP12001-047P1RCP1(M)
; CURRENT APPLICATION NUMBER: US/11/186,731
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/077,130
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-731-2

Query Match      58.5%; Score 31; DB 7; Length 2630;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 PwLEEE 8
Db      2584 PwLTEE 2589

RESULT 38
US-10-995-561-773
; Sequence 773, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 773
; LENGTH: 3803
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-773

Query Match      58.5%; Score 31; DB 6; Length 3803;
```

```
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 774
; LENGTH: 5406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-774

Query Match      58.5%; Score 31; DB 6; Length 5406;
Best Local Similarity 71.4%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3 PWLEEEE 9
      ||| |||
Db      2524 PWLMEKE 2530

RESULT 39
US-10-995-561-771
; Sequence 771, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 771
; LENGTH: 3960
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-771

Query Match      58.5%; Score 31; DB 6; Length 3960;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3 PWLEEEE 9
      ||| |||
Db      2524 PWLMEKE 2530

RESULT 40
US-10-995-561-777
; Sequence 777, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 777
; LENGTH: 5335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-777

Query Match      58.5%; Score 31; DB 6; Length 5335;
Best Local Similarity 71.4%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3 PWLEEEE 9
      ||| |||
Db      2432 PWLMEKE 2438

RESULT 41
US-10-995-561-774
; Sequence 774, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
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; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 774
; LENGTH: 5406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-774

Query Match      58.5%; Score 31; DB 6; Length 5406;
Best Local Similarity 71.4%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3 PWLEEEE 9
      ||| |||
Db      2503 PWLMEKE 2509

RESULT 42
US-10-995-561-779
; Sequence 779, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 779
; LENGTH: 5415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-779

Query Match      58.5%; Score 31; DB 6; Length 5415;
Best Local Similarity 71.4%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3 PWLEEEE 9
      ||| |||
Db      2524 PWLMEKE 2530

RESULT 43
US-10-995-561-775
; Sequence 775, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 775
; LENGTH: 5464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-775

Query Match      58.5%; Score 31; DB 6; Length 5464;
Best Local Similarity 71.4%; Pred. No. 1.8e+03;
```

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 3 PWLEEE 9  
Db 2524 PWLMEKE 2530

## RESULT 44

US-10-995-561-776  
; Sequence 776, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 776  
; LENGTH: 5935  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-995-561-776

Query Match 58.5%; Score 31; DB 6; Length 5935;  
Best Local Similarity 71.4%; Pred. No. 2e+03;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEE 9  
Db 3026 PWLMEKE 3032

## RESULT 45

US-11-186-731-5  
; Sequence 5, Application US/11186731  
; Publication No. US2005025521A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Acton, Susan L.  
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family  
; TITLE OF INVENTION: Members and Uses Therefor  
; FILE REFERENCE: MPI2001-047P/RCPI (M)  
; CURRENT APPLICATION NUMBER: US/11/186,731  
; CURRENT FILING DATE: 2005-07-21  
; PRIOR APPLICATION NUMBER: US/10/077,130  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: 60/269201  
; PRIOR FILING DATE: 2001-02-15  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 7968  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-186-731-5

Query Match 58.5%; Score 31; DB 7; Length 7968;  
Best Local Similarity 83.3%; Pred. No. 2.5e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEE 8  
Db 7922 PWLTEE 7927

## RESULT 46

US-10-929-988-14  
; Sequence 14, Application US/10929988  
; Publication No. US20050277588A1

; GENERAL INFORMATION:  
; APPLICANT: CWIRLA, STEVEN E.  
; APPLICANT: BALU, PALANI  
; APPLICANT: DUFFIN, DAVID J.  
; APPLICANT: PIPLANI, SUNILA  
; APPLICANT: MERRILL, BARBARA MCEOWEN  
; APPLICANT: SCHATZ, PETER JOSEPH  
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY  
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED  
; TITLE OF INVENTION: USES  
; FILE REFERENCE: 0300-0014  
; CURRENT APPLICATION NUMBER: US/10/929,988  
; CURRENT FILING DATE: 2004-08-30  
; PRIOR APPLICATION NUMBER: US/09/620,091  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 491  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-929-988-14

Query Match 56.6%; Score 30; DB 6; Length 10;  
Best Local Similarity 80.0%; Pred. No. 9.2;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWL 5  
Db 4 EGPWV 8

## RESULT 47

US-10-929-988-164  
; Sequence 164, Application US/10929988  
; Publication No. US20050277588A1  
; GENERAL INFORMATION:  
; APPLICANT: CWIRLA, STEVEN E.  
; APPLICANT: BALU, PALANI  
; APPLICANT: DUFFIN, DAVID J.  
; APPLICANT: PIPLANI, SUNILA  
; APPLICANT: MERRILL, BARBARA MCEOWEN  
; APPLICANT: SCHATZ, PETER JOSEPH  
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY  
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED  
; TITLE OF INVENTION: USES  
; FILE REFERENCE: 0300-0014  
; CURRENT APPLICATION NUMBER: US/10/929,988  
; CURRENT FILING DATE: 2004-08-30  
; PRIOR APPLICATION NUMBER: US/09/620,091  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 491  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 164  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-929-988-164

Query Match 56.6%; Score 30; DB 6; Length 12;  
Best Local Similarity 80.0%; Pred. No. 11;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWL 5  
Db 7 EGPWV 11

## RESULT 48

US-10-929-988-190  
; Sequence 190, Application US/10929988  
; Publication No. US20050277589A1  
; GENERAL INFORMATION:  
; APPLICANT: CWIRLA, STEVEN E.  
; APPLICANT: BALU, PALANI  
; APPLICANT: DUFFIN, DAVID J.  
; APPLICANT: PIPLANI, SUNILA  
; APPLICANT: MERRILL, BARBARA MCEOWEN  
; APPLICANT: SCHATZ, PETER JOSEPH  
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY  
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED  
; TITLE OF INVENTION: US8  
; FILE REFERENCE: 0300-0014  
; CURRENT APPLICATION NUMBER: US/10/929,988  
; CURRENT FILING DATE: 2004-08-30  
; PRIOR APPLICATION NUMBER: US/09/620,091  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 491  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 190  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-929-988-190

Query Match 56.6%; Score 30; DB 6; Length 18;  
Best Local Similarity 80.0%; Pred. No. 16;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWL 5  
Db 10 EGPWV 14  
|||:

## RESULT 49

US-10-467-657-390  
; Sequence 390, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 390  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-390

Query Match 56.6%; Score 30; DB 6; Length 118;  
Best Local Similarity 55.6%; Pred. No. 85;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9  
Db 69 EGDWLIDKE 77  
|||:|

## RESULT 50

US-11-165-141-4  
; Sequence 4, Application US/11165141  
; Publication No. US20050266485A1  
; GENERAL INFORMATION:  
; APPLICANT: Preenell, Scott R.  
; APPLICANT: Xu, Wenfeng  
; APPLICANT: Novak, Julia E.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Grant, Francis J.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19  
; FILE REFERENCE: 00-108  
; CURRENT APPLICATION NUMBER: US/11/165,141  
; CURRENT FILING DATE: 2005-06-23  
; PRIOR APPLICATION NUMBER: US/09/995,898  
; PRIOR FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: US 60/253,561  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 60/267,211  
; PRIOR FILING DATE: 2001-02-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 203  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-165-141-4

Query Match 56.6%; Score 30; DB 7; Length 203;  
Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EGPWLEER 8  
Db 88 KSPWVESE 95  
:|:|

Search completed: January 3, 2006, 09:55:46  
Job time : 7.42857 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:05 ; Search time 90.8571 Seconds  
(without alignments)  
43.523 Million cell updates/sec

Title: US-10-759-832-7

Perfect score: 53

Sequence: 1 EGPWLEERE 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 1000 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	9	2	Aaw24399 Anti-gastr
2	53	100.0	9	3	Aay59434 Antigastr
3	53	100.0	9	3	Aay51305 Human gas
4	53	100.0	9	8	ADH89212 Gastrin G
5	53	100.0	10	8	ADH89213 Gastrin G
6	53	100.0	10	9	AEC05673 Gastrin p
7	53	100.0	11	9	ADW00245 Human wil
8	53	100.0	12	2	AAR06245 Antigenic
9	53	100.0	13	9	ADY37657 Human G17
10	53	100.0	15	2	AAR74297 Human gas
11	53	100.0	16	2	AAR74295 Human gas
12	53	100.0	16	3	AAY49309 Human hep
13	53	100.0	16	6	ABP73035 Peptide s
14	53	100.0	17	2	AAW65184 Gastrin f
15	53	100.0	17	2	AAW24398 Carboxy-a
16	53	100.0	17	4	AAU05580 Human Jan
17	53	100.0	17	4	AAW91246 Gastrin r
18	53	100.0	17	4	AAW59273 KS2-pepti
19	53	100.0	17	5	AAU76504 Protein k
20	53	100.0	17	7	ADF72769 Chemosele
21	53	100.0	17	8	ADF72934 Biotinyla
22	53	100.0	17	8	ADH10240 Peptide s
23	53	100.0	17	8	ADH89206 Gastrin G
24	53	100.0	17	8	ADH89223 Gastrin G

25	53	100.0	17	8	ADK00577	Immunogen
26	53	100.0	17	8	ADL02105	Phosphope
27	53	100.0	17	8	ADN03334	Exemplary
28	53	100.0	17	8	ADR42169	Gastrin r
29	53	100.0	17	8	ADT49596	Human mat
30	53	100.0	17	8	ADU48550	Gastrin-1
31	53	100.0	17	8	ADU48549	Gastrin-1
32	53	100.0	17	9	ADV16301	Human gas
33	53	100.0	17	9	ADV16302	Human gas
34	53	100.0	17	9	ADW00243	Human var
35	53	100.0	17	9	ADW00242	Human wil
36	53	100.0	17	9	ADW71906	Non-phosp
37	53	100.0	17	9	AEA08308	PTK domai
38	53	100.0	17	9	AEA36970	Phosphory
39	53	100.0	17	9	AEA52649	Kinase bi
40	53	100.0	17	9	AEB25345	Peptide u
41	53	100.0	17	9	AEB77639	Gastrin-1
42	53	100.0	17	9	AEC05671	Gastrin p
43	53	100.0	18	2	AAW24397	Glycine-e
44	53	100.0	18	8	ADH89207	Glycine e
45	53	100.0	18	8	ADT49597	Human gas
46	53	100.0	18	9	AEC05677	Gastrin p
47	53	100.0	19	9	AEC05672	Gastrin t
48	53	100.0	19	9	AEC05674	Gastrin t
49	53	100.0	20	9	AEC05675	Gastrin T
50	53	100.0	27	9	AEC05676	Gastrin T
51	53	100.0	34	8	ADT49598	Human gas
52	53	100.0	35	8	ADT49599	Human gas
53	50	94.3	12	2	AAW62740	Gastrin h
54	50	94.3	12	2	ADY37667	Human G17
55	50	94.3	17	2	AAW62739	Gastrin h
56	50	94.3	17	4	ADU24445	Novel glu
57	50	94.3	17	8	ADU46719	Gastrin 1
58	50	94.3	17	8	ADZ71375	N-termina
59	50	94.3	17	9	ABW92577	Glutamin
60	50	94.3	17	2	AAW31639	Human gly
61	50	94.3	18	4	AAW72381	Human pro
62	50	94.3	18	4	AAW72385	Human gly
63	50	94.3	21	2	AAW31641	Gastrin p
64	50	94.3	21	4	AAW72383	Human pro
65	50	94.3	28	9	ADW00244	Human wil
66	50	94.3	33	7	ABR83022	Gastrin-r
67	50	94.3	33	8	ADL92093	Big gastr
68	50	94.3	33	9	ADW00233	Human wil
69	50	94.3	33	9	ADW00234	Human var
70	50	94.3	34	2	AAW62734	Gastrin h
71	50	94.3	34	2	AAW31638	Amidated
72	50	94.3	34	4	AAW91247	Gastrin r
73	50	94.3	34	4	AAW72380	Human pro
74	50	94.3	34	4	AAW72386	Human ami
75	50	94.3	34	5	ABW82195	Gastrin 3
76	50	94.3	34	8	ADJ68390	Human hea
77	50	94.3	34	8	ADJ68390	Human hea
78	50	94.3	34	8	ADJ68390	Human hea
79	50	94.3	34	8	ADJ68390	Human hea
80	50	94.3	34	8	ADJ68390	Human hea
81	50	94.3	34	8	ADJ68390	Human hea
82	50	94.3	34	9	ADV16299	Human gas
83	50	94.3	34	9	ADV16299	Human gas
84	50	94.3	34	9	ADU77733	Gastrin p
85	50	94.3	34	9	ADU77733	Gastrin p
86	50	94.3	34	9	ADW00240	Human wil
87	50	94.3	34	9	ADW00241	Human var
88	50	94.3	34	9	ABW77640	Big gastr
89	50	94.3	34	9	ABW98014	Gastrin 3
90	50	94.3	34	9	ABW98013	Gastrin 3
91	50	94.3	35	2	AAW31637	Amidated
92	50	94.3	35	4	AAW72379	Immunogen
93	50	94.3	47	2	AAW62750	Immunogen
94	50	94.3	52	2	ABW62749	Immunogen
95	50	94.3	52	2	ABW62749	Immunogen
96	50	94.3	69	2	AAW62745	Immunogen
97	50	94.3	74	2	AAW31636	Human pro

98	50	94.3	74	4	AAy72378	Human pro	171	39	73.6	525	9	ADY19677	PRO polyp
99	50	94.3	80	8	ADT54946	Human pro	172	39	73.6	525	9	ADY15710	PRO polyp
100	50	94.3	100	4	AAy72384	Human pre	173	39	73.6	529	7	ADP76407	Novel hum
101	50	94.3	101	1	AAp90331	Recombina	174	39	73.6	529	8	ADP54623	Human PRO
102	50	94.3	101	8	ADU48551	Gastrin-3	175	39	73.6	539	8	ADS12013	Human the
103	50	94.3	101	9	ADU77736	Gastrin p	176	39	73.6	551	3	AAH13598	Streptomy
104	50	94.3	101	9	ABE98017	Gastrin 7	177	39	73.6	567	7	ADB85487	Human agg
105	49	92.5	17	9	AEAS1268	Ligand-co	178	39	73.6	619	6	ABU45553	Protein e
106	49	92.5	18	8	ADO51612	Phosphory	179	39	73.6	628	7	ADB85485	Human agg
107	49	92.5	19	5	AAU74405	LyA3-Gast	180	39	73.6	752	7	ADB85483	Human agg
108	49	92.5	19	7	ADP45101	Kemptide.	181	39	73.6	753	7	ADB85481	Human agg
109	49	92.5	19	9	ADW76494	Peptide #	182	39	73.6	763	7	ADB85492	Human agg
110	48	90.6	11	8	ADH89211	Gastrin G	183	39	73.6	880	4	ABB71719	Drosophil
111	48	90.6	11	8	ADT54952	Human pro	184	39	73.6	929	3	AAH41226	Human ORF
112	48	90.6	13	8	ADT54965	Human pro	185	39	73.6	930	2	AAW75426	Human agg
113	48	90.6	16	1	AAp71246	Non-radio	186	39	73.6	930	7	ADB85503	Human agg
114	48	90.6	16	3	ABH13767	Tyrosine	187	39	73.6	930	7	ADB85479	Human agg
115	48	90.6	16	9	ADW00236	Human var	188	39	73.6	930	8	ADQ17600	Human sof
116	48	90.6	16	9	ADW00235	Human wil	189	39	73.6	930	8	ADR99240	ADAMTS.
117	48	90.6	17	5	ABB82194	Gastrin 1	190	39	73.6	960	8	ADJ50369	Oil-asso
118	48	90.6	17	8	ADO70140	Gastrin p	191	39	73.6	1108	8	ADJ49373	Oil-asso
119	48	90.6	17	8	ADO70139	Gastrin p	192	39	73.6	1108	8	ADJ49646	Oil-asso
120	48	90.6	17	8	ADT54950	Human pro	193	39	73.6	1413	5	AAE21729	Human PKI
121	48	90.6	17	9	ADU77735	Gastrin p	194	39	73.6	1460	7	ADC59465	Novel hum
122	48	90.6	17	9	ADU77734	Gastrin p	195	39	73.6	1460	8	ADU04632	Human KIA
123	48	90.6	17	9	ABE98015	Gastrin 1	196	38	71.7	6	ADH89209	Gastrin G	
124	48	90.6	17	9	ABE98016	Gastrin 1	197	38	71.7	6	ADT49600	Human gas	
125	48	90.6	18	8	ADT54949	Human pro	198	38	71.7	12	2	AAE06246	Antigenic
126	46	86.8	18	8	ADN29118	Human bio	199	38	71.7	12	3	AAy49303	Human hep
127	45	84.9	238	5	AAE62741	Gastrin h	200	38	71.7	12	3	AAy51309	Human gas
128	45	84.9	238	8	AAU93061	Arabidops	201	38	71.7	12	6	ABP73032	Peptide s
129	45	84.9	238	8	ADD30031	Plant yie	202	38	71.7	12	9	ADY37660	Human G17
130	45	84.9	238	8	ADI44105	Plant tra	203	38	71.7	17	8	ADT54960	Human pro
131	45	84.9	238	8	ADI61441	A. thalia	204	38	71.7	18	8	ADT54957	Human pro
132	45	84.9	238	8	ADO02415	Thalecres	205	38	71.7	44	3	AAH33343	Eucalyptu
133	44	83.0	14	2	AAO6249	Antigenic	206	38	71.7	49	3	AAH33176	Eucalyptu
134	44	83.0	14	9	ADY37666	Human G17	207	38	71.7	62	6	ABO01749	Rice Myb-
135	43	81.1	7	8	ADH89210	Gastrin G	208	38	71.7	62	8	ADJ77717	Rice Myb-
136	42	79.2	17	8	ADT54959	Human pro	209	38	71.7	76	3	AAH33168	Eucalyptu
137	42	79.2	18	8	ADT54956	Human pro	210	38	71.7	94	2	AAH331902	Soybean c
138	42	79.2	18	8	ADT54955	Human pro	211	38	71.7	146	4	AAH43599	Human pol
139	42	79.2	542	9	ABM96322	M. xanthu	212	38	71.7	146	8	ADM24620	Human PRO
140	41	77.4	248	7	ADCO1289	Enterohae	213	38	71.7	179	6	ABO01743	Maize Myb
141	41	77.4	262	8	ADX92011	Plant ful	214	38	71.7	179	8	ADJ77705	Corn Myb-
142	41	77.4	273	2	AAy05831	Arabidops	215	38	71.7	196	6	ADA55578	Human pro
143	41	77.4	273	8	ABO43112	A. thalia	216	38	71.7	203	8	ADX91109	Plant ful
144	41	77.4	273	8	ADO01749	Thalecres	217	38	71.7	205	6	ABR41137	Human DIT
145	41	77.4	368	8	ADY25276	Plant ful	218	38	71.7	205	6	ADJ48497	Maize oil
146	40	75.5	122	5	ABG60002	Human DIT	219	38	71.7	221	6	ABO01748	Rice Myb-
147	40	75.5	182	4	AAU16252	Human nov	220	38	71.7	221	8	ADJ77715	Rice Myb-
148	40	75.5	182	6	ABU55321	Human nov	221	38	71.7	232	8	ADX87958	Plant ful
149	40	75.5	211	6	ABR41442	Human DIT	222	38	71.7	232	8	ADX78815	Plant ful
150	40	75.5	213	7	ADL22757	Human dis	223	38	71.7	234	8	ADO01763	Thalecres
151	40	75.5	310	8	ADJ49001	Oil-asso	224	38	71.7	248	8	ADN73599	Thale cre
152	40	75.5	349	6	ADA15583	A. thalia	225	38	71.7	256	8	ADN73599	Thale cre
153	40	75.5	349	7	ADD55756	Thalecres	226	38	71.7	258	7	ADD30312	Plant yie
154	40	75.5	349	8	ADO01721	Thalecres	227	38	71.7	258	8	ADI44233	Plant tra
155	40	75.5	612	7	ABM85299	Human pro	228	38	71.7	264	8	ADX74712	Plant ful
156	40	75.5	870	9	AEA20008	Novel hum	229	38	71.7	278	2	AAW37811	Tobacco M
157	40	75.5	920	7	ADB80357	Human MDD	230	38	71.7	317	4	AAH73687	Human oxi
158	40	75.5	2214	8	ADN10916	Phaffia r	231	38	71.7	317	5	ABB08430	Amino aci
159	39	73.6	174	7	ADM07206	Human Nm2	232	38	71.7	317	6	ABB99478	Amino aci
160	39	73.6	336	5	ABP41746	Human ova	233	38	71.7	317	8	ADJ88319	Human eny
161	39	73.6	492	7	ABR84659	Human tru	234	38	71.7	318	5	ABP60935	Zymomonas
162	39	73.6	498	2	AAH13270	Lymphocyt	235	38	71.7	325	7	ADD30244	Plant yie
163	39	73.6	498	2	AAH87089	Human imm	236	38	71.7	325	8	ADI44101	Plant tra
164	39	73.6	525	6	ADA26247	Human LAG	237	38	71.7	325	8	ADJ49247	Oil-asso
165	39	73.6	525	7	ADFL13710	Tumor-Ass	238	38	71.7	325	8	ADO02405	Thalecres
166	39	73.6	525	7	ADFL13709	Tumor-Ass	239	38	71.7	329	6	ABU21136	Protein e
167	39	73.6	525	8	ADP12408	Protein e	240	38	71.7	340	8	ADY10688	Plant ful
168	39	73.6	525	8	ADQ17787	Human sof	241	38	71.7	369	4	AAH47594	Human DHD
169	39	73.6	525	8	ADS73722	Human lym	242	38	71.7	369	4	AAU14291	Human nov
170	39	73.6	525	8	ADS10759	Human the	243	38	71.7	369	5	ABB08431	Amino aci

244	38	71.7	369	8	ADJ88321	Adj88321 Human bet	317	729	7	ADF61818	Human BRC
245	38	71.7	369	8	ADQ15168	Adq15168 Human can	318	729	8	ADL23955	Deubiquit
246	38	71.7	373	6	ABO00708	AbO00708 Novel hum	319	752	2	AAW98883	Human A-M
247	38	71.7	374	6	ADW72635	Adw72635 Plant ful	320	769	4	ABG21454	Novel hum
248	38	71.7	390	6	ABR41163	AbR41163 Human DIT	321	961	8	ADG73342	Arabidops
249	38	71.7	501	5	AAO15583	AaO15583 Human PYR	322	1431	9	ADV97898	Murine pr
250	38	71.7	501	7	ADP94741	AdP94741 Human PYR	323	70	8	Adf45238	Human INP
251	38	71.7	548	8	ADS73344	AdS73344 Arabidops	324	98	8	AdS73348	Secale ce
252	38	71.7	581	8	ADY24033	AdY24033 Plant ful	325	99	4	ABH15846	Human ner
253	38	71.7	662	7	ABM90165	Abm90165 Rice abio	326	118	5	ABP00831	Human ORF
254	38	71.7	894	8	ADN23878	Adn23878 Bacterial	327	118	5	ABP00831	Human ORF
255	38	71.7	920	8	ADN23879	Adn23879 Bacterial	328	121	7	ADM03886	Human pro
256	38	71.7	991	9	ADV44751	AdV44751 Human nuc	329	161	8	ADX70925	Plant ful
257	37	69.8	50	4	AAE62001	Aae62001 A-myb pro	330	167	3	AAG32234	Arabidops
258	37	69.8	50	4	AAE62000	Aae62000 B-myb pro	331	193	3	AAG32233	Arabidops
259	37	69.8	50	4	AAE62002	Aae62002 C-myb pro	332	193	6	ABU49576	Protein e
260	37	69.8	102	8	ADR09430	AdR09430 Human pro	333	195	3	AAE24633	Arabidops
261	37	69.8	106	9	AEC05458	Aec05458 Mouse C-M	334	197	8	ADS73347	Hordeum v
262	37	69.8	173	7	ABO75581	AbO75581 Pseudomon	335	210	7	ABO74059	Pseudomon
263	37	69.8	206	6	ABO01758	AbO01758 Soybean M	336	241	6	ABP77400	N. gonorr
264	37	69.8	206	8	ADJ77735	AdJ77735 Soybean M	337	241	6	ABU37415	Protein e
265	37	69.8	250	8	ADT71530	AdT71530 Human CGD	338	261	4	AAE70543	Human PRO
266	37	69.8	254	8	ADS73346	AdS73346 Adiantum	339	261	6	ABO01372	Human pro
267	37	69.8	265	4	ABG16395	AbG16395 Novel hum	340	261	6	ABO01373	Human pro
268	37	69.8	274	4	ABG22354	AbG22354 Novel hum	341	261	6	ABO01366	Human pro
269	37	69.8	274	4	AAU31494	Aau31494 Novel hum	342	261	6	ABO01366	Human pro
270	37	69.8	278	4	ABG21451	AbG21451 Novel hum	343	261	8	ADN96118	Human NOV
271	37	69.8	301	3	AAE41485	Aae41485 Arabidops	344	261	8	ADN96110	Human NOV
272	37	69.8	301	8	ADN73669	Adn73669 Thale cre	345	261	8	ADN96116	Human NOV
273	37	69.8	304	4	AAE02541	Aae02541 A. thalia	346	263	3	AAG32232	Arabidops
274	37	69.8	304	5	AAU92594	Aau92594 Arabidops	347	271	7	ADC08052	Rice prot
275	37	69.8	304	7	ADP30740	AdP30740 Plant yie	348	286	4	ABG07914	Novel hum
276	37	69.8	304	7	ADP37249	AdP37249 Plant yie	349	288	3	AAE06991	Arabidops
277	37	69.8	304	8	ADL43793	AdL43793 Plant tra	350	288	3	AAE06990	Arabidops
278	37	69.8	304	8	ADO01705	AdO01705 Thalecres	351	322	3	AAE06990	Arabidops
279	37	69.8	304	9	AEA27069	Aea27069 Stress to	352	322	3	AAE06989	Arabidops
280	37	69.8	318	3	AAE41484	Aae41484 Arabidops	353	331	3	AAE06989	Arabidops
281	37	69.8	325	7	ADC97159	AdC97159 E. faeciu	354	331	3	AAE06982	Arabidops
282	37	69.8	337	8	ADN47876	AdN47876 Thermococ	355	350	3	AAE48107	Arabidops
283	37	69.8	367	3	AAE46455	Aae46455 Arabidops	356	352	3	AAE32355	Arabidops
284	37	69.8	367	3	AAE04911	Aae04911 Arabidops	357	361	6	AAE60881	Mevalonat
285	37	69.8	367	7	ADP55848	AdP55848 Thalecres	358	361	6	AAE29749	Protein e
286	37	69.8	367	8	ADI43505	AdI43505 Plant tra	359	361	6	ABU97219	Enzyme po
287	37	69.8	367	8	ADO01719	AdO01719 Thalecres	360	362	4	AAE01937	Arabidops
288	37	69.8	367	9	AEA26741	Aea26741 Stress to	361	362	7	ADD55722	Thalecres
289	37	69.8	373	3	AAE46454	Aae46454 Arabidops	362	362	8	ABO01697	Thalecres
290	37	69.8	373	3	AAE04910	Aae04910 Arabidops	363	362	8	ABO04889	Murine ca
291	37	69.8	398	4	AAE96622	Aae96622 Putative	364	365	7	ADC96963	E. faeciu
292	37	69.8	398	8	ADS43175	AdS43175 Bacterial	365	368	8	ADX97296	Plant ful
293	37	69.8	497	8	ADP03083	AdP03083 GFP-M&M p	366	389	5	ADH48786	NOV30 pro
294	37	69.8	530	9	ABE06261	Aeb06261 Amino aci	367	393	7	ADD30742	Plant yie
295	37	69.8	574	4	ABE60930	AbE60930 Drosophil	368	393	8	ADI43799	Plant tra
296	37	69.8	636	9	ADY54319	AdY54319 Mouse Myb	369	397	9	ABM90750	M. xanthu
297	37	69.8	640	8	ABM80820	Abm80820 Tumour-as	370	505	8	ADS73343	Arabidops
298	37	69.8	640	8	ADP56094	AdP56094 Human PRO	371	524	8	ADM74233	Human NOV
299	37	69.8	640	8	ADP73354	AdP73354 Human Rmy	372	524	4	AAE70540	Human PRO
300	37	69.8	640	9	ADX05522	AdX05522 Cyclin-de	373	525	4	AAE70541	Human PRO
301	37	69.8	640	9	ADY19860	AdY19860 PRO polyP	374	525	4	AAE70541	Human PRO
302	37	69.8	640	9	ADY54321	AdY54321 Human Myb	375	525	6	ABO01369	Human pro
303	37	69.8	651	8	ADP66286	AdP66286 Human pro	376	525	6	ABO01367	Human pro
304	37	69.8	651	8	ABE59671	AbE59671 Drosophil	377	525	6	ABO01368	Human pro
305	37	69.8	691	4	ABE59671	AbE59671 Drosophil	378	525	8	ADN96106	Human NOV
306	37	69.8	700	2	AAE03663	Aae03663 Human myb	379	525	8	ADN96108	Human NOV
307	37	69.8	700	4	AAE40233	Aae40233 Human pol	380	525	8	ADN96110	Human NOV
308	37	69.8	700	6	ABR92125	AbR92125 Human cer	381	526	8	ADN96110	Human NOV
309	37	69.8	700	7	ADD14182	AdD14182 Human src	382	526	4	ABG08397	Novel hum
310	37	69.8	700	7	ADN95317	AdN95317 Human BEC	383	526	4	ABG08397	Novel hum
311	37	69.8	700	8	ADL12338	AdL12338 Human ste	384	526	6	ABO01370	Human pro
312	37	69.8	700	8	ADL70593	AdL70593 Cervical	385	527	6	ABO01375	Human pro
313	37	69.8	700	8	ABM82242	Abm82242 Tumour-as	386	527	8	ADN96112	Human NOV
314	37	69.8	711	7	ADG75747	AdG75747 Human pro	387	527	8	ADN96122	Human NOV
315	37	69.8	724	4	AAE42019	Aae42019 Human pol	388	543	6	ABO01371	Human pro
316	37	69.8	729	2	AAW47538	Aaw47538 Homo sapi	389	543	6	ABO01374	Human pro

390	36	67.9	543	8	ADM74229	Adm74229 Human NOV	463	35	66.0	117	7	ADH88255	Adh88255 Enterococ
391	36	67.9	543	8	ADN96120	Adn96120 Human NOV	464	35	66.0	121	4	ABG17138	Abg17138 Novel hum
392	36	67.9	544	5	ABP69306	Abp69306 Human pol	465	35	66.0	121	5	ABB99084	Abb99084 Human zin
393	36	67.9	588	8	ADS73321	Ads73321 Tobacco 3	466	35	66.0	121	7	ADC33343	Adc33343 Human nov
394	36	67.9	637	9	ABX339871	Abx339871 L. pneumo	467	35	66.0	122	6	ABO01772	Ab001772 Bread whe
395	36	67.9	642	9	ABX336461	Abx336461 L. pneumo	468	35	66.0	122	8	ADJ77763	Adj77763 Wheat Myb
396	36	67.9	680	6	ABU335728	Abu335728 Protein e	469	35	66.0	125	3	AAG44889	Aag44889 Zea may
397	36	67.9	715	8	ADX95897	Adx95897 Plant ful	470	35	66.0	126	3	AAB33184	Aab33184 Eucalyptu
398	36	67.9	776	7	ADD31027	Add31027 Plant yie	471	35	66.0	126	6	ABO01753	Ab001753 Rice Myb-
399	36	67.9	776	8	ADI43929	Adi43929 Plant tra	472	35	66.0	126	8	ADJ77725	Adj77725 Rice Myb-
400	36	67.9	776	8	ADS73341	Ads73341 Arabidops	473	35	66.0	130	3	ABX33154	Abx33154 Eucalyptu
401	36	67.9	776	9	AEA26665	Aea26665 Stress to	474	35	66.0	136	6	ADA15579	Ada15579 A. thalia
402	36	67.9	779	4	AAM79958	Aam79958 Human pro	475	35	66.0	136	8	ADO01713	Ado01713 Thalecres
403	36	67.9	779	4	AAM79974	Aam79974 Human pro	476	35	66.0	146	3	AAB33155	Aab33155 Eucalyptu
404	36	67.9	779	4	ABG00880	Abg00880 Novel hum	477	35	66.0	149	6	AAU16218	Aau16218 Human nov
405	36	67.9	788	8	ADS73315	Ads73315 Rice 3 Rm	478	35	66.0	149	6	ABU55287	Abu55287 Human nov
406	36	67.9	792	8	ADN27045	Adn27045 Bacterial	479	35	66.0	151	5	ABG59819	Abg59819 Human sec
407	36	67.9	804	8	ADQ66097	Adq66097 Novel hum	480	35	66.0	156	3	AAG44280	Aag44280 Arabidops
408	36	67.9	811	6	ABR58290	AbR58290 BC00343 p	481	35	66.0	158	3	AAG44888	Aag44888 Zea may
409	36	67.9	816	6	ABR58329	AbR58329 XM_035861	482	35	66.0	159	3	AAB33206	Aab33206 Pinus rad
410	36	67.9	816	4	ABG25783	Abg25783 Novel hum	483	35	66.0	162	6	ADA48106	Ada48106 Rice prot
411	36	67.9	816	4	ABG04035	Abg04035 Novel hum	484	35	66.0	162	7	ABM85964	Abm85964 Rice abio
412	36	67.9	823	6	ABO14746	Ab014746 Novel hum	485	35	66.0	164	8	ADJ48845	Adj48845 Oil-asso
413	36	67.9	829	5	AAE15854	Aae15854 Human SBZ	486	35	66.0	171	7	ABM86186	Abm86186 Rice abio
414	36	67.9	853	5	AAE15853	Aae15853 Human SEZ	487	35	66.0	192	3	AAB33255	Aab33255 Eucalyptu
415	36	67.9	865	6	ABR41371	AbR41371 Human DIT	488	35	66.0	196	8	ADX70806	Adx70806 Plant ful
416	36	67.9	868	6	ABR41418	AbR41418 Human DIT	489	35	66.0	215	8	ADY06469	Ady06469 Plant ful
417	36	67.9	869	7	ADB64378	AdB64378 Human pro	490	35	66.0	216	4	AAE04182	Aae04182 Human gen
418	36	67.9	884	6	ABU05307	Abu05307 Human dia	491	35	66.0	224	8	ADY70917	Ady70917 Plant ful
419	36	67.9	925	4	AAO13881	Aao13881 Human pol	492	35	66.0	233	8	ADQ65132	Adq65132 Novel hum
420	36	67.9	993	4	AAH70537	Aah70537 Human PRO	493	35	66.0	250	9	ADW17378	Adw17378 Eucalyptu
421	36	67.9	993	8	ADU73298	AdU73298 Rice 3 Rm	494	35	66.0	257	3	AAG36350	Aag36350 Arabidops
422	36	67.9	993	8	ADU24061	AdU24061 Human asp	495	35	66.0	257	6	ADA48652	Ada48652 Rice prot
423	36	67.9	994	4	AAH70538	Aah70538 Human PRO	496	35	66.0	257	7	ABM90166	Abm90166 Rice abio
424	36	67.9	994	5	AAU81976	Aau81976 Human sec	497	35	66.0	261	7	ADD30200	Add30200 Plant yie
425	36	67.9	995	8	ADT06978	Adt06978 Arabidops	498	35	66.0	261	8	ADI41801	Adi41801 Plant tra
426	36	67.9	1042	8	ADH73319	AdH73319 Tobacco 3	499	35	66.0	261	9	AEA26693	Aea26693 Stress to
427	36	67.9	1090	4	ABG04713	Abg04713 Novel hum	500	35	66.0	263	3	AAG36349	Aag36349 Arabidops
428	36	67.9	1177	4	ABG28191	Abg28191 Novel hum	501	35	66.0	264	5	ABJ10414	Abj10414 Myb-relat
429	36	67.9	1177	4	ABG02336	Abg02336 Novel hum	502	35	66.0	264	7	ADM26396	Adm26396 Hyperther
430	36	67.9	1282	7	ABM88185	Abm88185 Rice abio	503	35	66.0	264	8	ADH50112	Adh50112 Wheat Myb
431	36	67.9	1282	8	ADI45253	Adi45253 Rice isop	504	35	66.0	268	8	ADY23758	Ady23758 Plant ful
432	36	67.9	1596	5	AAE20271	Aae20271 Human lun	505	35	66.0	269	3	AAG36348	Aag36348 Arabidops
433	36	67.9	2097	4	ABG17329	Abg17329 Novel hum	506	35	66.0	269	9	ADW17409	Adw17409 Eucalyptu
434	36	67.9	2097	7	ADC33271	AdC33271 Human nov	507	35	66.0	276	6	ABU05299	Abu05299 Human dia
435	35	66.0	8	2	AAW21347	Aaw21347 Gastrin p	508	35	66.0	277	8	ADI42106	Adi42106 Plant tra
436	35	66.0	8	8	ADW39615	Adw39615 HMG CoA r	509	35	66.0	279	8	ADQ37109	Adq37109 Cell prol
437	35	66.0	14	9	ABE98019	AbE98019 Gastrin 1	510	35	66.0	279	8	ADY73766	Ady73766 Plant ful
438	35	66.0	45	3	AAH33398	Aah33398 Pinus rad	511	35	66.0	280	3	AAG31515	Aag31515 Arabidops
439	35	66.0	61	3	AAH33369	Aah33369 Pinus rad	512	35	66.0	280	4	AAH68353	Aah68353 Amino aci
440	35	66.0	61	3	AAH33355	Aah33355 Eucalyptu	513	35	66.0	280	8	ADO61587	Ado61587 Transcrip
441	35	66.0	61	3	AAH33353	Aah33353 Eucalyptu	514	35	66.0	280	9	AEA26637	Aea26637 Stress to
442	35	66.0	62	3	AAH33404	Aah33404 Pinus rad	515	35	66.0	281	9	ADW17381	Adw17381 Eucalyptu
443	35	66.0	66	3	AAH33299	Aah33299 Pinus rad	516	35	66.0	282	3	AAG27683	Aag27683 Arabidops
444	35	66.0	69	4	AAU61949	Aau61949 Propionib	517	35	66.0	282	7	ADB31821	AdB31821 Plant (A.
445	35	66.0	69	6	ABM58468	Abm58468 Propionib	518	35	66.0	282	7	ADD30604	Add30604 Plant yie
446	35	66.0	75	4	ABG17139	Abg17139 Novel hum	519	35	66.0	282	8	ADI44109	Adi44109 Plant tra
447	35	66.0	76	3	AAH332796	Aah332796 Eucalyptu	520	35	66.0	282	8	ADI61449	Adi61449 A. thalia
448	35	66.0	78	3	AAH33205	Aah33205 Pinus rad	521	35	66.0	282	8	ADO02425	Ado02425 Thalecres
449	35	66.0	80	4	ABG04742	Abg04742 Novel hum	522	35	66.0	282	8	ADO02047	Ado02047 Thalecres
450	35	66.0	80	7	ABB31798	Abb31798 Human nov	523	35	66.0	286	5	AAU93191	Aau93191 Arabidops
451	35	66.0	84	4	ABB37698	Abb37698 Peptide #	524	35	66.0	286	7	ADD31061	Add31061 Plant yie
452	35	66.0	84	5	ABG40539	Abg40539 Human pep	525	35	66.0	286	8	ADI41923	Adi41923 Plant tra
453	35	66.0	85	3	AAH32820	Aah32820 Eucalyptu	526	35	66.0	289	9	AEA26955	Aea26955 Stress to
454	35	66.0	85	8	ABO54913	Ab054913 Human gen	527	35	66.0	289	9	ADW17767	Adw17767 Pinus rad
455	35	66.0	88	8	ADT56823	Adt56823 Plant pol	528	35	66.0	294	9	ADW17767	Adw17767 Pinus rad
456	35	66.0	90	8	ABO01767	Ab001767 Soybean M	529	35	66.0	296	8	ADY22298	Ady22298 Plant ful
457	35	66.0	90	8	ADJ77753	Adj77753 Soybean M	530	35	66.0	298	9	ADW17412	Adw17412 Eucalyptu
458	35	66.0	102	3	AAH32823	Aah32823 Eucalyptu	531	35	66.0	299	8	ADI61439	Adi61439 A. thalia
459	35	66.0	106	3	AAH32824	Aah32824 Arabidops	532	35	66.0	299	8	ADO02411	Ado02411 Thalecres
460	35	66.0	115	5	ABJ10424	Abj10424 Myb-relat	533	35	66.0	301	7	ABM86709	Abm86709 Rice abio
461	35	66.0	115	5	ABB06845	Abb06845 Human nGP	534	35	66.0	302	5	ABJ10415	Abj10415 Myb-relat
462	35	66.0	115	8	ADH50132	Adh50132 Maize Myb	535	35	66.0	302	8	ADH50114	Adh50114 Maize Myb

536	35	66.0	302	9	Aea26953	Stress to	609	35	66.0	343	8	ADx71573	Plant ful
537	35	66.0	303	9	Adw17415	Eucalyptu	610	35	66.0	343	8	Adx68254	Plant ful
538	35	66.0	304	8	Adx77578	Plant ful	611	35	66.0	345	3	Ag34523	Arabidops
539	35	66.0	304	8	Adx71311	Plant ful	612	35	66.0	345	7	ADDD31007	Plant yie
540	35	66.0	305	9	Adw17416	Eucalyptu	613	35	66.0	345	8	Adi44401	Plant tra
541	35	66.0	307	8	Adi42124	Plant tra	614	35	66.0	345	8	Adt56119	Plant pol
542	35	66.0	307	8	Ado02658	Thalecres	615	35	66.0	347	8	Adi42130	Plant tra
543	35	66.0	307	9	Aea26887	Stress to	616	35	66.0	347	9	Adw18327	Eucalyptu
544	35	66.0	310	5	ABP60871	Rickettsi	617	35	66.0	347	9	Aea26941	Stress to
545	35	66.0	310	8	Adi42129	Plant tra	618	35	66.0	348	8	Adt58583	Plant pol
546	35	66.0	311	8	Ado62276	Transcrip	619	35	66.0	350	8	Adx96719	Plant ful
547	35	66.0	311	9	Aea26945	Stress to	620	35	66.0	351	4	AAE01925	Arabidops
548	35	66.0	313	8	Adx89567	Plant ful	621	35	66.0	351	7	Ado30566	Plant yie
549	35	66.0	313	8	Adx71586	Plant ful	622	35	66.0	351	8	Adi43587	Plant tra
550	35	66.0	313	7	ABO63718	Klebsiell	623	35	66.0	351	8	Ado02031	Thalecres
551	35	66.0	316	9	Adw17773	Pinus rad	624	35	66.0	351	8	Ado03391	Thalecres
552	35	66.0	319	6	ADA15491	A. thalia	625	35	66.0	351	9	Aea26779	Stress to
553	35	66.0	319	6	Ado01755	Thalecres	626	35	66.0	352	3	AAAG47793	Arabidops
554	35	66.0	319	8	Adx70903	Plant ful	627	35	66.0	357	9	Adw18315	Eucalyptu
555	35	66.0	321	8	Adi42127	Plant tra	628	35	66.0	365	3	Ag330853	Arabidops
556	35	66.0	321	8	Adj49239	Oil-assoc	629	35	66.0	365	8	ADJ49928	Oil-assoc
557	35	66.0	321	8	Ado02661	Thalecres	630	35	66.0	365	8	ADJ49928	Oil-assoc
558	35	66.0	321	8	Adt58404	Plant pol	631	35	66.0	365	8	Ado02043	Thalecres
559	35	66.0	321	9	Aea26985	Stress to	632	35	66.0	368	8	Adx69157	Plant ful
560	35	66.0	323	3	Ag52567	Arabidops	633	35	66.0	371	8	Adi42131	Plant tra
561	35	66.0	323	3	Ag52567	Arabidops	634	35	66.0	371	9	Aea26943	Stress to
562	35	66.0	323	6	ABO01754	Arabidops	635	35	66.0	372	2	AAW47095	Murine DM
563	35	66.0	323	6	ABO01754	Rice Myb-	636	35	66.0	383	8	ADY11415	Plant ful
564	35	66.0	323	8	Adi43585	Plant tra	636	35	66.0	383	8	ADY11415	Plant ful
565	35	66.0	323	8	Adj77727	Rice Myb-	637	35	66.0	401	8	Adx71412	Plant ful
566	35	66.0	323	8	Ado03389	Thalecres	638	35	66.0	401	8	Adn18641	Bacterial
567	35	66.0	323	8	Adt55619	Plant pol	639	35	66.0	401	8	Adi41930	Bacterial
568	35	66.0	324	9	Aea26777	Stress to	640	35	66.0	411	9	Adw17427	Eucalyptu
569	35	66.0	324	5	ABP60924	Arabidops	641	35	66.0	412	3	AAAB33303	Pinus rad
570	35	66.0	324	5	ABP60924	Rhizobium	642	35	66.0	417	8	ADRO9452	Human pro
571	35	66.0	324	7	AdB31833	Plant (A.	643	35	66.0	420	7	ADD46279	Human pro
572	35	66.0	324	7	AdD55710	Thalecres	644	35	66.0	420	7	ADDE62900	Human pro
573	35	66.0	324	7	AdE31463	Plant yie	645	35	66.0	420	9	ADX08158	Cyclin-de
574	35	66.0	324	8	Adi44119	Plant tra	646	35	66.0	428	7	ABM86263	Rice abio
575	35	66.0	324	8	Ado02441	Thalecres	647	35	66.0	428	7	ABM90243	Rice abio
576	35	66.0	326	5	AdU93118	Arabidops	648	35	66.0	439	8	ADX93847	Plant ful
577	35	66.0	326	8	Adt56080	Plant pol	649	35	66.0	444	9	Adw17791	Pinus rad
578	35	66.0	327	9	Adw17776	Pinus rad	650	35	66.0	460	9	ABM96390	M. xanthu
579	35	66.0	328	4	AAW25666	Human pro	651	35	66.0	461	9	Adw18482	Pinus rad
580	35	66.0	332	4	AAE02468	Arabidops	652	35	66.0	481	9	Adw18468	Pinus rad
581	35	66.0	332	6	ABO01768	Soybean M	653	35	66.0	484	7	ABO67205	Klebsiell
582	35	66.0	332	7	AdB37067	Plant yie	654	35	66.0	485	9	Adw17792	Pinus rad
583	35	66.0	332	8	Adi41583	Plant tra	655	35	66.0	485	9	Adw17753	Pinus rad
584	35	66.0	332	8	Adj77755	Soybean M	656	35	66.0	485	9	Adw17755	Pinus rad
585	35	66.0	332	8	Ado01771	Thalecres	657	35	66.0	486	4	AB95746	Human pro
586	35	66.0	332	8	Aea26749	Stress to	658	35	66.0	493	8	ABM85129	Human dia
587	35	66.0	333	3	Ag43779	Arabidops	659	35	66.0	506	6	ADA34236	Acinetoba
588	35	66.0	333	9	Aea26951	Stress to	660	35	66.0	511	5	AAU77781	Human bra
589	35	66.0	334	8	Adt58635	Plant pol	661	35	66.0	511	5	AAU77781	Human bra
590	35	66.0	334	8	Aea26947	Stress to	662	35	66.0	521	7	ADJ69949	Human bra
591	35	66.0	335	7	AdB31825	Plant (A.	663	35	66.0	525	4	ABB71642	Drosophil
592	35	66.0	335	7	AdB31825	Plant (A.	664	35	66.0	529	4	AAAG81124	Mycobacte
593	35	66.0	335	7	AdB31825	Plant yie	665	35	66.0	529	5	ABU05756	M. tuberc
594	35	66.0	335	8	Adi43603	Plant tra	666	35	66.0	530	7	ABU05756	M. tuberc
595	35	66.0	335	8	Ado02215	Thalecres	667	35	66.0	534	5	ABP41206	Human ova
596	35	66.0	335	8	Ado03407	Thalecres	668	35	66.0	534	5	ABP41206	Human ova
597	35	66.0	335	9	Aea26677	Stress to	669	35	66.0	559	6	ABU54574	Human NOV
598	35	66.0	337	8	Adx69102	Plant ful	670	35	66.0	569	6	ABU63346	Human sul
599	35	66.0	338	8	Aea26949	Stress to	671	35	66.0	569	7	AAE38587	Human 252
600	35	66.0	340	9	Adw17754	Pinus rad	672	35	66.0	569	7	ADH60970	Human 252
601	35	66.0	341	3	Ag43778	Arabidops	673	35	66.0	569	8	ADJ57911	Human ext
602	35	66.0	341	8	Adi42125	Plant tra	674	35	66.0	569	8	ADJ57911	Human ext
603	35	66.0	341	8	Adi42126	Plant tra	675	35	66.0	569	8	ADU47474	Human 252
604	35	66.0	341	8	Ado02660	Thalecres	676	35	66.0	572	5	AAO15116	Bacillus
605	35	66.0	341	8	Ado02659	Thalecres	677	35	66.0	576	2	AAJ06477	Human tum
606	35	66.0	341	8	Adx66275	Plant ful	678	35	66.0	576	2	AAJ49546	Human Nsp
607	35	66.0	341	9	Aea26889	Stress to	679	35	66.0	576	2	AAJ49545	Human Nsp
608	35	66.0	342	7	Adm26693	Hyperther	680	35	66.0	576	2	AAJ49547	Human Nsp
							681	35	66.0	576	2	AAJ49541	Human PRO

682	35	66.0	576	3	RAY51932	Aay51932 Human PRO	755	34	64.2	123	4	AAU30775	Aau30775 Novel hum
683	35	66.0	576	3	RAY51939	Aay51939 Human PRO	756	34	64.2	125	8	ADX97072	Adx97072 Plant ful
684	35	66.0	576	3	RAY93684	Aay93684 Amino aci	757	34	64.2	126	4	ABG07387	Abg07387 Novel hum
685	35	66.0	576	7	ADJ58649	Adj58649 Human PRO	758	34	64.2	131	4	ABG13883	Abg13883 Novel hum
686	35	66.0	576	7	ADJ58650	Adj58650 Human PRO	759	34	64.2	135	4	ABG28547	Abg28547 Novel hum
687	35	66.0	576	7	ADJ58651	Adj58651 Human PRO	760	34	64.2	135	8	ADJ75551	Adj75551 Plant ful
688	35	66.0	576	7	ADJ58629	Adj58629 Human PRO	761	34	64.2	139	5	ABJ10425	Abj10425 Myb-relat
689	35	66.0	576	8	ABM82020	Abm82020 Tumour-as	762	34	64.2	139	8	ADH50134	Adh50134 Rice Myb-
690	35	66.0	576	9	AEA16698	Aea16698 Human SH2	763	34	64.2	142	4	ABG24585	Abg24585 Novel hum
691	35	66.0	576	9	AEA16720	Aea16720 Human SH2	764	34	64.2	142	9	ABE36718	Aeb36718 L. pneumo
692	35	66.0	576	9	AEA16718	Aea16718 Human SH2	765	34	64.2	152	3	AAG09858	Aag09858 Arabidops
693	35	66.0	576	9	AEA16719	Aea16719 Human SH2	766	34	64.2	152	3	AAG13102	Aag13102 Arabidops
694	35	66.0	583	5	RAE25389	Aae25389 Human NZM	767	34	64.2	160	3	AAG09857	Aag09857 Arabidops
695	35	66.0	623	8	ADX91232	Adx91232 Plant ful	768	34	64.2	160	6	ABU07428	Abu07428 Protein d
696	35	66.0	679	4	ABG24073	Abg24073 Novel hum	769	34	64.2	162	3	ABJ33249	Abj33249 Eucalyptu
697	35	66.0	679	4	ABG10378	Abg10378 Novel hum	770	34	64.2	169	8	ADJ48931	Adj48931 Oil-assoc
698	35	66.0	686	6	ABP96223	Abp96223 Human nuc	771	34	64.2	170	3	ABJ33107	Abj33107 Pinus rad
699	35	66.0	704	4	AM78755	Aam78755 Human pro	772	34	64.2	170	3	ABG13389	Abg13389 Novel hum
700	35	66.0	729	4	ABG19268	Abg19268 Novel hum	773	34	64.2	170	9	AEA23698	Aea23698 Human PRO
701	35	66.0	739	4	ABG03917	Abg03917 Novel hum	774	34	64.2	175	3	ABG33268	Abg33268 Pinus rad
702	35	66.0	760	9	ADX08071	Adx08071 Cyclin-de	775	34	64.2	176	3	ABG33283	Abg33283 Pinus rad
703	35	66.0	761	2	AAW47093	Aaw47093 Murine cy	776	34	64.2	176	3	AAG36520	Aag36520 Arabidops
704	35	66.0	770	7	ADI21651	Adi21651 Novel hum	777	34	64.2	178	8	ADJ90416	Adj90416 Plant ful
705	35	66.0	771	7	ADI21730	Adi21730 Novel hum	778	34	64.2	184	4	ABG00764	Abg00764 Novel hum
706	35	66.0	790	6	ADA55066	Ada55066 Human pro	779	34	64.2	184	4	ABG27110	Abg27110 Novel hum
707	35	66.0	790	7	ADC31848	Adc31848 Human nov	780	34	64.2	191	3	ABG33222	Abg33222 Eucalyptu
708	35	66.0	790	7	ADJ71094	Adj71094 Human hea	781	34	64.2	191	4	ABG07138	Abg07138 Novel hum
709	35	66.0	804	6	ABO07126	Ab007126 Novel hum	782	34	64.2	191	8	ADJ90788	Adj90788 Plant ful
710	35	66.0	826	4	ABG21280	Abg21280 Novel hum	783	34	64.2	191	8	ADJ90817	Adj90817 Plant ful
711	35	66.0	893	7	ADB65350	Adb65350 Human pro	784	34	64.2	194	4	ABG16269	Abg16269 Novel hum
712	35	66.0	893	7	ADC31323	Adc31323 Human nov	785	34	64.2	194	9	ADM18323	Adm18323 Eucalyptu
713	35	66.0	893	7	ADJ70016	Adj70016 Human hea	786	34	64.2	195	3	ABG33294	Abg33294 Eucalyptu
714	35	66.0	895	8	ADS41795	Ads41795 Bacterial	787	34	64.2	195	4	ABG17375	Abg17375 Novel hum
715	35	66.0	1252	4	AAW79739	Aaw79739 Human pro	788	34	64.2	202	3	AAG18017	Aag18017 Arabidops
716	35	66.0	1276	4	ABG11806	Abg11806 Novel hum	789	34	64.2	202	3	AG227866	Ag227866 Arabidops
717	35	66.0	1694	7	ADJ70470	Adj70470 Human hea	790	34	64.2	204	6	ABO01757	Ab001757 Soybean M
718	35	66.0	4773	7	ADJ95094	Adj95094 Novel NOV	791	34	64.2	204	6	ABO01760	Ab001760 Soybean M
719	35	66.0	4868	8	ADM68813	Adm68813 Mosquito	792	34	64.2	204	8	ADJ77739	Adj77739 Soybean M
720	34	64.2	22	3	RAY87625	Aay87625 Influenza	793	34	64.2	204	8	ADJ77733	Adj77733 Soybean M
721	34	64.2	41	8	ABO56871	Ab056871 Human gen	794	34	64.2	205	3	ABG33293	Abg33293 Eucalyptu
722	34	64.2	49	5	ADK36247	Adk36247 Novel hum	795	34	64.2	205	8	ADJ48511	Adj48511 Oil-assoc
723	34	64.2	53	5	ADK35077	Adk35077 Novel hum	796	34	64.2	206	3	AAG27865	Aag27865 Arabidops
724	34	64.2	55	3	ABG33378	Abg33378 Pinus rad	797	34	64.2	206	3	AAG18016	Aag18016 Arabidops
725	34	64.2	55	5	ADK36336	Adk36336 Novel hum	798	34	64.2	206	6	ABO01759	Ab001759 Soybean M
726	34	64.2	56	3	ABG33379	Abg33379 Pinus rad	799	34	64.2	206	7	ADD30198	Add30198 Plant yie
727	34	64.2	57	3	ABG33331	Abg33331 Eucalyptu	800	34	64.2	206	7	ADJ37063	Adj37063 Plant yie
728	34	64.2	58	3	ABG33389	Abg33389 Eucalyptu	801	34	64.2	206	7	ADJ37083	Adj37083 Plant yie
729	34	64.2	58	3	ABG50021	Abg50021 Arabidops	802	34	64.2	206	7	ADJ31531	Adj31531 Plant yie
730	34	64.2	60	3	ABG33359	Abg33359 Pinus rad	803	34	64.2	206	8	ADI41795	Adi41795 Plant tra
731	34	64.2	61	3	ABG33376	Abg33376 Pinus rad	804	34	64.2	206	8	ADI61431	Adi61431 A. thalia
732	34	64.2	61	3	ABG33376	Abg33376 Pinus rad	805	34	64.2	206	8	ADJ77737	Adj77737 Soybean M
733	34	64.2	62	3	ABG33366	Abg33366 Pinus rad	806	34	64.2	206	8	ADO02429	Ado02429 Thalecres
734	34	64.2	64	3	ABG33348	Abg33348 Eucalyptu	807	34	64.2	206	9	AEA26601	Aea26601 Stress to
735	34	64.2	65	2	RAY12416	Aay12416 Human 5'	808	34	64.2	207	8	ADJ70663	Adj70663 Plant ful
736	34	64.2	67	3	ABG33391	Abg33391 Eucalyptu	809	34	64.2	208	8	ABO01756	Ab001756 Soybean M
737	34	64.2	71	4	AAW82636	Aaw82636 Human imm	810	34	64.2	208	8	ADJ77731	Adj77731 Soybean M
738	34	64.2	78	3	ABG33285	Abg33285 Pinus rad	811	34	64.2	211	4	ABG24589	Abg24589 Novel hum
739	34	64.2	82	8	ADP45510	Adp45510 Human AKA	812	34	64.2	211	8	ADJ70661	Adj70661 Plant ful
740	34	64.2	87	9	ADZ59786	Adz59786 Human int	813	34	64.2	211	8	ADJ89608	Adj89608 Plant ful
741	34	64.2	90	4	AAU60311	Aau60311 Propionib	814	34	64.2	213	3	ABG36283	Abg36283 Human pro
742	34	64.2	90	6	ABM56830	Abm56830 Propionib	815	34	64.2	214	3	AAG24971	Aag24971 Arabidops
743	34	64.2	93	4	ABB15873	Abb15873 Human ner	816	34	64.2	214	3	AAG45932	Aag45932 Arabidops
744	34	64.2	94	3	ABG33198	Abg33198 Pinus rad	817	34	64.2	214	8	ADI43519	Adi43519 Plant tra
745	34	64.2	94	6	ABO01755	Ab001755 Soybean M	818	34	64.2	214	8	ADO01761	Ado01761 Thalecres
746	34	64.2	94	8	ADJ77729	Adj77729 Soybean M	819	34	64.2	214	9	ADO03345	Ado03345 Thalecres
747	34	64.2	99	4	ABG16275	Abg16275 Novel hum	820	34	64.2	214	9	AEA26747	Aea26747 Stress to
748	34	64.2	103	8	ADT58644	Adt58644 Plant pol	821	34	64.2	217	6	ABO01773	Ab001773 Pea Myb-r
749	34	64.2	106	8	ADJ79080	Adj79080 Plant ful	822	34	64.2	217	8	ADJ77764	Adj77764 Pea Myb-r
750	34	64.2	114	3	ABG32825	Abg32825 Eucalyptu	823	34	64.2	221	8	ADJ70653	Adj70653 Plant ful
751	34	64.2	116	4	ABG28581	Abg28581 Novel hum	824	34	64.2	226	7	ABO43136	Ab043136 A. thalia
752	34	64.2	116	6	ABO00761	Ab000761 Polypepti	825	34	64.2	226	7	ADD55728	Add55728 Thalecres
753	34	64.2	122	7	ABO43148	Ab043148 A. thalia	826	34	64.2	226	7	ADD30420	Add30420 Plant yie
754	34	64.2	122	7	ADD55856	Add55856 Thalecres	827	34	64.2	226	8	ADI43507	Adi43507 Plant tra

828	34	64.2	226	8	AD003333	Ado03333 Thalecres	901	34	64.2	274	6	ABU21702	Abu21702 Protein e
829	34	64.2	226	8	ADX73011	Adx73011 Plant ful	902	34	64.2	274	8	ADX73048	Adx73048 Plant ful
830	34	64.2	226	9	AEA26743	Aea26743 Stress to	903	34	64.2	275	3	AAB33046	Aab33046 Pinus tra
831	34	64.2	235	6	AB001761	Ab001761 Soybean M	904	34	64.2	275	8	ADI42077	Adi42077 Plant tra
832	34	64.2	235	8	ADJ77741	Adj77741 Soybean M	905	34	64.2	275	3	ADO02620	Ado02620 Thalecres
833	34	64.2	236	8	ADJ77087	Adj77087 Plant ful	906	34	64.2	276	3	ADQ41252	Adq41252 Arabidops
834	34	64.2	239	7	ADE37091	Ade37091 Plant yie	907	34	64.2	276	9	ADZ67575	Adz67575 Arabidops
835	34	64.2	239	8	ADI41793	Adi41793 Plant tra	908	34	64.2	279	4	ABG21482	Abg21482 Novel hum
836	34	64.2	239	8	ADO02407	Ado02407 Thalecres	909	34	64.2	280	4	ABG21093	Abg21093 Novel hum
837	34	64.2	239	8	ADJ79279	Adj79279 Plant ful	910	34	64.2	280	8	ADJ79361	Adj79361 Plant ful
838	34	64.2	240	3	AG30516	Aag30516 Arabidops	911	34	64.2	284	8	ADJ66610	Adj66610 HYP33.3KD
839	34	64.2	241	4	ABG21816	Abg21816 Novel hum	912	34	64.2	285	3	AG411251	Aga411251 Arabidops
840	34	64.2	242	7	ADM04305	Adm04305 Human pro	913	34	64.2	285	4	ABG24540	Abg24540 Novel hum
841	34	64.2	243	7	ABG07320	Abg07320 Novel hum	914	34	64.2	285	8	ADN72611	Adn72611 Thale cre
842	34	64.2	243	6	ABU44709	Abu44709 Protein e	915	34	64.2	287	4	ABG21864	Abg21864 Novel hum
843	34	64.2	245	4	ABG67834	Aab67834 Amino aci	916	34	64.2	292	7	ADC08061	Adc08061 Rice prot
844	34	64.2	245	7	ADJ31827	Adj31827 Plant (A.	917	34	64.2	292	8	ABM82757	Abm82757 Human dia
845	34	64.2	245	7	ADJ31085	Adj31085 Plant yie	918	34	64.2	293	4	AG641108	Aag641108 Echerich
846	34	64.2	245	8	ADI44025	Adi44025 Plant tra	919	34	64.2	296	8	ADJ89305	Adj89305 Plant ful
847	34	64.2	245	8	ADO02245	Ado02245 Thalecres	920	34	64.2	297	7	ADD30462	Add30462 Plant yie
848	34	64.2	246	8	ADO01703	Ado01703 Thalecres	921	34	64.2	297	8	ADI44435	Adi44435 Plant tra
849	34	64.2	249	6	AG54570	Aag54570 Zea mays	922	34	64.2	299	2	AAR05369	Aar05369 Protein c
850	34	64.2	248	7	ABM74373	Abm74373 DNA clone	923	34	64.2	299	4	ABG21685	Abg21685 Novel hum
851	34	64.2	249	3	AG26239	Aag26239 Arabidops	924	34	64.2	299	4	ABG24558	Abg24558 Novel hum
852	34	64.2	249	3	AG30515	Aag30515 Arabidops	925	34	64.2	299	9	ADM17386	Adm17386 Eucalyptu
853	34	64.2	249	4	AAE02557	Aae02557 A. thalia	926	34	64.2	301	3	AG41493	Aag41493 Arabidops
854	34	64.2	249	6	ADI15467	Adi15467 A. thalia	927	34	64.2	301	3	AG19261	Aag19261 Arabidops
855	34	64.2	249	8	ADJ43077	Adj43077 Plant tra	928	34	64.2	301	3	AG05799	Aag05799 Arabidops
856	34	64.2	249	8	ADO03221	Ado03221 Thalecres	929	34	64.2	301	4	ABG30331	Abg30331 Novel hum
857	34	64.2	249	8	ADO2409	Ado2409 Thalecres	930	34	64.2	302	4	ABG24511	Abg24511 Novel hum
858	34	64.2	252	4	AAW16199	Aam16199 Peptide #	931	34	64.2	302	8	ADY12833	Ady12833 Plant ful
859	34	64.2	252	4	ABB35176	Abb35176 Peptide #	932	34	64.2	303	8	ADX66564	Adx66564 Plant ful
860	34	64.2	252	4	ABM28687	Aam28687 Peptide #	933	34	64.2	304	8	ADX91441	Adx91441 Plant ful
861	34	64.2	252	4	ABB30008	Abb30008 Peptide #	934	34	64.2	305	3	AG411493	Aag411493 Arabidops
862	34	64.2	252	4	ABM20616	Abb20616 Protein #	935	34	64.2	305	4	AAE02555	Aae02555 A. thalia
863	34	64.2	252	4	AAW68381	Aam68381 Human bon	936	34	64.2	305	5	AAU92396	Aau92396 Arabidops
864	34	64.2	252	4	AAW56011	Aam56011 Human bra	937	34	64.2	305	5	ABP65541	Abp65541 Bifidobac
865	34	64.2	252	4	ABG50053	Abg50053 Human liv	938	34	64.2	305	7	ABO43108	Abo43108 A. thalia
866	34	64.2	252	4	ABM03929	Aam03929 Peptide #	939	34	64.2	305	7	ABE31561	Abe31561 Plant yie
867	34	64.2	252	4	ABG07390	Abg07390 Novel hum	940	34	64.2	305	7	ABO73970	Abo73970 Pseudomon
868	34	64.2	252	5	ABG37946	Abg37946 Human pep	941	34	64.2	305	8	ADI43809	Adi43809 Plant tra
869	34	64.2	252	8	ADX66591	Adx66591 Plant ful	942	34	64.2	305	8	ADO01753	Ado01753 Thalecres
870	34	64.2	257	3	AG454569	Aag54569 Zea mays	943	34	64.2	305	9	AEA27073	Aea27073 Stress to
871	34	64.2	258	5	ABJ10408	Abj10408 Myb-relat	944	34	64.2	307	4	ABP66293	Aab66293 Putative
872	34	64.2	258	8	ADH50100	Adh50100 Rice Myb-	945	34	64.2	308	3	AAV68240	Aay68240 Murine cl
873	34	64.2	259	4	ABG24545	Abg24545 Novel hum	946	34	64.2	308	3	AAV52894	Aay52894 Murine cl
874	34	64.2	260	4	ABG26923	Abg26923 Novel hum	947	34	64.2	308	4	ABM58655	Aab58655 Murine cl
875	34	64.2	260	8	ADJ78378	Adj78378 Plant ful	948	34	64.2	309	3	AGI19260	Aag19260 Arabidops
876	34	64.2	261	7	ABM86277	Abm86277 Rice abio	949	34	64.2	309	3	AGG54568	Aag54568 Zea mays
877	34	64.2	262	7	ABM86326	Abm86326 Rice abio	950	34	64.2	309	3	AGG05798	Aag05798 Arabidops
878	34	64.2	263	7	ABO79530	Abo79530 Pseudomon	951	34	64.2	309	3	AG46465	Aag46465 Arabidops
879	34	64.2	264	4	ABG29775	Abg29775 Novel hum	952	34	64.2	309	4	ABM67830	Aab67830 Amino aci
880	34	64.2	265	4	ABG01843	Abg01843 Novel hum	953	34	64.2	309	7	ADD55850	Ad55850 Thalecres
881	34	64.2	266	3	AG440124	Aag440124 Arabidops	954	34	64.2	309	7	ADD55762	Ad55762 Thalecres
882	34	64.2	266	3	AGG22138	Aag22138 Arabidops	955	34	64.2	309	7	ADD31067	Ad31067 Plant yie
883	34	64.2	266	4	AAE01890	Aae01890 Arabidops	956	34	64.2	309	8	ADI43805	Adi43805 Plant tra
884	34	64.2	266	8	ADI43513	Adi43513 Plant tra	957	34	64.2	309	8	ADO01745	Ado01745 Thalecres
885	34	64.2	266	8	ADO01739	Ado01739 Thalecres	958	34	64.2	309	8	ADO01737	Ado01737 Thalecres
886	34	64.2	272	9	ADV42256	Adv42256 Plant tra	959	34	64.2	309	8	ADJ94465	Adj94465 Plant ful
887	34	64.2	273	4	AAE01914	Aae01914 Arabidops	960	34	64.2	309	9	AEA26639	Aea26639 Stress to
888	34	64.2	273	4	AAE01930	Aae01930 Arabidops	961	34	64.2	309	9	AEA26989	Aea26989 Stress to
889	34	64.2	273	4	AAE02542	Aae02542 A. thalia	962	34	64.2	310	3	AAG20312	Aag20312 Arabidops
890	34	64.2	273	6	ADAI5585	Adai5585 A. thalia	963	34	64.2	310	3	AGX38738	Aag38738 Arabidops
891	34	64.2	273	7	ABO43123	Abo43123 A. thalia	964	34	64.2	310	8	ADJ72328	Adj72328 Plant ful
892	34	64.2	273	7	ADD55700	Ad55700 Thalecres	965	34	64.2	310	8	ADY25077	Ady25077 Plant ful
893	34	64.2	273	7	ADD30744	Ad30744 Plant yie	966	34	64.2	311	4	ABG21674	Abg21674 Novel hum
894	34	64.2	273	8	ADI41577	Adi41577 Plant tra	967	34	64.2	312	3	AG42946	Aag42946 Arabidops
895	34	64.2	273	8	ADI43515	Adi43515 Plant tra	968	34	64.2	312	3	ABG17260	Aag17260 Arabidops
896	34	64.2	273	8	ADO03341	Ado03341 Thalecres	969	34	64.2	312	4	ABG01795	Abg01795 Novel hum
897	34	64.2	273	8	ADO01751	Ado01751 Thalecres	970	34	64.2	312	4	ABG24541	Abg24541 Novel hum
898	34	64.2	273	8	ADO01743	Ado01743 Thalecres	971	34	64.2	313	2	AAW01159	Aw01159 Sorbitol
899	34	64.2	273	8	ABM82758	Abm82758 Human dia	972	34	64.2	313	8	ADX67486	Adx67486 Plant ful
900	34	64.2	273	8	ABM82756	Abm82756 Human dia	973	34	64.2	318	4	ABG01336	Abg01336 Novel hum

974 34 64.2 318 7 ABO61852  
 975 34 64.2 320 3 AAG17259  
 976 34 64.2 320 3 AAG42945  
 977 34 64.2 320 4 AAE02556  
 978 34 64.2 320 5 AAU93119  
 979 34 64.2 320 6 ADA15513  
 980 34 64.2 320 7 ADD55760  
 981 34 64.2 320 7 ADD31021  
 982 34 64.2 320 8 ADI43801  
 983 34 64.2 320 8 ADO01731  
 984 34 64.2 320 9 AEA27071  
 985 34 64.2 321 5 AAU75802  
 986 34 64.2 321 9 AEB35983  
 987 34 64.2 321 9 AEB36160  
 988 34 64.2 323 4 ABG07394  
 989 34 64.2 323 5 AAU93178  
 990 34 64.2 323 7 ADC35158  
 991 34 64.2 323 8 ADI43715  
 992 34 64.2 324 8 ADY25074  
 993 34 64.2 325 9 ADW17775  
 994 34 64.2 326 8 ADI43400  
 995 34 64.2 329 8 ADX72849  
 996 34 64.2 330 4 ABG15760  
 997 34 64.2 331 4 ABG07384  
 998 34 64.2 332 8 ADX93398  
 999 34 64.2 333 6 ADA15591  
 1000 34 64.2 333 8 ADO01765

## ALIGNMENTS

RESULT 1  
 AAU24399 standard; peptide; 9 AA.  
 AC AAU24399;  
 XX  
 DT 13-MAR-1998 (first entry)  
 XX  
 DE Anti-gastrin-17 immunogen.  
 XX  
 KW Glycine-extended gastrin-17; gastrointestinal tumour; immunogen;  
 KW colorectal adenocarcinoma; antibody; progastrin; cholecystochinin B;  
 XX anti-gastrin-17; anti-G-17.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 9  
 FT /note= "Glu modified by a peptide spacer conjugated to a  
 FT diphtheria toxoid"  
 XX  
 PN WO9728821-A1.  
 XX  
 XX 14-AUG-1997.  
 XX  
 XX 07-FEB-1997; 97WO-US002029.  
 XX  
 XX 08-FEB-1996; 96US-0011411P.  
 XX  
 XX (APHT-) APHTON CORP.  
 XX  
 XX Gevas PC, Karr SL, Grimes S, Michaeli D, Watson SA;  
 XX  
 XX WPI; 1997-415075/38.  
 XX  
 XX Treatment of glycine-extended gastrin-17-dependent gastrointestinal  
 FT tumours - using anti-G17 immunogenic composition, especially for  
 FT treatment of colorectal adenocarcinomas.  
 XX  
 XX Example 1; Fig 1C; 37pp; English.  
 XX

CC The present sequence represents a specific example of an anti-gastrin-17  
 CC immunogen, comprising the N-terminal 9 amino acids of gastrin-17  
 CC conjugated to an immunogenic carrier such as Diphtheria toxoid, by a  
 CC spacer peptide. This immunogenic composition is used in a new treatment  
 CC of glycine-extended gastrin-17 (G17-Gly)-dependent gastrointestinal  
 CC tumours. Anti-G17 immunogens raise antibodies which bind both the  
 CC amidated and glycine-extended forms of G17. Neutralisation of progastrin  
 CC G17-Gly prohormone by the antibodies inhibits the growth of tumour cells  
 CC dependent on progastrin G17-Gly as growth stimulator or inducer. The  
 CC method is especially for the treatment of colorectal adenocarcinomas in  
 CC humans. The novel method is non-invasive, selectively reversible, does  
 CC not damage normal tissue, does not require frequent repeated treatments  
 CC and does not cross the blood brain barrier  
 XX  
 XX Sequence 9 AA;  
 SQ  
 Query Match 100.0%; Score 53; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 EGPWLEEEER 9  
 Db 1 EGPWLEEEER 9  
 |||||  
 RESULT 2  
 AAU59434  
 ID AAU59434 standard; peptide; 9 AA.  
 XX  
 AC AAU59434;  
 XX  
 DT 21-MAR-2000 (first entry)  
 XX  
 DE Antigastrin-G17 immunogen.  
 XX  
 KW Antigastrin-G17 immunogen; tumour; tumour growth factor;  
 KW gastrin-dependent tumour; therapy.  
 XX  
 OS Rattus sp.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "pyroglutamic acid"  
 XX  
 PN WO9959628-A2.  
 XX  
 XX 25-NOV-1999.  
 XX  
 XX 14-MAY-1999; 99WO-US010750.  
 XX  
 XX 15-MAY-1998; 98US-0085687P.  
 XX  
 XX (APHT-) APHTON CORP.  
 XX  
 XX Gevas PC, Grimes S, Karr SL, Watson SA, Michaeli D;  
 XX  
 XX WPI; 2000-072406/06.  
 XX  
 XX Combination therapy, useful for treating tumors, especially.  
 XX  
 XX Claim 7; Page 23; 25pp; English.  
 XX  
 XX This sequence represents an antigastrin-G17 immunogen. The invention  
 CC relates to a method for treating tumors by immunologically neutralising  
 CC a tumour growth factor and administering one or more chemotherapeutic  
 CC agents. The method is useful for treating tumors, especially gastrin-  
 CC dependent tumors, including colorectal, stomach, pancreatic and  
 CC hepatocellular adenocarcinomas. The combination of anti-G17 immunisation  
 CC and chemotherapeutic agents increases the therapeutic effects in  
 CC controlling or inhibiting colorectal tumour growth over chemotherapy  
 CC alone  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 100.0%; Score 53; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
 DB 1 EGPWLEEE 9  
 |||||

RESULT 3  
 AAY51305  
 ID AAY51305 standard; peptide; 9 AA.  
 XX  
 AC AAY51305;  
 DT 14-APR-2000 (first entry)  
 XX Human gastrin aminoterminal (1-9) G17 peptide.  
 XX Immunogenic; treatment; hypergastrinemia; gastrin G17; gastrin G34;  
 KW pernicious anemia; anti-ulcer; proton pump inhibitor; colorectal disease.  
 KW  
 OS Homo sapiens.  
 XX WO9959631-A1.  
 PN 25-NOV-1999.  
 XX  
 PD 14-MAY-1999; 99WO-US010751.  
 XX  
 PF 15-MAY-1998; 98US-0085714P.  
 XX  
 PR (APHT-) APHTON CORP.  
 PA Gevas PC, Grimes S, Karr S, Michaeli D, Watson S;  
 PI WPI; 2000-116301/10.  
 DR Treating or preventing hypergastrinemia comprising administration of,  
 XX e.g. anti-gastrin antibodies.  
 XX Disclosure; Page 11; 44pp; English.  
 XX This invention describes a novel method for the treatment or preventing  
 CC hypergastrinemia by administering to a patient a gastrin G17 and/or G34  
 CC peptide fragment linked by an amino acid spacer to an immunogenic  
 CC carrier. The methods are used to treat hypergastrinemic patients,  
 CC particularly those with pernicious anemia, those receiving treatment with  
 CC anti-ulcer agents such as proton pump inhibitors (particularly omeprazole  
 CC or lansoprazole) or H<sub>2</sub> receptor blocking agents or antagonists, or those  
 CC having colorectal disorders or diseases. This sequence represents the  
 CC human gastrin G17 peptide which is used to illustrate the method of the  
 CC invention  
 XX  
 SQ Sequence 9 AA;  
 Query Match 100.0%; Score 53; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
 DB 1 EGPWLEEE 9  
 |||||

RESULT 4  
 ADH89212  
 ID ADH89212 standard; peptide; 9 AA.  
 XX  
 AC ADH89212;  
 XX 06-MAY-2004 (first entry)  
 DT

XX Gastrin G-17 peptide fragment 1-9, SEQ ID 7.  
 DE Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;  
 XX gastrin G-34; gonadotropin releasing hormone; GnRH;  
 KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;  
 KW thyroid cancer; lung cancer; reproductive system cancer.  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "Pyroglutamic acid"  
 FT  
 FT WO2004004687-A2.  
 XX 15-JAN-2004.  
 XX 03-JUL-2003; 2003WO-US021176.  
 XX 03-JUL-2002; 2002US-0394179P.  
 XX (APHT-) APHTON CORP.  
 PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 XX Michaeli D, Grimes S, Barenholz Y, Even-Chen S;  
 PI WPI; 2004-099340/10.  
 XX  
 DR Injectible liposomal composition for delivery of a water-soluble  
 XX substance e.g. vaccine for preventing pregnancy, comprises several  
 PT liposomal vesicles comprising a high weight ratio of lipid to  
 PT encapsulated water-soluble substance.  
 XX  
 PS Claim 14; SEQ ID NO 7; 73pp; English.  
 XX The present invention relates to injectable liposomal compositions (I)  
 CC for delivery of a water-soluble substance e.g. immunomimic peptides. (I)  
 CC comprises several liposomal vesicles comprising a high weight ratio of a  
 CC lipid to an encapsulated water-soluble substance so as to achieve a high  
 CC efficiency of encapsulation. The immunomimic peptide is chosen from  
 CC gastrin G-17 (ADH89206 to ADH89213 and ADH89223), gastrin G-34 (ADH89217-  
 CC ADH89219), gonadotropin releasing hormone (GnRH) peptide (ADH89220 and  
 CC ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-  
 CC ADH89222 and ADH89225). (I) comprising vaccines directed against hormone  
 CC or hormone cognate receptors, where the vaccine comprises at least one:  
 CC hormone-immunomimic peptide such as gastrin G-17 or G-34 is useful for  
 CC treating gastrointestinal malignancy, and non-gastrointestinal tumors  
 CC such as thyroid and lung cancer; or GnRH or hCG immunomimic peptide is  
 CC useful as contraceptive and for treating cancers in male and female  
 CC reproductive systems.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 100.0%; Score 53; DB 8; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
 DB 1 EGPWLEEE 9  
 |||||

RESULT 5  
 ADH89213  
 ID ADH89213 standard; peptide; 10 AA.  
 XX  
 AC ADH89213;  
 XX 06-MAY-2004 (first entry)  
 DT  
 XX Gastrin G-17 peptide fragment 1-10, SEQ ID 8.  
 DE  
 XX

KW Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;  
 KW gastrin G-34; gonadotropin releasing hormone; GnRH;  
 KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;  
 KW thyroid cancer; lung cancer; reproductive system cancer.  
 OS Synthetic.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "Pyroglutamic acid"  
 FT  
 XX  
 XX EPI564554-A1.  
 PN 17-AUG-2005.  
 XX  
 PD  
 XX  
 XX 12-FEB-2004; 2004EP-00075439.  
 PN 12-FEB-2004; 2004EP-00075439.  
 XX  
 PR (PEPS-) PEPSAN SYSTEMS BV.  
 PF (UYUT-) UNIV UTRECHT HOLDING BV.  
 XX  
 PA Akrestejn GJ, Hensen EJ, Scibelli A, Van Der Most RG, Meloen RH;  
 XX Turkstra JA;  
 PI WPI; 2005-573732/59.  
 XX  
 DR Affinity-binding assay for selecting antigen specific immune cells, by  
 XX contacting cell having four copies of target molecule with two labeled  
 XX binding molecules, detecting cells staining with each label, selecting  
 XX cells binding both labels.  
 XX  
 XX Example 3; Page 11; 45pp; English.  
 PS  
 XX The present invention relates to an affinity-binding assay for selecting  
 XX antigen specific immune cells. The method involves contacting particle  
 XX such as a cell having four copies of target molecule with two binding  
 XX molecules specific for the target molecule, where first of the binding  
 XX molecules is associated with a first label and a second of the binding  
 XX molecules is associated with a second label, detecting cells staining  
 XX with each label and selecting cells binding both labels. The invention  
 XX also provides a method for detection of early B cell populations in  
 XX vaccine development. The invention is useful for the preparation of an  
 XX antibody. The present sequence is a gastrin peptide. This sequence is an  
 XX immunogenic peptide used as a vaccine.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 53; DB 9; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.051;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 EGPWLEEEE 9  
 Db 1 EGPWLEEEE 9  
 |||||  
 RESULT 7  
 ADW00245  
 ID ADW00245 standard; peptide; 11 AA.  
 XX  
 AC ADW00245;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 XX Human wild type gastrin-17 peptide aa 1-11.  
 DE  
 XX  
 XX antidiabetic; gastrin receptor; cholecystokinin receptor;  
 KW gastrin receptor modulator; CCK receptor modulator; gastrin; diabetes;  
 KW fasting blood glucose; insulin.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "pyroglutamic acid"  
 FT  
 XX US200426682-A1.

KW Injectable liposomal composition for delivery of a water-soluble  
 KW substance e.g. vaccine for preventing pregnancy, comprises several  
 KW liposomal vesicles comprising a high weight ratio of lipid to  
 KW encapsulated water-soluble substance.  
 OS  
 XX  
 XX Claim 14; SEQ ID NO 8; 73pp; English.  
 PS  
 XX The present invention relates to injectable liposomal compositions (I)  
 XX for delivery of a water-soluble substance e.g. immunomimic peptides. (I)  
 XX comprises several liposomal vesicles comprising a high weight ratio of a  
 XX lipid to an encapsulated water-soluble substance so as to achieve a high  
 XX efficiency of encapsulation. The immunomimic peptide is chosen from  
 XX gastrin G-17 (ADH89206 to ADH89213 and ADH89223), gastrin G-34 (ADH89217-  
 XX ADH89219), gonadotropin releasing hormone (GnRH) peptide (ADH89220 and  
 XX ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-  
 XX ADH89222 and ADH89225). (I) comprising vaccines directed against hormone  
 XX or hormone cognate receptors, where the vaccine comprises at least one:  
 XX hormone-immunomimic peptide such as gastrin G-17 or G-34 is useful for  
 XX treating gastrointestinal malignancy, and non-gastrointestinal tumors  
 XX such as thyroid and lung cancer; or GnRH or hCG immunomimic peptide is  
 XX useful as contraceptive and for treating cancers in male and female  
 XX reproductive systems.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 53; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.051;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 EGPWLEEEE 9  
 Db 1 EGPWLEEEE 9  
 |||||  
 RESULT 6  
 AEC05673  
 ID AEC05673 standard; peptide; 10 AA.  
 XX  
 AC AEC05673;  
 XX  
 DT 20-OCT-2005 (first entry)  
 XX  
 XX Gastrin peptide #2.  
 DE  
 XX  
 XX Vaccine; development; antibody production; immunogenicity; gastrin;  
 KW hormone.  
 KW

XX 30-DEC-2004.  
 XX PD  
 XX PF  
 XX PF  
 XX 21-NOV-2003; 2003US-00719450.  
 XX PR  
 XX 22-OCT-2002; 2002US-0420187P.  
 XX PR  
 XX 22-OCT-2002; 2002US-0420399P.  
 XX PR  
 XX 21-NOV-2002; 2002US-0428100P.  
 XX PR  
 XX 22-NOV-2002; 2002US-0428562P.  
 XX PR  
 XX 03-DEC-2002; 2002US-0430590P.  
 XX PR  
 XX 22-OCT-2003; 2002US-00691123.  
 XX PR  
 XX 14-NOV-2003; 2003US-0519933P.  
 XX PA  
 XX (CRUZ/) CRUZ A.  
 XX PI  
 XX Cruz A;  
 XX WPI; 2005-074216/08.  
 XX DR  
 XX Pharmaceutical composition useful for treating diabetes, comprises a  
 PT gastrin compound having an extended activity upon administration to a  
 PT subject in comparison with native gastrin.  
 XX  
 XX Claim 1; Page; 25pp; English.  
 XX  
 XX The invention relates to a pharmaceutical composition (I) comprising a  
 CC gastrin compound (C1) having an extended activity upon administration to  
 CC a subject in comparison with native gastrin. (I) or C1 is useful for  
 CC treating a subject having diabetes, which involves administering C1 or a  
 CC modified gastrin capable of covalently reacting with a serum protein,  
 CC where the frequency of administering the gastrin compound is less than  
 CC frequency of administration of a native gastrin. The method further  
 CC involves measuring a physiological indicator of islet neogenesis,  
 CC measuring fasting blood glucose (FBG), and decreasing insulin dependency.  
 CC The modified gastrin comprises a sequence of native gastrin capable of  
 CC binding to the gastrin/CK receptor and an amino terminal cysteine or  
 CC lysine. (I) or C1 is useful for maintaining for an extended period of  
 CC time an increased gastrin serum level compared with the serum level of a  
 CC peptide having an amino acid sequence of a native gastrin, which involves  
 CC administering C1. (I) Contains gastrin compositions having longer active  
 CC function than native gastrin peptides, and has a longer half-life in  
 CC circulation in a subject. This sequence corresponds to amino acids 1-11  
 CC of the wild type gastrin-17 peptide used in the invention. (Note: this  
 CC sequence is not given in the specification but is generated using  
 CC information given by the inventors in the Claims section).  
 XX  
 XX Sequence 11 AA;  
 SQ  
 Query Match 100.0%; Score 53; DB 9; Length 11;  
 Best Local Similarity 100.0%; Pred. NO. 0.057;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEE 9  
 DB 1 EGPWLEEE 9  
 RESULT 8  
 AAR06245  
 ID AAR06245 standard; peptide; 12 AA.  
 AC  
 XX AAR06245;  
 XX  
 XX 09-JAN-2003 (revised)  
 DT 07-DEC-1990 (first entry)  
 DT  
 XX Antigenic peptide fragment selected from the 12 N-terminal AAs of  
 DE heptadecagastrin (G17).  
 DE  
 XX Gastrin; tumours; peptic ulcers; diphtheria toxoid; tetanus toxin.  
 KW  
 XX Unidentified.  
 OS  
 XX

PN EP380230-A.  
 XX  
 XX PD 01-AUG-1990.  
 XX PF  
 XX 17-JAN-1990; 90EP-00300456.  
 XX PR  
 XX 24-JAN-1989; 89US-00301353.  
 XX PR 12-MAY-1989; 89US-00351193.  
 XX  
 XX (APHT-) APHTON CORP.  
 XX PI Gevas PC, Grimes S, Karr SL, Littenberg RL;  
 XX WPI; 1990-233029/31.  
 XX DR  
 XX Immunogens against gastrin peptide(s) - used to induce antibodies that  
 PT specifically neutralise single form of gastrin, G17 or G34.  
 PT  
 XX Claim 6; Page 19; 32pp; English.  
 XX  
 XX Antigenic fragments may be attached to an immunogenic carrier and used to  
 CC raise Abs to a specific single form of Gastrin ie. G17 or G34. Peptide  
 CC fragments capable of binding to these Abs are useful in neutralising anti  
 CC -gastrin Abs in vivo. (Updated on 09-JAN-2003 to add missing OS field.)  
 XX  
 XX Sequence 12 AA;  
 SQ  
 Query Match 100.0%; Score 53; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.062;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEE 9  
 DB 1 EGPWLEEE 9  
 RESULT 9  
 ADY37657  
 ID ADY37657 standard; peptide; 13 AA.  
 AC  
 XX ADY37657;  
 XX  
 XX 05-MAY-2005 (first entry)  
 DT  
 XX Human G17 N-terminal peptide fragment, residues 1-12 #1.  
 DE  
 KW Cytostatic; Gastrointestinal-Gen.; Antiulcer; Vaccine; pharmaceutical;  
 KW hormone; gastrin; heptadecagastrin; ulcer; duodenal ulcer; stomach ulcer;  
 KW tumor.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "Pyroglutamic acid"  
 FT  
 XX US6861510-B1.  
 PN  
 XX 01-MAR-2005.  
 XX PD  
 XX 06-JUN-1995; 95US-00465917.  
 XX PF  
 XX 24-JAN-1989; 89US-00301353.  
 XX PR 12-MAY-1989; 89US-00351193.  
 XX PR 23-JAN-1990; 90US-00721638.  
 XX PR 23-JAN-1990; 90WO-US000520.  
 XX PR 19-APR-1991; 91US-00679212.  
 XX PR 30-MAR-1994; 94US-00219773.  
 XX  
 XX (APHT-) APHTON CORP.  
 XX PI Gevas PC, Karr SL, Grimes S, Littenberg RL;  
 XX

XX

XX Gastroesophageal reflux disease; GERD; gastrin; anti-gastrin antibody;  
 KW histamine H<sub>2</sub>; proton pump inhibitor; acid output; stomach; therapy;  
 KW esophagitis; immunogen; human; heptadecagastrin; immunomimic; G17.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Modified-site 1  
 FT /label= pGlu  
 FT /note= "pyroglutamate"  
 FT Peptide  
 FT /note= "carboxy-terminal spacer"  
 FT  
 XX WO9959612-A1.  
 PN  
 XX  
 XX 25-NOV-1999.  
 PD  
 XX  
 XX 14-MAY-1999; 99WO-US010734.  
 PF  
 XX  
 XX 15-MAY-1998; 98US-0085610P.  
 PR  
 XX (APHT-) APHTON CORP.  
 PA  
 XX Gevas PC, Grimes S, Karr S, Michaeli D;  
 PI WPI; 2000-062378/05.  
 XX  
 XX Method for treatment of gastroesophageal reflux disease (GERD).  
 PT  
 XX  
 XX Example 5; Page 13; 24pp; English.  
 PS  
 XX The invention relates to the treatment of gastroesophageal reflux disease  
 CC (GERD) that comprises administering to a patient an immunogenic  
 CC composition which generates anti-gastrin antibodies, which bind to  
 CC gastrin, in a patient; and administering histamine H<sub>2</sub> antagonist or a  
 CC proton pump inhibitor. The method provides a more effective method for  
 CC controlling acid output by the stomach. The therapy is less costly. High  
 CC gastrin levels associated with standard therapies are neutralized and  
 CC undesirable side effects are reduced. The method permits a reduced dosage  
 CC of acid reducing agent both at the acid producing level as well as the  
 CC acid production stimulating level (gastrin). Reduction of dosages is  
 CC desirable for prolonged treatment of GERD. In a combination therapy with  
 CC H<sub>2</sub> agonists or proton pump inhibitors, anti-gastrin 17 antibody titers  
 CC can be maintained by occasional booster shots while gastric acid  
 CC inhibitor dosing is reduced. Immunization allows a sufficient time for  
 CC the esophagitis to completely heal and no surgery is required. The  
 CC present sequence represents a human heptadecagastrin (G17) immunomimic  
 CC followed by a carboxy-terminal spacer  
 XX  
 SQ Sequence 16 AA;  
 Query Match 100.0%; Score 53; DB 3; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.083;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEE 9  
 Db 1 EGPWLEEEE 9  
 RESULT 13  
 ABP73035  
 ID ABP73035 standard; peptide; 16 AA.  
 XX  
 AC ABP73035;  
 XX  
 XX 03-JUN-2003 (first entry)  
 DT  
 XX Peptide specific for the induction of immune response to G17.  
 DE  
 XX Cancer; lung; oesophagus; liver; immunogen; hormone; gastrin 17; G17;

KW gastrin receptor; cholecystokinin-B; CCK-B; Barrett's condition;  
 KW gastrin-induced tumour; immune response.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Modified-site 1  
 FT /note= "pyroglutamic acid"  
 FT Peptide  
 FT /note= "spacer"  
 FT  
 XX WO2003005955-A2.  
 PN  
 XX 23-JAN-2003.  
 PD  
 XX 09-JUL-2002; 2002WO-US021768.  
 PF  
 XX 09-JUL-2001; 2001US-0303868P.  
 PR  
 XX (APHT-) APHTON CORP.  
 PA  
 XX Gevas PC, Michaeli D, Grimes S;  
 PI WPI; 2003-229433/22.  
 XX  
 XX Treating cancerous or pre-cancerous conditions of the lung, esophagus or  
 PT liver, by administering an immunogen which induces antibodies in the  
 PT patient against G17 and/or cholecystokinin-B/gastrin receptors.  
 XX  
 XX Example 1; Page 7; 27pp; English.  
 PS  
 XX The specification describes a method of treating a cancerous or pre-  
 CC cancerous condition of the lung, oesophagus or liver. The method involves  
 CC administering to a patient an immunogen which induces antibodies in the  
 CC patient against peptide hormone gastrin 17 (G17) and/or a gastrin  
 CC receptor, e.g. cholecystokinin (CCK)-8. The method is useful for treating  
 CC cancerous or pre-cancerous condition of lung, oesophagus or liver, where  
 CC the condition is cancer, or Barrett's condition. The treatment prevents  
 CC or delays progression of the Barrett's oesophagus to a cancerous state.  
 CC The method is also useful for treating the growth of a gastrin-induced  
 CC tumour or pre-cancerous lesion of the lung, liver or oesophagus. ABP73032  
 CC -35 represent peptides which induce specific immune responses to G17. The  
 CC peptides comprise an amino terminal fragment of G17 and a carboxy-  
 CC terminal spacer  
 XX  
 SQ Sequence 16 AA;  
 Query Match 100.0%; Score 53; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.083;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEE 9  
 Db 1 EGPWLEEEE 9  
 RESULT 14  
 AAW65184  
 ID AAW65184 standard; peptide; 17 AA.  
 XX  
 AC AAW65184;  
 XX  
 XX 02-OCT-1998 (first entry)  
 DT  
 XX Gastrin fragment analogue.  
 DE  
 XX Bradykinin; N-benzylglycine; agonist; receptor study; antagonist;  
 KW achiral; analgesic; angiotensin II; gastrin.  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH



PT diseases or disorders such as osteoarthritis, rheumatoid arthritis.  
 XX  
 PS Example 6; Page 18; 55pp; English.  
 XX  
 CC The sequence represents a synthetic biotinylated peptide substrate for  
 CC human Janus kinase 3 (JAK3). The invention relates to the use of JAK/STAT  
 CC (Janus kinase/signal transducer and activator of transcription)  
 CC inhibitors other than debrromymenaldesine (DBH) and hymenaldesine (H)  
 CC for inhibiting the progression or the likelihood of developing diseases  
 CC involving cartilage degradation, and for regulating the expression of pro  
 CC -inflammatory agents or cytokines in a chondrocyte, and cartilage  
 CC degrading enzymes in a cell. A JAK3/STAT inhibitor of the invention is  
 CC useful for inhibiting progression or likelihood of developing  
 CC osteoarthritis or rheumatoid arthritis. The inhibitor is also useful for  
 CC treating other JAK/STAT-mediated diseases or disorders, including T cell-  
 CC mediated disorders, mast cell-mediated disorders, type 2 (cytokine  
 CC hypersensitivity) disorders, B cell lymphoma, and myeloid diseases. T  
 CC cell-mediated disorders include human T cell leukaemia/lymphoma virus  
 CC (HTLV)-1, Szory's syndrome, c-abl transformation, natural killer-like T  
 CC cell lymphomas (NK-like tumours) and graft-vs-host disease; cytokine  
 CC hypersensitivity disorders include Leishmaniasis, leprosy, allergy and  
 CC viral infections; mast cell-mediated disorders include hay fever, asthma,  
 CC hives and anaphylaxis; and leukaemias and lymphomas include acute  
 CC lymphocytic and lymphoblastic leukaemias, B cell lymphomas and leukaemias  
 CC of myeloid origin. DBH and H are useful as therapeutic agents in cancers  
 CC in which JAK3 plays a role in the initiation or progression of  
 CC tumorigenesis  
 XX  
 SQ Sequence 17 AA;  
 Query Match 100.0%; Score 53; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEE 9  
 DB 1 EGPWLEEE 9  
 RESULT 17  
 AAB91246  
 ID AAB91246 standard; peptide; 17 AA.  
 XX  
 AC AAB91246;  
 XX  
 DT 22-JUN-2001 (first entry)  
 XX  
 DE Gastrin releasing peptide (GRP) SEQ ID NO:422.  
 XX  
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimide; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200069900-A2.  
 XX  
 PD 23-NOV-2000.  
 XX  
 PF 17-MAY-2000; 2000WO-US013576.  
 XX  
 PR 17-MAY-1999; 99US-0134406P.  
 PR 10-SEP-1999; 99US-0153406P.  
 PR 15-OCT-1999; 99US-0159783P.  
 XX  
 FA (CONJ-) CONJUCHEM INC.  
 XX  
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;  
 XX  
 DR WPI, 2001-112059/12.  
 XX  
 PT Modifying and attaching therapeutic peptides to albumin prevents

PT peptidase degradation, useful for increasing length of in vivo activity.  
 XX  
 PS Disclosure; Page 336; 733pp; English.  
 XX  
 CC The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimide and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity in  
 CC vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 17 AA;  
 Query Match 100.0%; Score 53; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEE 9  
 DB 1 EGPWLEEE 9  
 RESULT 18  
 AAB59273  
 ID AAB59273 standard; peptide; 17 AA.  
 XX  
 AC AAB59273;  
 XX  
 DT 27-MAR-2001 (first entry)  
 XX  
 DE KS2-peptide substrate.  
 XX  
 KW Phosphorylation; kinase; insulin.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200075167-A2.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 09-JUN-2000; 2000WO-US016025.  
 XX  
 PR 09-JUN-1999; 99US-0138311P.  
 PR 10-JUN-1999; 99US-0138438P.  
 PR 08-JUL-1999; 99US-00349733.  
 PR 28-APR-2000; 2000US-0200594P.  
 XX  
 PA (LJLB-) LJL BIOSYSTEMS INC.  
 XX  
 PI Sportsman JR, Hoekstra MF, Lee SK, Cairns N, Kauvar LM;  
 XX  
 DR WPI, 2001-091201/10.  
 XX  
 PT Assay for detecting phosphorylation and dephosphorylation modification of  
 PT proteins by contacting luminescence peptide with a binding partner and  
 PT measuring change in luminescence polarization.  
 XX  
 PS Claim 70; Page 70; 89pp; English.  
 XX  
 CC The present invention relates to detecting addition or removal of a  
 CC phosphate group to or from a substrate. The method involves contacting a  
 CC luminescent peptide with a binding partner that binds specifically to a

CC phosphorylated peptide without regard to the particular amino acid  
CC sequence of the peptide. The method is useful for detecting  
CC phosphorylation and dephosphorylation modifications of proteins,  
CC including kinases and phosphatases. The methods can be used to study the  
CC kinase activity of different receptors e.g. the insulin receptor and to  
CC find agonists and antagonists of these receptors  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 53; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.089;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EGPWLEEE 9  
Db 1 EGPWLEEE 9  
RESULT 19  
ID AAU76504 standard; peptide; 17 AA.  
AC AAU76504;  
DT 05-JUN-2002 (first entry)  
DE Protein kinase A (PKA) substrate #3.  
XX Protein kinase A; phosphorylation.  
XX Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /label= OTHER  
FT /note= "Pyroglutamic acid"  
XX  
FN US6335176-B1.  
XX  
PD 01-JAN-2002.  
XX  
PF 16-OCT-1998; 98US-00174216.  
XX  
PF 16-OCT-1998; 98US-00174216.  
XX (PHAR-) PHARMACOPEIA INC.  
XX  
PI Inglesse J, Glickman JF;  
XX  
DR WPI; 2002-194620/25.  
XX  
PT Reagent for phosphorylating a compound, comprises a moiety that is  
PT specifically reactive with reactive site chain of the compound, a linking  
PT moiety and a peptide sequence comprising kinase substrate.  
XX  
PS Disclosure; Col 8; 26pp; English.  
XX  
XX The invention relates to a reagent (I) for incorporation of a  
CC phosphorylation site by reaction with a reactive side chain of a compound  
CC to be phosphorylated. (I) comprises a structure A-B-C, where A is a  
CC moiety that is specifically reactive with a reactive side chain, C is a  
CC peptide sequence comprising kinase substrate, and B is a linking moiety  
CC selected from any one of the 19 compounds given in the specification e.g.  
CC N-gamma-maleimidobutyryloxy-succinamide ester. (I) is useful for  
CC phosphorylation, by reacting (I) with a compound to be phosphorylated  
CC (e.g. protein or polypeptide) and then phosphorylating the resulting  
CC product using a protein kinase under phosphorylating conditions  
CC comprising 32P-phosphate or 33P-phosphate. The phosphorylated compounds  
CC are useful in assays such as drug discovery. The method is suitable for  
CC radioactively phosphorylating already synthesised proteins, without the  
CC need to carry out recombinant methods to incorporate an amino acid  
CC sequence. The method is highly adaptable and can be used to phosphorylate  
CC a broad variety of compounds that contain reactive site groups. (I)

CC avoids production of proteins having an inaccessible kinase substrate  
CC sequence as can result from known recombinant methods. Introduction of  
CC multiple phosphorylation sites in proteins is possible merely by  
CC increasing the ratio of reagent to protein, and the method of  
CC phosphorylating does not interfere with the protein's function or become  
CC inaccessible as a result of protein folding. The method allows labeled  
CC products to be obtained that have a higher specific activity than is  
CC normally obtained with recombinant methods. The present sequence  
CC represents a protein kinase A (PKA) peptide substrate used in examples  
CC that demonstrate the method of the invention  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 53; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.089;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EGPWLEEE 9  
Db 1 EGPWLEEE 9  
RESULT 20  
ID ADF72769 standard; peptide; 17 AA.  
XX  
AC ADF72769;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Chemoselective self-assembled monolayer binding peptide.  
XX  
KW immobilizing; functional organic molecule; predetermined density;  
KW mixed monolayer surface; MMS; reducing end; peracetylated sugar;  
KW chemoselective; self-assembled monolayer; SAM.  
XX  
OS Unidentified.  
XX  
PN WO2003018854-A2.  
XX  
PD 06-MAR-2003.  
XX  
PF 27-AUG-2002; 2002WO-US027195.  
XX  
PR 27-AUG-2001; 2001US-0315261P.  
PR 28-AUG-2001; 2001US-0315544P.  
PR 15-FEB-2002; 2002US-0356765P.  
PR 15-FEB-2002; 2002US-0358412P.  
PR 19-FEB-2002; 2002US-0357136P.  
PR 20-FEB-2002; 2002US-0375023P.  
PR 26-APR-2002; 2002US-0380259P.  
XX  
PA (SURP-) SURFACE LOGIX INC.  
XX  
PI Hodneland C, Campbell S, Duffy D, Agosto M, Wang E;  
XX  
XX WPI; 2003-393250/37.  
XX  
XX Immobilizing functional organic molecule in a predetermined density on a  
PT mixed monolayer surface, by contacting the surface with the organic  
PT molecule to form a covalent bond and to immobilize the organic molecule.  
XX  
PS Disclosure; Fig 40; 234pp; English.  
XX  
XX The invention relates to a novel method for immobilizing a functional  
CC organic molecule in a predetermined density on a mixed monolayer surface  
CC (MMS). The novel method comprises a first monolayer moiety (MM1) having a  
CC covalent bond forming reactive group and a second monolayer moiety (MM2)  
CC having an inert group. The method involves contacting MMS with the  
CC functional organic molecule to form a covalent bond between the  
CC functional organic molecule and MM1 to immobilize the functional organic  
CC molecule. The novel method of the invention is useful for immobilizing a  
CC functional organic molecule in a predetermined density on a mixed

CC monolayer surface, where the functional organic molecule is selected from  
 CC oligopeptides, peptides, polypeptides, oligonucleotides,  
 CC oligonucleosides, carbohydrates, proteins, nucleosides,  
 CC enzymes, enzyme substrates, ligands, receptors, antibodies, antigens,  
 CC lipids, and small molecules, but preferably a carbohydrate. The  
 CC carbohydrate comprises a reducing end, the reducing end comprises a  
 CC peracetylated sugar having an n-pentenyl group. This sequence represents  
 CC a peptide which binds to the chemoselective self-assembled monolayer's  
 CC (SAM's) at the B-terminal, relating to the novel method of the invention.  
 XX  
 XX Sequence 17 AA;

Query Match 100.0%; Score 53; DB 7; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9

Db 1 EGPWLEEE 9

# RESULT 21

ADP72934  
 ID ADP72934 standard; peptide; 17 AA.

XX AC ADP72934;

XX DT 26-FEB-2004 (first entry)

XX DE Biotinylated substrate biotin.

XX KW bisubstituted pyrazine compounds; Antiallergic; Antiasthmatic;  
 XX KW Antinflammatory; Dermatological; Antirheumatic; Antiarthritic;  
 XX KW Immunosuppressive; Antidiabetic; Antithyroid; Nootropic; Neuroprotective;  
 XX KW Virucide; Hepatotropic; Anti-HIV; Cytostatic;  
 XX KW JAK-2 tyrosine protein kinase inhibitor.

XX OS Synthetic.

XX PN WO2003099796-A1.

XX PD 04-DEC-2003.

XX PF 23-MAY-2003; 2003WO-AU000629.

XX PR 23-MAY-2002; 2002AU-00002515.

XX PR 26-JUL-2002; 2002US-039970P.

XX PA (CYTO-) CYTOPIA PTY LTD.

XX PI Burns CJ, Bu X, Wilks AF;

XX DR WPI; 2004-053219/05.

XX PT New disubstituted pyrazine useful for treating a protein kinase  
 PT associated disorders e.g. allergic asthma, rheumatic disease, systemic  
 PT lupus erythematosus and rheumatoid arthritis.

XX PS Disclosure; SEQ ID NO 7; 42pp; English.

XX CC The present invention relates to bisubstituted pyrazine compounds. The  
 CC compounds potentially modulates protein kinase signal transduction by  
 CC affecting the enzymatic activity of RTKs, CKs and/or STKs mediated  
 CC signal transduction pathways. The present sequence represents  
 CC a biotinylated substrate biotin.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 53; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9

Db 1 EGPWLEEE 9

# RESULT 22

ADH10240

ID ADH10240 standard; peptide; 17 AA.

XX AC ADH10240;

XX DT 11-MAR-2004 (first entry)

XX DE Peptide substrate used in kinase assays.

XX KW Pyrazine; protein kinase; signal transduction; Janus kinase; TYK2;  
 XX KW antiallergic; antiasthmatic; antinflammatory; dermatological;  
 XX KW antirheumatic; antiarthritic; immunosuppressive; muscular; antidiabetic;  
 XX KW antithyroid; nootropic; neuroprotective; virucide; hepatotropic;  
 XX KW anti-HIV; cytostatic; tyrosine protein kinase.

XX OS Synthetic.

XX PN WO2003099811-A1.

XX PD 04-DEC-2003.

XX PF 23-MAY-2003; 2003WO-AU000628.

XX PR 23-MAY-2002; 2002AU-00002514.

XX PR 26-JUL-2002; 2002US-039898P.

XX PA (CYTO-) CYTOPIA PTY LTD.

XX PI Wilks AF, Bu X, Burns CJ;

XX DR WPI; 2004-081905/08.

XX PT New disubstituted pyrazines useful for treating protein kinase associated  
 PT disorders, e.g. allergic asthma, rheumatic disease, systemic lupus  
 PT erythematosus and rheumatoid arthritis.

XX PS Example 61; Page 73; 53pp; English.

XX CC The invention relates to disubstituted pyrazines of specified formula.  
 CC The novel compounds are potent modulators of protein kinases (such as  
 CC tyrosine kinase and serine/threonine kinase) mediated signal transduction  
 CC pathways. They are used for treating a protein kinase (such as a receptor  
 CC tyrosine kinase (e.g. EGF, HER3, HER4, IR, IGF-1R, IRP, PDGFR-  
 CC alpha, PDGFR-beta, CSF1R, C-Kit, C-fms, Flk-1R, Flk4, KDR/Flk-1, Flt-1,  
 CC FGFR-1R, FGFR-2R, FGFR-3R, FGF-4R), cellular tyrosine kinase (e.g. Src,  
 CC Fcrk, Btk, Csk, Abi, ZAP70, Fes/Fps, Fak, Ack, Yes, Fyn, Lyn, Lck, Blk,  
 CC Hck, Fgr and Yrk), a tyrosine kinase (e.g. JAK1 - JAK3, TYK2) and a  
 CC serine/threonine kinase (e.g. ERK2, c-jun, p38MAPK, PKA, PKC, a  
 CC cyclin-dependent kinase, CDK1 - CDK11) associated disease state e.g.  
 CC atopy (e.g. allergic asthma, atopic dermatitis (Eczema), allergic  
 CC rhinitis); cell mediated hypersensitivity (e.g. allergic contact  
 CC dermatitis and hypersensitivity pneumonitis); rheumatic disease (e.g.  
 CC systemic lupus erythematosus, rheumatoid arthritis, juvenile arthritis,  
 CC Sjogren's syndrome, scleroderma, polymyositis, ankylosing spondylitis,  
 CC psoriatic arthritis), other autoimmune disease (e.g. Type I diabetes,  
 CC autoimmune thyroid disorders, and Alzheimer's disease), viral disease  
 CC (e.g. Epstein Barr Virus (EBV), hepatitis B, hepatitis C, HIV, HTLV 1,  
 CC Varicella-Zoster virus, human papilloma virus), and cancer (e.g.  
 CC leukemia, lymphoma and prostate cancer). The present sequence represents  
 CC a peptide substrate used in kinase assays.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 53; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9



Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
 |||||  
 Db 1 EGPWLEEE 9

RESULT 25  
 ADK00577  
 ID ADK00577 standard; peptide; 17 AA.  
 XX  
 AC ADK00577;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Immunogenic lipopeptide of the invention #113.  
 XX  
 KW T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;  
 KW Antifertility; vaccine; antibody.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004014956-A1.  
 XX  
 PD 19-FEB-2004.  
 XX  
 PF 12-AUG-2003; 2003WO-AU001018.  
 XX  
 PR 12-AUG-2002; 2002US-0402838P.  
 XX  
 PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.  
 XX  
 PI Jackson D, Zeng W;  
 XX  
 DR WPI; 2004-238735/22.  
 XX  
 PT Novel lipopeptide comprising polypeptide having amino acid sequence of T  
 PT helper cell epitope and B cell epitope, conjugated to lipid moieties,  
 PT useful for eliciting immune response against group A Streptococcus  
 PT antigen.  
 XX  
 PS Claim 36; SEQ ID NO 113; 194pp; English.  
 XX  
 CC The present invention relates to a lipopeptide comprising polypeptide  
 CC conjugated to lipid moieties, where polypeptide contains amino acid  
 CC sequence of T helper cell epitope and B cell epitope, where amino acid  
 CC sequences are different, and internal lysine residues or internal lysine  
 CC analog residues for covalent attachment of each of lipid moieties through  
 CC aeg; amino group or terminal side chain group of lysine or lysine  
 CC analog. The peptides are useful in eliciting the production of antibody  
 CC against an antigenic B cell epitope in a subject, and are useful for  
 CC antibody production, synthetic vaccine production, diagnostic method  
 CC employing antibodies and antibody ligands and immunotherapy for  
 CC veterinary and human medicine. The method efficiently elicits the  
 CC production of antibody against antigenic B cell epitope. The present  
 CC sequence represents a novel immunogenic lipopeptide comprising T helper  
 CC and B cell epitopes.  
 XX  
 SQ Sequence 17 AA;  
 Query Match 100.0%; Score 53; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
 |||||  
 Db 1 EGPWLEEE 9

RESULT 26  
 ADL02105  
 ID ADL02105 standard; peptide; 17 AA.  
 XX

AC ADL02105;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Phosphopeptide.  
 XX  
 KW phosphopeptide; binding solution; high-throughput screening;  
 KW cellular phosphoprotein status; signal transduction; mitosis;  
 KW cell proliferation; phosphoprotein expression profile.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "N-terminal biotinyl"  
 FT Modified-site 17 /note= "C-terminal amidated"  
 FT  
 XX  
 PN US2004038306-A1.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PF 02-MAY-2003; 2003US-00428192.  
 XX  
 PR 03-MAY-2002; 2002US-0377733P.  
 PR 28-JUN-2002; 2002US-0393059P.  
 PR 30-AUG-2002; 2002US-0407255P.  
 PR 14-JAN-2003; 2003US-0440252P.  
 XX  
 PA (AGNE/) AGNEW B.  
 PA (BEC/) BEECHEM J.  
 PA (GEEK/) GEE K.  
 PA (HAUG/) HAUGLAND R.  
 PA (LIU/) LIU J.  
 PA (MART/) MARTIN V.  
 PA (PATT/) PATTON W.  
 PA (STEI/) STEINBERG T.  
 XX  
 PI Agnew B, Beechem J, Gee K, Haugland R, Liu J, Martin V;  
 PI Patton W, Steinberg T;  
 XX  
 DR WPI; 2004-267637/25.  
 XX  
 CC Binding solution useful for binding, detecting and isolating  
 CC phosphorylated target molecules, comprises metal chelating part or  
 CC phosphate-binding compound having chemical part, linker and metal-  
 CC chelating part, salt and acid.  
 XX  
 PS Example 29; Page 51; 83pp; English.  
 XX  
 CC The invention relates to a binding solution (BS), comprising a 1,2-bis(2-  
 CC aminophenoxy)-ethane-N,N',N'-tetraacetic acid (BAPTA) metal chelating  
 CC part or a phosphate-binding compound having a chemical part, linker and  
 CC metal-chelating part, salt comprising trivalent metal ions and an acid.  
 CC The (BS) is useful for binding a phosphorylated target molecule in a  
 CC sample, detecting an immobilised phosphorylated target molecule from a  
 CC sample and isolating phosphorylated target molecule from a sample. The  
 CC (BS) is also useful in the field of proteomics, molecular biology, high-  
 CC throughput screening and diagnostics. The (BS) is useful for analysis and  
 CC monitoring of phosphorylated target molecules. The (BS) is useful to  
 CC generate data that are used as reference point for human patients or  
 CC animal sample for diagnosis of disease, progression of disease, and/or  
 CC predisposition for disease. The (BS) is useful for gaining valuable  
 CC information of the effects of various drugs and compounds on the cellular  
 CC phosphoprotein status. The (BS) is useful for studying biological  
 CC phenomena such as signal transductions, mitosis, cell proliferation, etc.  
 CC The (BS) is useful for generating a comprehensive phosphoprotein  
 CC expression profile from any cell type or biological fluid of interest.  
 CC The (BS) specifically detects, isolates and/or quantitates phosphorylated  
 CC target molecules. The (BS) allows for rapid, sensitive, and non-  
 CC radioactive detection of variety of selected kinases and phosphatases.  
 CC The (BS) allows for high-throughput screening. The present sequence  
 CC represents the amino acid sequence of a phosphopeptide.

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XX SQ Sequence 17 AA;
Query Match 100.0%; Score 53; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

RESULT 27
ADN03334
ID ADN03334 standard; peptide; 17 AA.
XX AC ADN03334;
XX DT 17-JUN-2004 (first entry)
XX DE Exemplary peptide ligand for proteome analysis #60.
XX KW Peptide ligand; proteome; capture compound; mass spectrometry;
XX KW protein separation;
XX KW matrix assisted laser desorption ionisation-time of flight; MALDI-TOF.
XX OS Unidentified.
XX OS
XX PN US2003119021-A1.
XX PD 26-JUN-2003.
XX PF 16-JUL-2002; 2002US-00197954.
XX PR 16-JUL-2001; 2001US-0306019P.
XX PR 21-AUG-2001; 2001US-0314123P.
XX PR 11-MAR-2002; 2002US-0363433P.
XX PA (KOST/) KOSTER H.
XX PA (SIDD/) SIDDIQI S.
XX PA (LITT/) LITTLE D P.
XX PI Koester H, Siddiqi S, Little DP;
XX PF; 2004-059185/06.
XX PT Collection of capture compounds capable of binding to biomolecules to
XX PT form complexes that are stable under mass spectrometry conditions, useful
XX PT for analysis of biomolecules, especially proteins.
XX PS Disclosure; SEQ ID NO 60; 165pp; English.
XX CC The invention relates to a collection of capture compounds capable of
XX CC binding to biomolecules to form complexes that are stable under mass
XX CC spectrometry conditions. The formulae for the capture compounds comprises
XX CC sets of compounds of formula (I)-(III) given in the specification. Also
XX CC included are analysis of biomolecules (by contacting a composition
XX CC comprising a biomolecule with the above collection and identifying or
XX CC detecting bound biomolecules), separating protein conformers (by
XX CC contacting a composition comprising a biomolecule with the above
XX CC collection, separating the members of the collection and identifying
XX CC bound proteins), reducing diversity of a complex mixture of biomolecules
XX CC (by contacting the mixture with the above collection and separating each
XX CC set of complexes of capture compounds with biomolecules from the other
XX CC sets) and identifying phenotype-specific biomolecules (by sorting cells
XX CC from a single subject into sets according to a phenotype, contacting
XX CC mixtures of biomolecules from each set with the above collection and
XX CC comparing the patterns of biomolecule binding from each set). The
XX CC collection of capture compounds is useful for the analysis of
XX CC biomolecules, especially proteins (e.g. analysis of a proteome), using
XX CC mass spectrometry, especially matrix assisted laser desorption ionisation
XX CC -time of flight (MALDI-TOF) mass spectrometry. The present sequence is an
XX CC exemplary peptide ligand which may be incorporated into a capture

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XX SQ compound of the invention.
XX SQ Sequence 17 AA;
Query Match 100.0%; Score 53; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

RESULT 28
ADR42169
ID ADR42169 standard; peptide; 17 AA.
XX AC ADR42169;
XX DT 21-OCT-2004 (first entry)
XX DE Gastrin related peptide ligand, SEQ ID 60.
XX KW Human; ligand; Gastrin.
XX KW Homo sapiens.
XX OS
XX PN WO2004064972-A2.
XX PD 05-AUG-2004.
XX PF 16-JAN-2004; 2004WO-US001037.
XX PR 16-JAN-2003; 2003US-0441398P.
XX PA (HKPH-) HK PHARM INC.
XX PA (KOE/) KOESTER H.
XX PI Koester H, Little DP, Siddiqi SM, Grealish MP, Marappan S;
XX PI Haasman CP, Yip P;
XX PF; 2004-642213/62.
XX PT Identifying drug non-target biomolecules in mixture of biomolecules
XX PT involves interacting mixture of biomolecules with capture compounds
XX PT having high binding affinity and analyzing captured biomolecules to
XX PT identify drug non-targets.
XX PS Disclosure; SEQ ID NO 60; 368pp; English.
XX CC The present invention relates to a method for identifying drug non-target
XX CC biomolecules in a mixture of biomolecules. The method comprises
XX CC interacting mixture with capture compounds having moiety X which
XX CC covalently binds to biomolecules with high affinity, moiety Y that
XX CC increases selectivity of binding so that the capture compound binds to
XX CC fewer biomolecules, and moiety Z for presenting X and Y, and analysing
XX CC captured biomolecules to identify drug non-targets. The capture compound
XX CC also optionally comprises a sorting function moiety Q and or a solubility
XX CC function moiety W. The selectivity function moiety Y serves to modulate
XX CC the reactivity function by reducing the number of groups to which the
XX CC reactivity function moiety X bind, such as by steric hindrance and other
XX CC interactions. Y is optionally a peptide ligand (ADR42112-ADR42256).
XX SQ Sequence 17 AA;
Query Match 100.0%; Score 53; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

```

RESULT 29  
 ADT49596  
 ID ADT49596 standard, peptide; 17 AA.  
 XX  
 AC ADT49596;  
 XX  
 XX 30-DEC-2004 (first entry)  
 DT  
 DE Human mature gastrin 17 (G17) amino acid sequence.  
 XX  
 XX G17; gastrin; hormone; human; gastrin 17.  
 KW  
 XX Homo sapiens.  
 OS  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /label= pGlu  
 FT /note= "pyroglutamic acid"  
 FT Modified-site 17  
 FT /note= "amidated C-terminus"  
 FT  
 XX WO2004088326-A2.  
 PN  
 XX 14-OCT-2004.  
 PD  
 XX 29-MAR-2004; 2004WO-US009666.  
 XX PF  
 XX 28-MAR-2003; 2003US-0458244P.  
 PR  
 XX (APHT-) APHTON CORP.  
 PA (HUNT-) HUNTINGDON LIFE SCI LTD.  
 XX  
 XX Grimes S, Little J, McLoughlin L;  
 PI  
 XX WPI; 2004-719280/70.  
 DR  
 XX  
 XX Determining total or free amount of gastrin hormone in a biological fluid  
 PT sample comprises incubating the sample in the presence of an N-terminal  
 PT sequence gastrin peptide for binding to a C-terminal specific antibody.  
 XX  
 PS Disclosure; SEQ ID NO 1; 24pp; English.  
 XX  
 CC The invention relates to determining the total amount of gastrin or free  
 CC gastrin hormone in a biological fluid sample. The method involves (a)  
 CC obtaining a biological fluid sample comprising a gastrin hormone from a  
 CC patient; (b) providing an immobilized antibody that selectively binds a C  
 CC -terminal epitope of the gastrin hormone; (c) incubating the sample in  
 CC the presence of an N-terminal sequence gastrin peptide under conditions  
 CC for binding of the gastrin hormone in the sample to the antibody to  
 CC produce an immobilized complex of the antibody bound to the gastrin  
 CC hormone; (d) washing the immobilized complex to remove unbound antibody  
 CC and N-terminal sequence gastrin peptide, and incubating the complex with  
 CC a detectable marker-conjugated antibody that selectively binds an N-  
 CC terminal epitope of gastrin hormone to form an immobilized detectable  
 CC marker-conjugated antibody complex; (e) washing the immobilized  
 CC detectable marker-conjugated antibody complex, and incubating with a  
 CC development reagent; and (f) measuring the developed reagent to determine  
 CC the total amount of (free) gastrin hormone in the biological fluid  
 CC sample. The C-terminal selective antibody and/or the N-terminal selective  
 CC antibody is a monoclonal antibody. The gastrin hormone is gastrin-17  
 CC (G17) or glycine extended G17 (G17-Gly) and the C-terminal selective  
 CC antibody and the N-terminal selective antibody bind G17. The method is  
 CC useful for detecting and/or quantifying free or total amount of gastric  
 CC hormone peptides including antibody-bound, in a biological fluid. The  
 CC present sequence represents the amino acid sequence of mature G17, the  
 CC predominant form of little gastrins in human.  
 CC  
 SQ Sequence 17 AA;  
 XX  
 Query Match 100.0%; Score 53; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9  
 DB |||||  
 1 EGPWLEEEE 9  
 RESULT 30  
 ADU48550  
 ID ADU48550 standard; protein; 17 AA.  
 XX  
 AC ADU48550;  
 XX  
 XX 27-JAN-2005 (first entry)  
 DT  
 DE Gastrin-17 amino acid sequence.  
 XX  
 XX KGF; keratinocyte growth factor; gastrin-17; antilipemic;  
 KW antidiabetic; vasotropic; cerebroprotective; cardiant; antiarrhythmic;  
 KW antibacterial; immunosuppressive; antiinflammatory; gastrointestinal;  
 KW antitumor; hypotensive; nootropic; neuroprotective; anorectic;  
 KW dermatological; endocrine; respiratory; hepatotropic; gene therapy;  
 KW cell therapy; fibroblast growth factor.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "pyroglutamic acid"  
 FT  
 XX WO2004096853-A1.  
 PN  
 XX 11-NOV-2004.  
 PD  
 XX 30-APR-2004; 2004WO-CA000648.  
 XX PF  
 XX 30-APR-2003; 2003US-0509068P.  
 PR  
 XX (WARA-) WARATAH PHARM INC.  
 PA  
 XX Brand SJ, Cruz A;  
 PI  
 XX WPI; 2004-804727/79.  
 DR  
 XX  
 XX New pharmaceutical composition comprising a keratinocyte growth factor  
 PT (KGF) agonist and a gastrin compound, useful in treating or preventing  
 PT diabetes, hypertension, heart failure and obesity.  
 XX  
 PS Disclosure; SEQ ID NO 8; 58pp; English.  
 XX  
 CC The invention relates to a pharmaceutical composition comprising a  
 CC keratinocyte growth factor (KGF) agonist and a gastrin compound that  
 CC provides beneficial effects relative to each compound alone, and  
 CC optionally a carrier, excipient, or vehicle. The composition provides  
 CC sustained beneficial effects, and is in a form that provides normal blood  
 CC glucose levels in a subject that persist for a prolonged period of time  
 CC after administration. The composition further comprises amounts of a KGF  
 CC agonist and a gastrin compound in a form for chronic or acute therapy of  
 CC a subject in need, where the amounts are suboptimal relative to the  
 CC amount of each compound administered alone for treatment of diabetes. The  
 CC beneficial effects are reduced or absent islet inflammation, decreased  
 CC disease progression, increased survival, or decreased symptoms of a  
 CC disease or condition, and/or are sustained beneficial effects that  
 CC persist for a prolonged period of time after termination of treatment.  
 CC The composition is useful for the preparation of a medicament for the  
 CC treatment of a condition or disease, such as dyslipidaemia,  
 CC hyperglycaemia, severe hypoglycaemic episodes, stroke, left ventricular  
 CC hypertrophy, arrhythmia, bacteraemia, septicemia, irritable bowel  
 CC syndrome, functional dyspepsia, diabetes, catabolic changes after  
 CC surgery, stress induced hyperglycaemia, gastric ulcers, myocardial  
 CC infarction, impaired glucose tolerance, hypertension, Alzheimer's disease  
 CC and other central and peripheral neurodegenerative conditions, chronic  
 CC heart failure, fluid retentive states, metabolic syndrome and related  
 CC diseases, and disorders and obesity. The composition is also used to

CC promote and/or enhance soft tissue growth and regeneration, such as in  
 CC epidermolysis bullosa, chemotherapy induced alopecia, male-pattern  
 CC baldness, hyaline membrane disease and hepatic cirrhosis. The present  
 CC sequence represents a little gastrin (gastrin-17) peptide sequence.  
 XX  
 SQ Sequence 17 AA;

Query Match 100.0%; Score 53; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
 |||||  
 Db 1 EGPWLEEE 9

RESULT 31  
 ADU48549  
 ID ADU48549 standard; protein; 17 AA.  
 XX  
 AC ADU48549;  
 XX  
 DT 27-JAN-2005 (first entry)  
 XX  
 DE Gastrin-17 amino acid sequence.  
 XX

XX KGF; FGF; keratinocyte growth factor; gastrin-17; antilipaeamic;  
 KW antidiabetic; vasotropic; cerebroprotective; cardiant; antiarrhythmic;  
 KW antibacterial; immunosuppressive; antiinflammatory; gastrointestinal;  
 KW anticancer; hypotensive; nootropic; neuroprotective; anorectic;  
 KW dermatological; endocrine; respiratory; hepatotropic; gene therapy;  
 KW cell therapy; fibroblast growth factor.  
 XX

OS Unidentified.

XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "pyroglutamic acid"  
 FT

XX WO2004096853-A1.

XX 11-NOV-2004.

XX 30-APR-2004; 2004WO-CA000648.

XX 30-APR-2003; 2003US-0509068P.

XX (WARA-) WARATAH PHARM INC.

XX Brand SJ, Cruz A;

XX WPI; 2004-804727/79.

XX New pharmaceutical composition comprising a keratinocyte growth factor  
 PT (KGF) agonist and a gastrin compound, useful in treating or preventing  
 PT diabetes, hypertension, heart failure and obesity.  
 XX

PS Disclosure; SEQ ID NO 7; 58pp; English.

XX The invention relates to a pharmaceutical composition comprising a  
 CC keratinocyte growth factor (KGF) agonist and a gastrin compound that  
 CC provides beneficial effects relative to each compound alone, and  
 CC optionally a carrier, excipient, or vehicle. The composition provides  
 CC sustained beneficial effects, and is in a form that provides normal blood  
 CC glucose levels in a subject that persist for a prolonged period of time  
 CC after administration. The composition further comprises amounts of a KGF  
 CC agonist and a gastrin compound in a form for chronic or acute therapy of  
 CC a subject in need, where the amounts are suboptimal relative to the  
 CC amount of each compound administered alone for treatment of diabetes. The  
 CC beneficial effects are reduced or absent islet inflammation, decreased  
 CC disease progression, increased survival, or decreased symptoms of a  
 CC disease or condition, and/or are sustained beneficial effects that  
 CC persist for a prolonged period of time after termination of treatment.

CC The composition is useful for the preparation of a medicament for the  
 CC treatment of a condition or disease, such as dyslipidaemia,  
 CC hyperglycaemia, severe hypoglycaemic episodes, stroke, left ventricular  
 CC hypertrophy, arrhythmia, bacteraemia, septicemia, irritable bowel  
 CC syndrome, functional dyspepsia, diabetes, catabolic changes after  
 CC surgery, stress induced hyperglycaemia, gastric ulcers, myocardial  
 CC infarction, impaired glucose tolerance, hypertension, Alzheimer's disease  
 CC and other central and peripheral neurodegenerative conditions, chronic  
 CC heart failure, fluid retentive states, metabolic syndrome and related  
 CC diseases, and disorders and obesity. The composition is also used to  
 CC promote and/or enhance soft tissue growth and regeneration, such as in  
 CC epidermolysis bullosa, chemotherapy induced alopecia, male-pattern  
 CC baldness, hyaline membrane disease and hepatic cirrhosis. The present  
 CC sequence represents a little gastrin (gastrin-17) peptide sequence.  
 XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 53; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
 |||||  
 Db 1 EGPWLEEE 9

RESULT 32

ADV16301

ID ADV16301 standard; peptide; 17 AA.

XX

AC ADV16301;

XX

DT 10-FEB-2005 (first entry)

XX

DE Human gastrin-17 wild-type peptide.

XX

KW Gastrin-17; diabetes mellitus; insulin dependent diabetes;

KW Gastrin receptor modulator; CCK receptor modulator.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 1 /note= "Pyroglutamic acid, optionally absent"

FT Modified-site 17 /note= "C-terminal amide"

XX

PN US2004229810-A1.

XX

PD 18-NOV-2004.

XX

PF 03-DEC-2003; 2003US-00728082.

XX

PR 22-OCT-2002; 2002US-0420187P.

PR 22-OCT-2002; 2002US-0420399P.

PR 21-NOV-2002; 2002US-0428100P.

PR 22-NOV-2002; 2002US-0428562P.

PR 03-DEC-2002; 2002US-0430590P.

PR 22-OCT-2003; 2003US-00691123.

XX

PA (CRUZ/) CRUZ A.

XX

XX Cruz A;

XX WPI; 2005-037040/04.

XX

PT Pharmaceutical composition for treating subject with diabetes, has

PT gastrin compound having extended activity upon administration to subject

PT in comparison with native gastrin.

XX

PS Claim 2; SEQ ID NO 3; 24pp; English.

XX

CC The invention relates to a novel pharmaceutical composition comprising a

CC gastrin compound having an extended activity, upon administration to a  
 CC subject, in comparison with native gastrin. The compounds of the  
 CC invention may be useful for treating a subject having diabetes. This  
 CC involves measuring a physiological indicator of islet neogenesis and  
 CC fasting blood glucose (FBG). The method further involves decreasing  
 CC insulin dependency. Furthermore, the compounds may be useful for  
 CC maintaining an increase in gastrin serum level for an extended period of  
 CC time. The current sequence is that of the human gastrin-17 wild-type  
 CC peptide of the invention which may act as a stimulator of the gastrin or  
 CC CCK receptor.

SQ Sequence 17 AA;

Query Match 100.0%; Score 53; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
 |||||  
 Db 1 EGPWLEEE 9

RESULT 33  
 ADV16302  
 ID ADV16302 standard; peptide; 17 AA.

XX AC ADV16302;  
 XX DT 10-PEB-2005 (first entry)  
 XX DE Human gastrin-17 mutant peptide - M14L.

XX KW gastrin-34; diabetes mellitus; insulin dependent diabetes;  
 XX KW Gastrin receptor modulator; CCK receptor modulator; mutein.

XX OS Homo sapiens.  
 XX OS Synthetic.

XX FH Key Location/Qualifiers  
 XX FT Modified-site 1  
 XX FT /note= "Pyroglutamic acid, optionally absent"  
 XX FT Misc-difference 14  
 XX FT /note= "Wild-type Met substituted by Leu"  
 XX FT Modified-site 17  
 XX FT /note= "C-terminal amide"

XX PN US2004229810-A1.  
 XX PD 18-NOV-2004.  
 XX PF 03-DEC-2003; 2003US-00728082.  
 XX PR 22-OCT-2002; 2002US-0420187P.  
 XX PR 22-OCT-2002; 2002US-0420399P.  
 XX PR 21-NOV-2002; 2002US-0428100P.  
 XX PR 22-NOV-2002; 2002US-0428562P.  
 XX PR 03-DEC-2002; 2002US-0430590P.  
 XX PR 22-OCT-2003; 2003US-00691123.

XX PA (CRUZ/) CRUZ A.

XX PI Cruz A;  
 XX DR WPI; 2005-037040/04.

XX PT Pharmaceutical composition for treating subject with diabetes, has  
 XX FT gastrin compound having extended activity upon administration to subject  
 XX PT in comparison with native gastrin.

XX PS Claim 2; SEQ ID NO 4; 24pp; English.

XX CC The invention relates to a novel pharmaceutical composition comprising a  
 XX CC gastrin compound having an extended activity, upon administration to a

CC subject, in comparison with native gastrin. The compounds of the  
 CC invention may be useful for treating a subject having diabetes. This  
 CC involves measuring a physiological indicator of islet neogenesis and  
 CC fasting blood glucose (FBG). The method further involves decreasing  
 CC insulin dependency. Furthermore, the compounds may be useful for  
 CC maintaining an increase in gastrin serum level for an extended period of  
 CC time. The current sequence is that of the human gastrin-17 mutant peptide  
 CC of the invention which may act as a stimulator of the gastrin or CCK  
 CC receptor.

SQ Sequence 17 AA;

Query Match 100.0%; Score 53; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
 |||||  
 Db 1 EGPWLEEE 9

RESULT 34  
 ADM00243  
 ID ADM00243 standard; peptide; 17 AA.

XX AC ADM00243;  
 XX DT 24-MAR-2005 (first entry)  
 XX DE Human variant gastrin-17 (M14L) peptide.

XX KW antidiabetic; gastrin receptor; cholecystokinin receptor;  
 XX KW Gastrin receptor modulator; CCK receptor modulator; gastrin; diabetes;  
 XX KW fasting blood glucose; insulin.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 XX FT Modified-site 1  
 XX FT /note= "pyroglutamic acid"  
 XX FT Modified-site 17  
 XX FT /note= "amidated C-terminus"

XX PN US2004266682-A1.  
 XX PD 30-DEC-2004.

XX PF 21-NOV-2003; 2003US-00719450.  
 XX PR 22-OCT-2002; 2002US-0420187P.  
 XX PR 22-OCT-2002; 2002US-0420399P.  
 XX PR 21-NOV-2002; 2002US-0428100P.  
 XX PR 22-NOV-2002; 2002US-0428562P.  
 XX PR 03-DEC-2002; 2002US-0430590P.  
 XX PR 22-OCT-2003; 2003US-00691123.  
 XX PR 14-NOV-2003; 2003US-0519933P.

XX PA (CRUZ/) CRUZ A.

XX PI Cruz A;  
 XX DR WPI; 2005-074216/08.

XX PT Pharmaceutical composition useful for treating diabetes, comprises a  
 XX FT gastrin compound having an extended activity upon administration to a  
 XX PT subject in comparison with native gastrin.

XX PS Disclosure; Page 5; 25pp; English.

XX CC The invention relates to a pharmaceutical composition (I) comprising a  
 XX CC gastrin compound (CI) having an extended activity upon administration to  
 XX CC a subject in comparison with native gastrin. (I) or CI is useful for  
 XX CC treating a subject having diabetes, which involves administering CI or a

CC modified gastrin capable of covalently reacting with a serum protein,  
 CC where the frequency of administering the gastrin compound is less than  
 CC frequency of administration of a native gastrin. The method further  
 CC involves measuring a physiological indicator of islet neogenesis,  
 CC measuring fasting blood glucose (FBG), and decreasing insulin dependency.  
 CC The modified gastrin comprises a sequence of native gastrin capable of  
 CC binding to the gastrin/CKK receptor and an amino terminal cysteine or  
 CC lysine. (I) or C1 is useful for maintaining for an extended period of  
 CC time an increased gastrin serum level compared with the serum level of a  
 CC peptide having an amino acid sequence of a native gastrin, which involves  
 CC administering C1. (I) Contains gastrin compositions having longer active  
 CC function than native gastrin peptides, and has a longer half-life in  
 CC circulation in a subject. This sequence corresponds to the variant  
 CC gastrin-17(M14L) peptide used in the invention. (Note: this sequence  
 CC differs from sequence denoted as SEQ ID NO: 4 as given in the Sequence  
 CC Listing of the specification).

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 53; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
 Db 1 EGPWLEEEE 9

RESULT 35

ADW00242  
 ID ADW00242 standard; peptide; 17 AA.

XX AC ADW00242;

XX DT 24-MAR-2005 (first entry)

XX DE Human wild type gastrin-17 peptide.

XX KW antidiabetic; gastrin receptor; cholecystokinin receptor;  
 KW gastrin receptor modulator; CKK receptor modulator; gastrin; diabetes;  
 KW fasting blood glucose; insulin.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "pyroglutamic acid"  
 FT Modified-site 17 /note= "amidated C-terminus"

XX US2004266682-A1.

XX 30-DEC-2004.

XX 21-NOV-2003; 2003US-00719450.

XX 22-OCT-2002; 2002US-0420187P.

XX 22-OCT-2002; 2002US-0420399P.

XX 21-NOV-2002; 2002US-0428100P.

XX 22-NOV-2002; 2002US-0428582P.

XX 03-DEC-2002; 2002US-0430590P.

XX 22-OCT-2003; 2003US-00691123.

XX 14-NOV-2003; 2003US-0519933P.

XX (CRUZ/) CRUZ A.

XX Cruz A;

XX WPI; 2005-074216/08.

XX Pharmaceutical composition useful for treating diabetes, comprises a  
 PT gastrin compound having an extended activity upon administration to a  
 PT subject in comparison with native gastrin.

XX PS Disclosure; Page 4; 25pp; English.

XX CC The invention relates to a pharmaceutical composition (I) comprising a  
 CC gastrin compound (C1) having an extended activity upon administration to  
 CC a subject in comparison with native gastrin. (I) or C1 is useful for  
 CC treating a subject having diabetes, which involves administering C1 or a  
 CC modified gastrin capable of covalently reacting with a serum protein,  
 CC where the frequency of administering the gastrin compound is less than  
 CC frequency of administration of a native gastrin. The method further  
 CC involves measuring a physiological indicator of islet neogenesis,  
 CC measuring fasting blood glucose (FBG), and decreasing insulin dependency.  
 CC The modified gastrin comprises a sequence of native gastrin capable of  
 CC binding to the gastrin/CKK receptor and an amino terminal cysteine or  
 CC lysine. (I) or C1 is useful for maintaining for an extended period of  
 CC time an increased gastrin serum level compared with the serum level of a  
 CC peptide having an amino acid sequence of a native gastrin, which involves  
 CC administering C1. (I) Contains gastrin compositions having longer active  
 CC function than native gastrin peptides, and has a longer half-life in  
 CC circulation in a subject. This sequence corresponds to the wild type  
 CC gastrin-17 peptide used in the invention. (Note: this sequence differs  
 CC from sequence denoted as SEQ ID NO: 3 as given in the Sequence Listing of  
 CC the specification).

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 53; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
 Db 1 EGPWLEEEE 9

RESULT 36

ADW71906  
 ID ADW71906 standard; peptide; 17 AA.

XX AC ADW71906;

XX DT 07-APR-2005 (first entry)

XX DE Non-phosphopeptide used in detection assay.

XX KW High throughput screening; diagnostic.

XX OS Unidentified.

XX FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "Biotinyl glutamic acid"

XX US2005014197-A1.

XX 20-JAN-2005.

XX 09-APR-2004; 2004US-00821522.

XX 03-MAY-2002; 2002US-0377733P.

XX 28-JUN-2002; 2002US-0393059P.

XX 30-AUG-2002; 2002US-0407255P.

XX 14-JAN-2003; 2003US-0440252P.

XX 02-MAY-2003; 2003US-00428192.

XX 07-NOV-2003; 2003US-00703816.

XX (AGNE/) AGNEW B.

XX (GEEK/) GEE K R.

XX (MART/) MARTIN V V.

XX PI Agnew B, Gee KR, Martin VV;

XX WPI; 2005-111245/12.

XX Isolation of phosphorylated target molecule in sample useful in field of  
 PT e.g. proteomics, involves incubating sample and binding solution, and  
 PT separating phosphorylated target molecules from unphosphorylated  
 PT molecules by chromatography.

XX Example 29; Page 56; 96pp; English.

XX The present invention relates to a method for isolating a phosphorylated  
 CC target molecule in a sample. The method involves incubating sample and  
 CC binding solution and separating phosphorylated target molecules from  
 CC unphosphorylated molecules by chromatography. The invention is useful in  
 CC the field of proteomics, molecular biology, high-throughput screening and  
 CC diagnostics. The present sequence is the non-phosphopeptide used in  
 CC detection assay.

XX Sequence 17 AA;  
 SQ

Query Match 100.0%; Score 53; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9  
 Db |||||

Db 1 EGPWLEEE 9

RESULT 37  
 AEA08308

ID AEA08308 standard; peptide; 17 AA.

XX AEA08308;  
 AC

XX 28-JUL-2005 (first entry)  
 DT

XX PTK domain substrate peptide SEQ ID NO 10.  
 DE

XX imidazo[1,2-a]pyrazin-8-ylamine; kinase; Btk kinase; cancer; neoplasm;  
 KW cytostatic; immunosuppressive; antiinflammatory; antipsoriatic;  
 KW immunomodulator; antirheumatic; antidiabetic; antirheumatic;  
 KW antiparkinsonian; neuroprotective; nontropic; antidiabetic;  
 KW antibacterial; antitumor; immune disorder; autoimmune disease;  
 KW inflammation; psoriasis; chronic myelocytic leukemia;  
 KW gastrointestinal tumor; lung tumor; breast tumor; ovary tumor;  
 KW prostate tumor; renal tumor; head and neck tumor; colorectal tumor;  
 KW graft rejection; atherosclerosis; Alzheimer's disease; diabetes;  
 KW diabetic retinopathy; insulin resistance; rheumatoid arthritis;  
 KW Parkinson's disease; septic shock.

XX Unidentified.  
 OS

XX Key Location/Qualifiers  
 FH

FT Modified-site 1 /note= "biotinylated residue"  
 FT Modified-site 17 /note= "amidated residue"

XX WO2005047290-A2.  
 PN

XX 26-MAY-2005.  
 PD

XX 10-NOV-2004; 2004WO-US037433.  
 PF

XX 11-NOV-2003; 2003US-0519311P.  
 PR

XX (CELL-) CELLULAR GENOMICS INC.  
 PA

XX Currie KS, Desimone RW, Pippin DA, Darrow JW, Mitchell SA;  
 PI WPI; 2005-386327/39.

XX New imidazo[1,2-a]pyrazin-8-ylamine derivatives, useful to treat e.g.  
 XX cancer, autoimmune condition, inflammatory condition, psoriasis,  
 PT

PT atherosclerosis, Parkinson's disease, diabetes and septic shock, are  
 PT kinase modulators.

XX Example 4; SEQ ID NO 10; 236pp; English.

XX This invention describes novel imidazo[1,2-a]pyrazin-8-ylamine  
 CC derivatives and their salts, solvates, crystal forms, diastereomers and  
 CC prodrugs. The invention also describes 1) a method for identifying a  
 CC kinase comprising contacting an organism, cell or preparation comprising  
 CC contacting the kinase with a novel imidazo[1,2-a]pyrazin-8-ylamine  
 CC derivative and detecting modulation of an activity of a kinase and 2) a  
 CC method for identifying Btk comprising contacting the organism cell or  
 CC preparation comprising the contacting kinase with a imidazo[1,2-a]pyrazin  
 CC 8-ylamine derivative and detecting modulation of an activity of Btk. The  
 CC derivatives can be used for the treatment of cancer when administered  
 CC with at least one antitumor therapeutic (preferably a chemotherapeutic  
 CC agent and especially mitomycin C, carboplatin, taxol, cisplatin,  
 CC paclitaxel, etoposide or doxorubicin or a radiotherapeutic agent. The  
 CC derivatives are useful for manufacture of a medicament for the treatment  
 CC of kinase (Btk) implicated condition, preferably cancer, an autoimmune  
 CC and/or inflammatory condition, in a mammal (preferably human, dog or  
 CC cat). The derivatives are also useful to treat conditions, diseases  
 CC and/or disorders such as psoriasis, cancer (especially chronic  
 CC myelogenous leukemia, gastrointestinal stromal tumors, non-small cell  
 CC lung cancer, breast cancer, ovarian cancer, recurrent ovarian cancer,  
 CC prostate cancer such as hormonal refractory prostate cancer, kidney  
 CC cancer, head and neck cancer or colorectal cancer), immunoregulation  
 CC (e.g. graft rejection), atherosclerosis, rheumatoid arthritis,  
 CC Parkinson's disease, Alzheimer's disease, diabetes (especially insulin  
 CC resistance or diabetic retinopathy) and septic shock. The imidazo[1,2-  
 CC a]pyrazin-8-ylamine derivatives have effective pharmacological properties  
 CC such as oral bioavailability, low toxicity, low serum protein binding and  
 CC desirable in vitro and in vivo half-lives. This sequence represents a  
 CC biotinylated and amidated peptide which is a substrate for a PTK domain  
 CC assay.

XX Sequence 17 AA;

Query Match 100.0%; Score 53; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9

Db |||||

Db 1 EGPWLEEE 9

RESULT 38

AEA36970  
 ID AEA36970 standard; peptide; 17 AA.

XX AEA36970;

XX 11-AUG-2005 (first entry)

DE Phosphotyrosine ligand peptide, H-5458.

XX Immunoassay; fluorescence.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "Biotinylated"

XX WO2005050206-A2.

XX 02-JUN-2005.

XX 17-SEP-2004; 2004WO-US030711.

XX 17-SEP-2003; 2003US-0504322P.

XX 23-SEP-2003; 2003US-0505453P.

XX PA (MOLE-) MOLECULAR PROBES INC.  
XX PT Beechem J, Gee K, Hagen D, Johnson I, Kang HC, Pastula C;  
XX DR WPI; 2005-41777/42.  
XX PT Ligand-detection reagent useful for determining presence of target ligand  
XX PT e.g. phosphorylated biomolecule in biological sample comprises ligand-  
XX PT binding antibody and ligand analog to form an antibody-ligand analog  
XX PT complex.  
XX PS Disclosure; Page 38; 123pp; English.  
XX CC The present invention relates to a ligand-detection reagent, ligand  
XX CC analog and method for determining the presence of a ligand in a sample.  
XX CC The ligand-detection reagent comprises of a ligand-binding antibody and a  
XX CC ligand analog to form an antibody-ligand analog complex. The ligand  
XX CC analog is a fluorogenic compound and comprises a monovalent or divalent  
XX CC antibody binding domain and a covalently bonded reporter molecule. The  
XX CC ligand-detection reagent is useful in a competitive immunoassay for the  
XX CC detection and measurement of one or more target ligands in a biological  
XX CC sample. The present sequence is a phosphotyrosine ligand peptide. This  
XX CC peptide is specific for phosphotyrosine-binding antibodies that when  
XX CC conjugated to a reporter molecule forms a ligand analog.  
XX SQ Sequence 17 AA;  
Query Match 100.0%; Score 53; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.089;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EGPWLEEE 9  
Db 1 EGPWLEEE 9  
RESULT 39  
ID AEA52649 standard; peptide; 17 AA.  
XX AC AEA52649;  
XX DT 25-AUG-2005 (first entry)  
XX DB Kinase biotinylated substrate peptide.  
XX KW Pharmaceutical; kinase; atopy; hypersensitivity; rheumatism;  
XX KW autoimmune disease; viral infection; cancer; neurodegenerative disease;  
XX KW cardiovascular disease; inflammation; infection; PCR; primer; ss;  
XX KW dermatological; antiallergic; immunosuppressive; antirheumatic; virucide;  
XX KW cytostatic; neuroprotective; cardiovascular-gen.; antiinflammatory;  
XX KW antimicrobial; enzyme inhibition.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT Modified-site 1  
XX FT /note= "Biotinylated residue"  
XX FT Modified-site 17  
XX FT /note= "C-terminal amide"  
XX PN WO2005054230-A1.  
XX PP 16-JUN-2005.  
XX PR 03-DEC-2004; 2004WO-AU001690.  
XX PR 03-DEC-2003; 2003AU-00906686.  
XX PR 20-APR-2004; 2004AU-00902060.  
XX PA (CYTO-) CYTOPIA RES PTY LTD.  
XX PT New indole-containing derivatives useful for treating e.g. Kaposi's

PI XX Burns CJ, Wilks AF, Bu X;  
XX DR WPI; 2005-466876/47.  
XX PT New pyrazine derivatives are protein tyrosine kinase inhibitors useful to  
XX PT treat e.g. rheumatic diseases, atopy, other autoimmune diseases and  
XX PT diseases, cancer, inflammation, neurodegenerative diseases and  
XX PT cardiovascular diseases.  
XX XX Disclosure; Page 42; 75pp; English.  
XX CC The invention relates to pyrazine derivatives and their prodrugs, salts,  
XX CC hydrates, solvates, crystal forms and diastereomers. The pyrazine  
XX CC derivatives are useful for treating tyrosine kinase-associated diseases  
XX CC involving janus kinase (JAK) 1, JAK2, JAK3 or TYK2 (particularly atopy,  
XX CC cell mediated hypersensitivity, rheumatic diseases, other autoimmune  
XX CC diseases/viral diseases, cancer, neurodegenerative diseases and  
XX CC cardiovascular diseases), in medicaments for treating JAK-associated  
XX CC disease states and for treating diseases and conditions associated with  
XX CC inflammation and infection. This sequence represents a kinase  
XX CC biotinylated substrate peptide used in the scope of the invention.  
XX SQ Sequence 17 AA;  
Query Match 100.0%; Score 53; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.089;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EGPWLEEE 9  
Db 1 EGPWLEEE 9  
RESULT 40  
ID AEB25345 standard; peptide; 17 AA.  
XX AC AEB25345;  
XX DT 08-SEP-2005 (first entry)  
XX DE Peptide used in protein kinase inhibitor assay.  
XX KW Cancer; neoplasm; inflammation; gastrointestinal disorder;  
XX KW Alzheimers disease; neurological disease; degeneration; dementia;  
XX KW psychiatric disorder; cognitive disorder; arthritis; cytostatic;  
XX KW gastrointestinal-gen.; antiinflammatory; antipsoriatic;  
XX KW immunosuppressive; neuroprotective; anticonvulsant; nootropic;  
XX KW antiparkinsonian; cerebroprotective; anticonvulsant; nootropic;  
XX KW neuroleptic; antidepressant; CNS-gen.; vasotropic; vulnerary;  
XX KW antiarthritic.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT Modified-site 1  
XX FT /note= "N-terminal biotin label"  
XX PN WO2005061519-A1.  
XX PD 07-JUL-2005.  
XX PP 17-DEC-2004; 2004WO-US042631.  
XX PR 19-DEC-2003; 2003US-0531202P.  
XX PA (SYRR-) SYRRX INC.  
XX PI Gangloff AR, Nowakowski J, Parasselli BR, Stafford JA, Tennant MG;  
XX DR WPI; 2005-497745/50.  
XX PT New indole-containing derivatives useful for treating e.g. Kaposi's

PT sarcoma, Parkinson's disease, stroke, depression or hair loss.  
 XX Example; Page 87; 179pp; English.  
 PS  
 XX The present invention relates to novel indole-containing derivatives that  
 CC act as protein kinase inhibitors. These compounds are useful for  
 CC treating: cancer (e.g. non small-cell lung, bladder, head, neck, ovarian,  
 CC prostate, breast, colorectal, small-cell lung, genitourinary,  
 CC gastrointestinal cancer, squamous cell carcinoma, astrocytoma, Kaposi's  
 CC sarcoma, glioblastoma, melanoma or glioma); inflammation, inflammatory  
 CC bowel disease, psoriasis, or transplant rejection; for preventing or  
 CC treating dementia related diseases (e.g. frontotemporal dementia  
 CC Parkinson's type, Parkinson dementia complex of Guam, HIV dementia,  
 CC diseases with associated neurofibrillar tangle pathologies, predemented  
 CC states, vascular dementia, dementia with Lewy bodies, frontotemporal  
 CC dementia and dementia pugilistica), Alzheimer's disease and conditions  
 CC associated with kinases; for preventing or treating amyotrophic lateral  
 CC sclerosis, corticobasal degeneration, Down syndrome, Huntington's  
 CC disease, Parkinson's disease, postencephalic parkinsonism, progressive  
 CC supranuclear palsy, Pick's disease, Niemann-Pick's disease, stroke, head  
 CC trauma and other chronic neurodegenerative diseases, bipolar disease,  
 CC affective disorders, depression, schizophrenia, cognitive disorders, hair  
 CC loss and contraceptive medication; mild cognitive impairment, age-  
 CC associated memory impairment, age-related cognitive decline, cognitive  
 CC impairment no dementia, mild cognitive decline, mild neurocognitive  
 CC decline, late-life forgetfulness, memory impairment and cognitive  
 CC impairment and androgenetic alopecia; or for treating arthritis (all  
 CC claimed). The present sequence is that of a peptide used in a time-  
 CC resolved fluorescence resonance energy transfer detection method to  
 CC determine inhibition of protein kinase C-Kit by indole-containing  
 CC compounds of the invention.  
 XX Sequence 17 AA;  
 SQ Query Match 100.0%; Score 53; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089; 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEE 9  
 DB 1 EGPWLEEE 9  
 RESULT 41  
 AEB77639  
 ID AEB77639 standard; peptide; 17 AA.  
 XX AC AEB77639;  
 XX 06-OCT-2005 (first entry)  
 DT Gastrin-1 peptide - SEQ ID 61.  
 DE autism; nootropic; asperger syndrome; gastrin-1.  
 XX Unidentified.  
 OS US2005170333-A1.  
 XX US2005170333-A1.  
 XX 04-AUG-2005.  
 PD 03-FEB-2004; 2004US-00770712.  
 PF 03-FEB-2004; 2004US-00770712.  
 PR (VOJD/) VOJDANI A.  
 XX VOjdani A;  
 PI WPI; 2005-562713/57.  
 DR Determining etiology of autistic spectrum disorder in patient, by  
 XX determining level of infectious agent/toxic chemical/dietary protein

PT derived antigen in samples of patient, comparing it with normal level of  
 XX antigens of control subjects.  
 PS Disclosure; SEQ ID NO 61; 89pp; English.  
 XX The invention comprises a method of determining etiology of an autistic  
 CC spectrum disorder in a patient. The method involves determining the level  
 CC of an infectious agent, toxic chemical, or dietary protein derived  
 CC antigen, or their antibodies in samples of patient, and comparing  
 CC antigens/antibodies levels with normal levels of antigens/antibodies from  
 CC control subjects. The method of the invention is useful for determining  
 CC the etiology of an autistic spectrum disorder, such as autism, pervasive  
 CC development disorder and Asperger's syndrome. The present amino acid  
 CC sequence represents a peptide that was used in the exemplification of the  
 CC invention.  
 XX Sequence 17 AA;  
 SQ Query Match 100.0%; Score 53; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089; 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEE 9  
 DB 1 EGPWLEEE 9  
 RESULT 42  
 AEC05671  
 ID AEC05671 standard; peptide; 17 AA.  
 XX AC AEC05671;  
 XX 20-OCT-2005 (first entry)  
 DT Gastrin peptide #1.  
 DE Vaccine; development; antibody production; immunogenicity; gastrin;  
 XX hormone.  
 XX Unidentified.  
 OS Key Location/Qualifiers  
 FT Modified-site 1 /note= "Pyroglutamic acid"  
 FT EP1564554-A1.  
 XX EP1564554-A1.  
 XX 17-AUG-2005.  
 PD 12-FEB-2004; 2004EP-00075439.  
 PF 12-FEB-2004; 2004EP-00075439.  
 PR (PEPS-) PRESCAN SYSTEMS BV.  
 XX (UYUT-) UNIV UTRECHT HOLDING BV.  
 PA Akresteljn GJ, Hensen EJ, Scibelli A, Van Der Most RG, Meloen RH;  
 XX Turkstra JA;  
 XX WPI; 2005-573732/59.  
 DR Affinity-binding assay for selecting antigen specific immune cells, by  
 XX contacting cell having four copies of target molecule with two labeled  
 PT binding molecules, detecting cells staining with each label, selecting  
 PT cells binding both labels.  
 XX Disclosure; Page 6; 45pp; English.  
 PS The present invention relates to an affinity-binding assay for selecting  
 CC antigen specific immune cells. The method involves contacting particle  
 CC such as a cell having four copies of target molecule with two binding  
 CC molecules specific for the target molecule, where first of the binding

CC molecules is associated with a first label and a second of the binding  
 CC molecules is associated with a second label, detecting cells staining  
 CC with each label and selecting cells binding both labels. The invention  
 CC also provides a method for detection of early B cell populations in  
 CC vaccine development. The invention is useful for the preparation of an  
 CC antibody. The present sequence is a gastrin peptide. This sequence is an  
 CC immunogenic peptide used as a vaccine.  
 XX  
 SQ Sequence 17 AA;

Query Match 100.0%; Score 53; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
 |||||  
 Db 1 EGPWLEEEE 9

RESULT 43  
 AAW24397  
 ID AAW24397 standard; peptide; 18 AA.  
 AC AAW24397;  
 XX

DT 12-MAR-1998 (first entry)  
 XX

DE Glycine-extended gastrin-17.  
 XX

KW Glycine-extended gastrin-17; gastrointestinal tumour; immunogen;  
 KW colorectal adenocarcinoma; antibody; progastrin; cholecystokinin B;  
 KW anti-gastrin-17; anti-G17.  
 XX

OS Homo sapiens.  
 XX

PN WO9728821-A1.  
 XX

PD 14-AUG-1997.  
 XX

PF 07-FEB-1997; 97WO-US002029.  
 XX

PR 08-FEB-1996; 96US-0011411P.  
 XX

PA (APHT-) APHTON CORP.  
 XX

PI Gevas PC, Karr SL, Grimes S, Michaeli D, Watson SA;  
 XX

WPI; 1997-415075/38.  
 XX

XX Treatment of glycine-extended gastrin-17-dependent gastrointestinal  
 PT tumours - using anti-G17 immunogenic composition, especially for  
 PT treatment of colorectal adenocarcinomas.  
 XX

PS Example 1; Fig 1A; 37pp; English.  
 XX

CC The present sequence represents glycine-extended gastrin-17. Treatment of  
 CC glycine-extended gastrin-17 (G17-Gly)-dependent gastrointestinal tumours  
 CC comprises administering an anti-gastrin 17 (anti-G17) immunogenic  
 CC composition. Anti-G17 immunogens raise antibodies which bind both the  
 CC antitiated and glycine-extended forms of G17. Neutralisation of progastrin  
 CC dependent on progastrin G17-Gly as growth stimulator or inducer. The  
 CC method is especially for the treatment of colorectal adenocarcinomas in  
 CC humans. This novel method is non-invasive, selectively reversible, does  
 CC not damage normal tissue, does not require frequent repeated treatments  
 CC and does not cross the blood brain barrier  
 XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 53; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 0.094;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
 |||||  
 Db 1 EGPWLEEEE 9

RESULT 44

ADH89207  
 ID ADH89207 standard; peptide; 18 AA.  
 XX

AC ADH89207;  
 XX

DT 06-MAY-2004 (first entry)  
 XX

DE Glycine extended gastrin G-17 precursor peptide, SEQ ID 2.  
 XX

KW Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;  
 KW gastrin G-34; gonadotropin releasing hormone; GnRH;  
 KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;  
 KW thyroid cancer; lung cancer; reproductive system cancer.  
 XX

OS Synthetic.  
 XX

XX Key Location/Qualifiers  
 FH Modified-site 1

FT /note= "Pyroglutamic acid"  
 FT

PN WO2004004687-A2.  
 XX

PD 15-JAN-2004.  
 XX

XX 03-JUL-2003; 2003WO-US021176.  
 PF

XX 03-JUL-2002; 2002US-0394179P.  
 PR

XX (APHT-) APHTON CORP.  
 PA

XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 PA

XX Michaeli D, Grimes S, Barenholz Y, Even-Chen S;  
 PI

XX WPI; 2004-099340/10.  
 XX

XX Injectable liposomal composition for delivery of a water-soluble  
 PT substance e.g. vaccine for preventing pregnancy, comprises several  
 PT liposomal vesicles comprising a high weight ratio of lipid to  
 PT encapsulated water-soluble substance.  
 XX

PS Disclosure; SEQ ID NO 2; 73pp; English.  
 XX

CC The present invention relates to injectable liposomal compositions (I)  
 CC for delivery of a water-soluble substance e.g. immunomimic peptides. (I)  
 CC comprises several liposomal vesicles comprising a high weight ratio of a  
 CC lipid to an encapsulated water-soluble substance so as to achieve a high  
 CC efficiency of encapsulation. The immunomimic peptide is chosen from  
 CC gastrin G-17 (ADH89206 to ADH89213 and ADH89223), Gastrin G-34 (ADH89217-  
 CC ADH89219), gonadotropin releasing hormone (GnRH) peptide (ADH89220 and  
 CC ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-  
 CC ADH89222 and ADH89225). (I) comprising vaccines directed against hormone  
 CC or hormone cognate receptors, where the vaccine comprises at least one:  
 CC hormone-immunomimic peptide such as gastrin G-17 or G-34 is useful for  
 CC treating gastrointestinal malignancy, and non-gastrointestinal tumors  
 CC such as thyroid and lung cancer; or GnRH or hCG immunomimic peptide is  
 CC useful as contraceptive and for treating cancers in male and female  
 CC reproductive systems.  
 XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 53; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 0.094;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
 |||||  
 Db 1 EGPWLEEEE 9

## RESULT 45

ADT49597  
ID ADT49597 standard; peptide; 18 AA.

XX ADT49597;

XX 30-DEC-2004 (first entry)

XX Human gastrin 17 (G17)-Gly amino acid sequence.

XX G17; gastrin; hormone; human; G17-Gly; gastrin 17.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 1  
FT /label= pGlu  
FT /note= "pyroglutamic acid"

XX WO2004088326-A2.

XX 14-OCT-2004.

XX 29-MAR-2004; 2004WO-US009666.

XX 28-MAR-2003; 2003US-0458244P.

XX (APHT-) APTON CORP.

XX (HUNT-) HUNTINGDON LIFE SCI LTD.

XX Grimes S, Little J, McLoughlin L;

XX WPI; 2004-719280/70.

XX Determining total or free amount of gastrin hormone in a biological fluid  
XX sample comprises incubating the sample in the presence of an N-terminal  
XX sequence gastrin peptide for binding to a C-terminal specific antibody.

XX Disclosure; SEQ ID NO 2; 24pp; English.

XX The invention relates to determining the total amount of gastrin or free  
XX gastrin hormone in a biological fluid sample. The method involves (a)  
XX obtaining a biological fluid sample comprising a gastrin hormone from a  
XX patient; (b) providing an immobilized antibody that selectively binds a C  
XX -terminal epitope of the gastrin hormone; (c) incubating the sample in  
XX the presence of an N-terminal sequence gastrin peptide under conditions  
XX for binding of the gastrin hormone in the sample to the antibody to  
XX produce an immobilized complex of the antibody bound to the gastrin  
XX hormone; (d) washing the immobilized complex to remove unbound antibody  
XX and N-terminal sequence gastrin peptide, and incubating the complex with  
XX a detectable marker- conjugated antibody that selectively binds an N-  
XX terminal epitope of gastrin hormone to form an immobilized detectable  
XX marker-conjugated antibody complex; (e) washing the immobilized  
XX detectable marker-conjugated antibody complex, and incubating with a  
XX development reagent; and (f) measuring the developed reagent to determine  
XX the total amount of (free) gastrin hormone in the biological fluid  
XX sample. The C-terminal selective antibody and/or the N-terminal selective  
XX antibody is a monoclonal antibody. The gastrin hormone is gastrin-17  
XX (G17) or glycine extended G17 (G17-Gly) and the C-terminal selective  
XX antibody and the N-terminal selective antibody bind G17. The method is  
XX useful for detecting and/or quantifying free or total amount of gastric  
XX hormone peptides including antibody-bound, in a biological fluid. The  
XX present sequence represents the amino acid sequence of G17-Gly, an  
XX incomplete processed form of gastrin found as a minor component of little  
XX gastrins in human.

XX Sequence 18 AA;

Query Match 100.0%; Score 53; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.094; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 EGPWLEEE 9  
| | | | |  
Db 1 EGPWLEEE 9

## RESULT 46

AEC05677  
ID AEC05677 standard; peptide; 18 AA.

XX AC AEC05677;

XX 20-OCT-2005 (first entry)

XX Gastrin peptide.

XX Vaccine; development; antibody production; immunogenicity; gastrin;  
XX hormone.

XX Unidentified.

XX Key Location/Qualifiers  
FH Modified-site 1  
FT /note= "Pyroglutamic acid"FT Modified-site 18  
FT /note= "Biotinylated C-terminal amide"

XX EP1564554-A1.

XX 17-AUG-2005.

XX 12-FEB-2004; 2004EP-00075439.

XX 12-FEB-2004; 2004EP-00075439.

XX (PEPS-) PEPSCAN SYSTEMS BV.

XX (UYUT-) UNIV UTRECHT HOLDING BV.

XX Akrestejn GJ, Hensen EJ, Scibelli A, Van Der Most RG, Meloen RH;  
XX Turkstra JA;

XX WPI; 2005-573732/59.

XX Affinity-binding assay for selecting antigen specific immune cells, by  
XX contacting cell having four copies of target molecule with two labeled  
XX binding molecules, detecting cells staining with each label, selecting  
XX cells binding both labels.

XX Example 1; Page 6; 45pp; English.

XX The present invention relates to an affinity-binding assay for selecting  
XX antigen specific immune cells. The method involves contacting particle  
XX such as a cell having four copies of target molecule with two binding  
XX molecules specific for the target molecule, where first of the binding  
XX molecules is associated with a first label and a second of the binding  
XX molecules is associated with a second label, detecting cells staining  
XX with each label and selecting cells binding both labels. The invention  
XX also provides a method for detection of early B cell populations in  
XX vaccine development. The invention is useful for the preparation of an  
XX antibody. The present sequence is a gastrin peptide. This sequence is an  
XX immunogenic peptide used as a vaccine.

XX Sequence 18 AA;

Query Match 100.0%; Score 53; DB 9; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.094; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 EGPWLEEE 9  
| | | | |

Db 1 EGPWLEEE 9

```

RESULT 47
AEC05672
ID AEC05672 standard; peptide; 19 AA.
XX
XX AEC05672;
XX
XX 20-OCT-2005 (first entry)
XX
XX Gastrin tandem peptide #1.
XX
XX Vaccine; development; antibody production; immunogenicity; gastrin;
XX hormone.
XX
XX Synthetic.
XX OS Unidentified.
XX
XX
XX Key Location/Qualifiers
XX Modified-site 1 /note= "Pyroglutamic acid"
XX
XX EPI564554-A1.
XX
XX 17-AUG-2005.
XX
XX 12-FEB-2004; 2004EP-00075439.
XX
XX 12-FEB-2004; 2004EP-00075439.
XX
XX (PEPS-) PEPSCAN SYSTEMS BV.
XX PA (UYUT-) UNIV UTRECHT HOLDING BV.
XX
XX Akrestejn GJ, Hensen EJ, Scibelli A, Van Der Most RG, Meloen RH;
XX Turkstra JA;
XX
XX WPI; 2005-573732/59.
XX
XX Affinity-binding assay for selecting antigen specific immune cells, by
XX contacting cell having four copies of target molecule with two labeled
XX binding molecules, detecting cells staining with each label, selecting
XX cells binding both labels.
XX
XX Disclosure; Page 6; 45pp; English.
XX
XX The present invention relates to an affinity-binding assay for selecting
XX antigen specific immune cells. The method involves contacting particle
XX such as a cell having four copies of target molecule with two binding
XX molecules specific for the target molecule, where first of the binding
XX molecules is associated with a first label and a second of the binding
XX molecules is associated with a second label, detecting cells staining
XX with each label and selecting cells binding both labels. The invention
XX also provides a method for detection of early B cell populations in
XX vaccine development. The invention is useful for the preparation of an
XX antibody. The present sequence is a gastrin tandem peptide. This sequence
XX is an immunogenic peptide used as a vaccine.
XX
XX Sequence 19 AA;
XX
XX Query Match 100.0%; Score 53; DB 9; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 0.1;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 EGPWLEEEE 9
XX Db 1 EGPWLEEEE 9
XX
XX RESULT 48
AEC05674
ID AEC05674 standard; peptide; 19 AA.
XX
XX AEC05674;
XX
XX 20-OCT-2005 (first entry)
XX

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```

XX Gastrin tandem peptide #2.
DE
XX Vaccine; development; antibody production; immunogenicity; gastrin;
XX hormone.
XX
XX Synthetic.
XX OS Unidentified.
XX
XX Key Location/Qualifiers
XX Modified-site 1 /note= "Pyroglutamic acid"
XX
XX EPI564554-A1.
XX
XX 17-AUG-2005.
XX
XX 12-FEB-2004; 2004EP-00075439.
XX
XX 12-FEB-2004; 2004EP-00075439.
XX
XX (PEPS-) PEPSCAN SYSTEMS BV.
XX PA (UYUT-) UNIV UTRECHT HOLDING BV.
XX
XX Akrestejn GJ, Hensen EJ, Scibelli A, Van Der Most RG, Meloen RH;
XX Turkstra JA;
XX
XX WPI; 2005-573732/59.
XX
XX Affinity-binding assay for selecting antigen specific immune cells, by
XX contacting cell having four copies of target molecule with two labeled
XX binding molecules, detecting cells staining with each label, selecting
XX cells binding both labels.
XX
XX Example 3; Page 11; 45pp; English.
XX
XX The present invention relates to an affinity-binding assay for selecting
XX antigen specific immune cells. The method involves contacting particle
XX such as a cell having four copies of target molecule with two binding
XX molecules specific for the target molecule, where first of the binding
XX molecules is associated with a first label and a second of the binding
XX molecules is associated with a second label, detecting cells staining
XX with each label and selecting cells binding both labels. The invention
XX also provides a method for detection of early B cell populations in
XX vaccine development. The invention is useful for the preparation of an
XX antibody. The present sequence is a gastrin tandem peptide. This sequence
XX is an immunogenic peptide used as a vaccine.
XX
XX Sequence 19 AA;
XX
XX Query Match 100.0%; Score 53; DB 9; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 0.1;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 EGPWLEEEE 9
XX Db 1 EGPWLEEEE 9
XX
XX RESULT 49
AEC05675
ID AEC05675 standard; peptide; 20 AA.
XX
XX AEC05675;
XX
XX 20-OCT-2005 (first entry)
XX
XX Gastrin TDK 1 peptide.
XX
XX Vaccine; development; antibody production; immunogenicity; gastrin;
XX hormone.
XX
XX Synthetic.
XX

```

```

OS Unidentified.
XX
PH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 20 /note= "Pyroglutamic acid"
FT Modified-site 20 /note= "C-terminal amide"
FT
XX
XX BP1564554-A1.
XX
XX PD 17-AUG-2005.
XX
XX PD 12-FEB-2004; 2004EP-00075439.
XX
XX PD 12-FEB-2004; 2004EP-00075439.
XX
XX PA (PEPS-) PEPSKAN SYSTEMS BV.
XX PA (UYUT-) UNIV UTRECHT HOLDING BV.
XX
XX PI Akresteljn GJ, Hensen EJ, Scibelli A, Van Der Most RG, Meloen RH;
XX PI Turkstra JA;
XX
XX WPI; 2005-573732/59.
XX
XX Affinity-binding assay for selecting antigen specific immune cells, by
XX contacting cell having four copies of target molecule with two labeled
XX binding molecules, detecting cells staining with each label, selecting
XX cells binding both labels.
XX
XX Example 3; Page 6; 45pp; English.
XX
XX The present invention relates to an affinity-binding assay for selecting
XX antigen specific immune cells. The method involves contacting particle
XX such as a cell having four copies of target molecule with two binding
XX molecules specific for the target molecule, where first of the binding
XX molecules is associated with a first label, and a second of the binding
XX molecules is associated with a second label, detecting cells staining
XX with each label and selecting cells binding both labels. The invention
XX also provides a method for detection of early B cell populations in
XX vaccine development. The invention is useful for the preparation of an
XX antibody. The present sequence is a gastrin TDK 1 peptide. This sequence
XX is an immunogenic peptide used as a vaccine.
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 53; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9
|||||
|||||

RESULT 50
AEC05676
ID AEC05676 standard; peptide; 27 AA.
XX
XX AC AEC05676;
XX
XX DT 20-OCT-2005 (first entry)
XX
XX DE Gastrin TDK 2 peptide.
XX
XX KW Vaccine; development; antibody production; immunogenicity; gastrin;
XX KW hormone.
XX
XX OS Synthetic.
XX OS Unidentified.
XX
XX PH Key Location/Qualifiers
FT Modified-site 1 /note= "Pyroglutamic acid"

```

```

FT Misc-difference 13 /note= "D-form residue"
FT Misc-difference 26 /note= "D-form residue"
FT Modified-site 27 /note= "C-terminal amide"
XX
XX PN EP1564554-A1.
XX
XX PD 17-AUG-2005.
XX
XX PD 12-FEB-2004; 2004EP-00075439.
XX
XX PD 12-FEB-2004; 2004EP-00075439.
XX
XX PA (PEPS-) PEPSKAN SYSTEMS BV.
XX PA (UYUT-) UNIV UTRECHT HOLDING BV.
XX
XX PI Akresteljn GJ, Hensen EJ, Scibelli A, Van Der Most RG, Meloen RH;
XX PI Turkstra JA;
XX
XX WPI; 2005-573732/59.
XX
XX Affinity-binding assay for selecting antigen specific immune cells, by
XX contacting cell having four copies of target molecule with two labeled
XX binding molecules, detecting cells staining with each label, selecting
XX cells binding both labels.
XX
XX Example 3; Page 6; 45pp; English.
XX
XX The present invention relates to an affinity-binding assay for selecting
XX antigen specific immune cells. The method involves contacting particle
XX such as a cell having four copies of target molecule with two binding
XX molecules specific for the target molecule, where first of the binding
XX molecules is associated with a first label, and a second of the binding
XX molecules is associated with a second label, detecting cells staining
XX with each label and selecting cells binding both labels. The invention
XX also provides a method for detection of early B cell populations in
XX vaccine development. The invention is useful for the preparation of an
XX antibody. The present sequence is a gastrin TDK 2 peptide. This sequence
XX is an immunogenic peptide used as a vaccine.
XX
SQ Sequence 27 AA;
Query Match 100.0%; Score 53; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9
|||||
|||||

Search completed: January 3, 2006, 09:19:09
Job time : 111.857 secs

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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:05 ; Search time 9.42857 Seconds  
(without alignments)  
91.843 Million cell updates/sec

Title: US-10-759-832-7  
Perfect score: 53  
Sequence: 1 EGPWLEEE 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :  
PIR\_80:\*  
1: pirl:\*  
2: pirl2:\*  
3: pirl3:\*  
4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	94.3	33	2 A60506	big gastrin - Nort
2	50	94.3	101	1 GMDHUB	gastrin precursor
3	50	94.3	104	1 GMDCT	gastrin precursor
4	48	90.6	17	2 A60071	gastrin - rhesus m
5	48	90.6	104	1 GMDG	gastrin precursor
6	48	90.6	104	1 GMDGB	gastrin precursor
7	47	88.7	17	1 GMDH	gastrin - sheep
8	47	88.7	34	2 J50426	big gastrin - goat
9	47	88.7	104	1 GMDH	gastrin precursor
10	45	84.9	238	2 T46166	MB27 protein - Ar
11	43	81.1	16	2 A29541	little gastrin - C
12	43	81.1	335	2 C75119	deoxyhypusine synt
13	42	79.2	370	2 F64401	deoxyhypusine synt
14	41	77.4	248	2 C91080	hypothetical prote
15	41	77.4	248	2 D85925	hypothetical prote
16	41	77.4	273	1 J02390	MYB transcrip
17	41	77.4	293	2 T09758	MYB-related protei
18	40	75.5	33	1 GMDGB	big gastrin [valid
19	40	75.5	33	2 B29541	big gastrin - Chin
20	40	75.5	110	2 S20350	napin nla - rape
21	40	75.5	268	1 J00961	myb-related protei
22	40	75.5	745	2 A71448	probable MYB trans
23	39	73.6	204	2 C35878	class I major hist
24	39	73.6	377	2 A49885	MHC class I histoc
25	39	73.6	379	2 A35878	class I major hist
26	39	73.6	379	2 E35878	class I major hist
27	39	73.6	406	2 B35878	class I major hist
28	39	73.6	498	2 S11246	LAG-3 protein prec
29	39	73.6	960	2 T00808	hypothetical prote

30	38	71.7	234	2	T51666	myb-related transc
31	38	71.7	256	2	T49254	Myb DNA binding pr
32	38	71.7	278	2	T03850	Myb-related protei
33	38	71.7	325	2	T51509	probable transcrip
34	38	71.7	378	2	D82158	N-acetylglucosamin
35	38	71.7	529	2	T48253	myb-like protein -
36	38	71.7	894	2	T26149	hypothetical prote
37	38	71.7	910	2	A48403	alpha-actinin - Ca
38	38	71.7	920	2	T26147	hypothetical prote
39	38	71.7	985	2	T41135	hypothetical prote
40	38	71.7	4006	2	T09070	probable tenascin
41	37	69.8	106	2	S26636	napin nlb - rape
42	37	69.8	189	1	G69355	MJ653 homolog AFO
43	37	69.8	222	1	F69335	conserved hypotet
44	37	69.8	301	1	A37766	SEC14 protein - ye
45	37	69.8	301	2	T45859	R2R3-MYB transcrip
46	37	69.8	304	1	S71285	myb-related protei
47	37	69.8	333	2	A87443	GTP-binding protei
48	37	69.8	348	2	S11198	transforming protei
49	37	69.8	357	2	S18198	class I histocoma
50	37	69.8	365	2	JH0535	class I histocoma
51	37	69.8	365	2	JH0537	class I histocoma
52	37	69.8	365	2	JH0536	class I histocoma
53	37	69.8	365	2	I38439	MHC class I histoc
54	37	69.8	367	2	T01017	probable MYB fami
55	37	69.8	388	1	Q0YV	transforming prote
56	37	69.8	398	2	A75128	probable transamin
57	37	69.8	624	1	T51581	transforming prote
58	37	69.8	636	1	TVM5MB	transforming prote
59	37	69.8	640	1	A55073	transforming prote
60	37	69.8	686	1	S28050	transforming prote
61	37	69.8	700	1	S01991	transforming prote
62	37	69.8	704	1	S33704	transforming prote
63	37	69.8	715	4	TVM5MY	transforming prote
64	37	69.8	728	1	S36095	transforming prote
65	37	69.8	733	1	S33643	transforming prote
66	37	69.8	751	1	I49457	transforming prote
67	37	69.8	752	1	S03423	transforming prote
68	37	69.8	757	1	I50667	transforming prote
69	37	69.8	761	1	TVCHM	transforming prote
70	37	69.8	761	1	TVHUMB	transforming prote
71	37	69.8	952	2	T48510	MYB like protein -
72	36	67.9	96	2	D49850	ferredoxin 2(4Fe-4
73	36	67.9	193	2	B82063	conserved hypotet
74	36	67.9	203	2	E83166	hypothetical prote
75	36	67.9	226	2	A69904	hypothetical prote
76	36	67.9	241	2	C81971	hypothetical prote
77	36	67.9	241	2	F81026	conserved hypotet
78	36	67.9	263	2	F84770	hypothetical prote
79	36	67.9	330	2	T08351	hypothetical prote
80	36	67.9	352	1	S58293	myb-related protei
81	36	67.9	393	1	S22520	myb-related protei
82	36	67.9	535	2	E95929	probable methylcro
83	36	67.9	544	2	T40058	probable chromatin
84	36	67.9	680	2	D86925	probable acyl-CoA
85	36	67.9	715	2	T04452	transforming prote
86	36	67.9	776	2	E85384	probable myb-prote
87	36	67.9	834	1	WVXPJ	RNA replicase 2 (E
88	36	67.9	907	2	A24938	hypothetical T2 pr
89	36	67.9	925	2	S27320	nuclear antigen EB
90	35.5	67.0	285	2	A95846	probable ECF-sigma
91	35	66.0	215	2	T40957	hypothetical prote
92	35	66.0	218	2	A35216	FPD4 protein - fow
93	35	66.0	230	2	D70400	probable 2-oxoacid
94	35	66.0	257	2	T03825	myb protein homolo
95	35	66.0	261	2	T06650	myb-related protei
96	35	66.0	274	2	T07393	Myb-related transc
97	35	66.0	274	2	AG1678	D-alanyl-D-alanine
98	35	66.0	274	2	E69423	branched-chain ami
99	35	66.0	278	2	T51641	myb-related transc
100	35	66.0	279	2	T03830	probable myb facto
101	35	66.0	280	1	S26604	myb-related protei
102	35	66.0	280	2	T00737	myb-related protei

103	35	66.0	280	2	T51667	myb-related transcr	176	34	64.2	362	1	HLMSLD	MHC class I histoc
104	35	66.0	282	2	C96687	hypothetical prote	177	34	64.2	362	2	C60854	MHC class I histoc
105	35	66.0	282	2	B85327	probable transcrip	178	34	64.2	362	2	B60854	hypothetical prote
106	35	66.0	299	2	D17917	probable transcrip	179	34	64.2	364	2	B83152	hypothetical prote
107	35	66.0	310	2	B97777	thioredoxin-diulf	180	34	64.2	372	2	T00243	sopa protein - Esc
108	35	66.0	310	2	D71703	thioredoxin reduct	181	34	64.2	374	2	T05891	myb-related protei
109	35	66.0	311	2	T03827	myb protein homolo	182	34	64.2	376	2	T51673	hypothetical prote
110	35	66.0	316	1	JQ0956	myb-related protei	183	34	64.2	377	2	F96550	hypothetical prote
111	35	66.0	317	2	B83760	hypothetical prote	184	34	64.2	388	1	BVECAF	sopa protein - Esc
112	35	66.0	323	2	T51621	myb-like protein l	185	34	64.2	392	2	T05422	hypothetical prote
113	35	66.0	323	2	T51645	myb-related transcr	186	34	64.2	399	2	T47712	MYB transcription
114	35	66.0	324	2	B85064	MYB-like protein l	187	34	64.2	432	2	D64046	N-acetylmuramoyl-L
115	35	66.0	326	2	T49966	myb-related protei	188	34	64.2	460	2	JC5137	beta-glucosidase (
116	35	66.0	330	2	F96775	hypothetical prote	189	34	64.2	460	2	A96555	unknown protein (i
117	35	66.0	332	1	S58283	myb-related protei	190	34	64.2	525	2	C64313	conserved hypotet
118	35	66.0	333	2	T45720	probable transcrip	191	34	64.2	530	2	T48004	multifunctional am
119	35	66.0	343	2	S17677	NADH2 dehydrogenas	192	34	64.2	542	2	H84509	hypothetical prote
120	35	66.0	343	2	T52590	probable transcrip	193	34	64.2	576	2	S12792	protein-tyrosine k
121	35	66.0	347	2	T07398	myb-related transcr	194	34	64.2	591	2	F69837	asparagine synthas
122	35	66.0	365	2	D86470	F21H2.9 protein -	195	34	64.2	597	1	P21VTV	RNA-directed RNA p
123	35	66.0	368	2	T03828	myb protein - rice	196	34	64.2	636	2	I48689	gene NK10 protein
124	35	66.0	382	2	C86230	hypothetical prote	197	34	64.2	646	2	T01079	sulfate transport
125	35	66.0	387	2	S32934	aminotransferase p	198	34	64.2	676	2	C97775	acylamino-acid-rel
126	35	66.0	401	2	D71003	probable transamin	199	34	64.2	679	2	A83488	hypothetical prote
127	35	66.0	417	2	A33269	DNA primase (EC 2.	200	34	64.2	775	2	T49817	hypothetical prote
128	35	66.0	420	2	S45630	DNA primase chain	201	34	64.2	812	2	T16621	beta-glucosidase (
129	35	66.0	421	1	S26605	myb-related protei	202	34	64.2	845	1	GLVK	lipoxigenase (EC 1
130	35	66.0	421	1	S24244	myb-related protei	203	34	64.2	859	2	T06352	lipoxigenase (EC 1
131	35	66.0	456	2	T48291	hypothetical prote	204	34	64.2	889	2	T06339	tyrosine kinase -
132	35	66.0	459	2	S42647	photosystem II chl	205	34	64.2	888	2	I58378	hypothetical prote
133	35	66.0	459	2	D23342	photosystem II CP4	206	34	64.2	909	2	T33749	hypothetical prote
134	35	66.0	506	2	F83888	two-component resp	207	34	64.2	1034	2	T30574	beta-galactosidase
135	35	66.0	529	2	C70545	hypothetical prote	208	34	64.2	1064	2	A41542	adenylate cyclase
136	35	66.0	572	2	JC7833	kumamolysin precu	209	34	64.2	1112	2	S70522	acyclic nucleotide
137	35	66.0	627	2	S76462	hypothetical prote	210	34	64.2	1171	2	T35548	hypothetical prote
138	35	66.0	803	2	T18738	hypothetical prote	211	34	64.2	1186	2	T23327	adenomatous polypo
139	35	66.0	810	2	B71639	virB4 protein prec	212	34	64.2	1188	2	G72734	hypothetical prote
140	35	66.0	1059	2	B24872	retrovirus-related	213	34	64.2	1188	2	T23330	hypothetical prote
141	35	66.0	1239	2	S74355	hypothetical prote	214	34	64.2	1558	2	C89114	protein C37C3.6a l
142	34	64.2	83	2	A12000	hypothetical prote	215	34	64.2	2167	2	T34395	hypothetical prote
143	34	64.2	122	1	S58294	myb-related protei	216	34	64.2	2167	2	T34395	genome polyprotein
144	34	64.2	153	2	T04563	myb-related protei	217	34	64.2	5126	2	S40450	ryanodine receptor
145	34	64.2	198	1	JQ0959	myb-related protei	218	33.5	64.2	645	2	G01205	TYL protein - huma
146	34	64.2	205	1	JQ0958	myb-related protei	219	33	62.3	72	2	F83209	hypothetical prote
147	34	64.2	206	2	JL0058	H-2 class I histoc	220	33	62.3	88	2	A40485	nucleosapoid prote
148	34	64.2	206	2	JL0058	H-2 class I histoc	221	33	62.3	119	2	H72495	hypothetical prote
149	34	64.2	217	2	T06455	Myb26 protein - ga	222	33	62.3	152	2	D64839	probable protein-t
150	34	64.2	246	1	S71283	hypothetical prote	223	33	62.3	152	2	F85633	probable phosphata
151	34	64.2	246	1	D86197	hypothetical prote	224	33	62.3	152	2	B90771	probable phosphata
152	34	64.2	249	2	B84717	probable MYB fami	225	33	62.3	164	2	S75684	hypothetical prote
153	34	64.2	275	2	T02988	myb-related protei	226	33	62.3	180	2	B64353	hypothetical prote
154	34	64.2	284	2	T17222	hypothetical prote	227	33	62.3	196	2	S72716	4-coumarate-CoA li
155	34	64.2	287	2	A10782	probable transcrip	228	33	62.3	200	2	C85096	hypothetical prote
156	34	64.2	293	2	D64984	probable transcrip	229	33	62.3	212	2	H83305	probable radical a
157	34	64.2	293	2	C85854	probable transcrip	230	33	62.3	216	2	D96520	hypothetical prote
158	34	64.2	293	2	A98010	transcription fact	231	33	62.3	234	2	T36740	hypothetical prote
159	34	64.2	296	2	T06025	myb protein-like -	232	33	62.3	247	2	A72664	myb-related protei
160	34	64.2	297	2	T47857	myb-related protei	233	33	62.3	249	1	S68688	pullulanase secret
161	34	64.2	305	1	S71284	probable sulfatase	234	33	62.3	252	2	S11802	conserved hypotet
162	34	64.2	307	2	A71057	probable sulfatase	235	33	62.3	256	2	AG0483	hypothetical prote
163	34	64.2	307	2	G75088	probable MYB fami	236	33	62.3	265	2	A95298	probable Myb-like
164	34	64.2	309	2	T00503	probable MYB fami	237	33	62.3	278	2	C86383	conserved hypotet
165	34	64.2	310	2	T46035	MYB84 - Arabidop	238	33	62.3	286	2	G69399	probable sec14 cyt
166	34	64.2	320	2	C85440	myb-related protei	239	33	62.3	286	2	T38768	probable MYB fami
167	34	64.2	332	2	T51650	probable transcrip	240	33	62.3	298	2	H84785	homeotic protein -
168	34	64.2	336	2	S09532	int protein - phag	241	33	62.3	301	2	T14331	van protein - Ent
169	34	64.2	342	2	G71012	deoxyhypusine synt	242	33	62.3	303	2	JC1427	ribosomal large su
170	34	64.2	348	2	A85535	probable NAGC-like	243	33	62.3	304	2	D72316	conserved hypotet
171	34	64.2	348	2	E90684	probable NAGC-like	244	33	62.3	304	2	AB0390	hypothetical prote
172	34	64.2	348	2	B64768	yaif protein - Esc	245	33	62.3	309	2	B82460	hypothetical prote
173	34	64.2	349	2	A53340	interferon regulat	246	33	62.3	313	2	G69084	hypothetical prote
174	34	64.2	355	2	JR0385	NADH2 dehydrogenas	247	33	62.3	313	2	A48903	beta-lactamase - P
175	34	64.2	359	2	A10140	molybdenum transpo	248	33	62.3	313	2	D69900	conserved hypotet

249	33	62.3	313	2	T39974	hypothetical prote	322	33	62.3	1074	2	JC5928	semaphorin F precu
250	33	62.3	318	2	H75490	proline iminopecti	323	33	62.3	1096	2	TL6875	hypothetical prote
251	33	62.3	321	1	C64522	chemotaxis protein	324	33	62.3	1179	2	G75459	DNA-directed RNA p
252	33	62.3	322	2	G71984	probable chemotaxi	325	33	62.3	1181	2	C82500	ICMF-related prote
253	33	62.3	322	2	AF0847	hydrogenase isoenz	326	33	62.3	1200	2	S68258	DNA polymerase gam
254	33	62.3	322	2	S15201	hydrogenase expres	327	33	62.3	1252	2	T14272	cortactin-binding
255	33	62.3	322	2	B91077	HypE protein [impo	328	33	62.3	1363	2	I58375	protein-tyrosine k
256	33	62.3	322	2	B85922	hypothetical prote	329	33	62.3	1486	2	E96608	probable retroelem
257	33	62.3	324	2	A83316	thioredoxin-disulf	330	33	62.3	1500	1	JQ1348	carbamoyl-phosphat
258	33	62.3	327	2	T01038	myb-related protei	331	33	62.3	1500	1	SVRTCA	brain-specific ang
259	33	62.3	328	2	H83171	thiamin-monophosph	332	33	62.3	1522	2	T00028	hypothetical prote
260	33	62.3	329	2	F95298	aldehyde or keto o	333	33	62.3	1922	2	T00637	hypothetical prote
261	33	62.3	355	2	A80454	uroporphyrinogen d	334	33	62.3	2228	1	ZLNZSV	genome polyprotein
262	33	62.3	363	2	T27386	hypothetical prote	335	33	62.3	3388	1	GNWVDP	genome polyprotein
263	33	62.3	369	1	DEBSPF	pyruvate dehydroge	336	33	62.3	3391	1	GNWV16	genome polyprotein
264	33	62.3	371	1	DEBSPA	pyruvate dehydroge	337	33	62.3	3391	1	GNWV26	genome polyprotein
265	33	62.3	382	2	C90717	N-acetylglucosamin	338	33	62.3	3391	1	GNWVJA	genome polyprotein
266	33	62.3	382	2	C85567	N-acetylglucosamin	339	33	62.3	3391	2	JS0219	polyprotein - deng
267	33	62.3	382	2	A37018	N-acetylglucosamin	340	33	62.3	3396	1	A42551	genome polyprotein
268	33	62.3	383	2	C70845	probable naga prot	341	33	62.3	8243	2	T31307	type I fatty acid
269	33	62.3	384	2	AH0584	N-acetylglucosamin	342	32	60.4	47	2	A47204	feline class I maj
270	33	62.3	393	2	D96577	hypothetical prote	343	32	60.4	65	2	S51099	MHC class I histoc
271	33	62.3	398	2	H72660	probable N-Acylami	344	32	60.4	67	2	G72803	gp32.1 protein - M
272	33	62.3	399	2	B64488	hypothetical prote	345	32	60.4	75	2	T06013	hypothetical prote
273	33	62.3	405	2	T17211	hypothetical prote	346	32	60.4	87	2	S52230	HLA-A30 variant ex
274	33	62.3	405	2	T01218	hypothetical prote	347	32	60.4	95	2	S72980	hypothetical prote
275	33	62.3	412	2	A27290	permease [imported	348	32	60.4	102	2	F83231	hypothetical prote
276	33	62.3	422	2	C97569	hypothetical prote	349	32	60.4	130	2	AD2175	two-component resp
277	33	62.3	424	2	F84165	hypothetical prote	350	32	60.4	137	2	I80172	class I histocompa
278	33	62.3	424	2	T08229	probable transposa	351	32	60.4	137	2	I80175	class I histocompa
279	33	62.3	424	2	T08249	probable transposa	352	32	60.4	137	2	I80173	class I histocompa
280	33	62.3	427	2	C83591	N-carbamoyl-beta-a	353	32	60.4	137	2	I80176	class I histocompa
281	33	62.3	441	2	G82612	hypothetical prote	354	32	60.4	137	2	I80174	class I histocompa
282	33	62.3	460	2	S06469	photosystem II chl	355	32	60.4	137	2	I38875	MHC class I antige
283	33	62.3	461	2	S34498	photosystem II chl	356	32	60.4	137	2	I38860	MHC class I antige
284	33	62.3	461	2	S04025	photosystem II chl	357	32	60.4	137	2	I38874	MHC class I antige
285	33	62.3	462	2	S10397	finger protein kox	358	32	60.4	137	2	I38876	MHC class I antige
286	33	62.3	467	2	G83592	adenosylmethionine	359	32	60.4	146	2	AC2423	hypothetical prote
287	33	62.3	473	2	T07228	photosystem II chl	360	32	60.4	159	2	S63619	cymc protein - Kle
288	33	62.3	477	2	A24115	transcription init	361	32	60.4	181	2	I59188	MHC cell surface g
289	33	62.3	483	2	G64799	ybeV protein - Esc	362	32	60.4	184	2	B83578	probable transcrip
290	33	62.3	485	2	T25199	hypothetical prote	363	32	60.4	189	2	S74159	CGMP-gated cation
291	33	62.3	487	2	T34386	hypothetical prote	364	32	60.4	205	2	JC7975	HIV accessory prot
292	33	62.3	502	2	D95855	probable ABC trans	365	32	60.4	215	2	T51640	myb-related transc
293	33	62.3	544	2	T14748	hypothetical prote	366	32	60.4	216	2	C64994	InaA protein - Esc
294	33	62.3	544	2	F82557	hypothetical prote	367	32	60.4	216	2	B85863	hypothetical prote
295	33	62.3	548	2	F96663	hypothetical prote	368	32	60.4	216	2	H91018	InaA protein [impo
296	33	62.3	565	2	E91268	thiol disulfide in	369	32	60.4	218	2	D82372	conserved hypoteth
297	33	62.3	565	2	C86109	thiol disulfide in	370	32	60.4	222	2	A75129	hypothetical prote
298	33	62.3	565	2	S56364	inner membrane cop	371	32	60.4	225	2	D71002	hypothetical prote
299	33	62.3	575	1	JC5432	glycoprotein 6-alp	372	32	60.4	225	2	G72291	hypothetical prote
300	33	62.3	579	2	B86926	acyl-CoA synthetas	373	32	60.4	226	2	AG1496	conserved hypoteth
301	33	62.3	579	2	D87063	probable acyl-CoA	374	32	60.4	226	2	AH1138	conserved hypoteth
302	33	62.3	580	2	B70668	probable acyl-CoA	375	32	60.4	235	2	S70219	sipa protein - Sal
303	33	62.3	582	2	B87204	probable acyl-CoA	376	32	60.4	239	2	H96028	conserved hypoteth
304	33	62.3	592	2	JC7709	testis-specific ki	377	32	60.4	243	2	T25190	hypothetical prote
305	33	62.3	599	2	S75363	hypothetical prote	378	32	60.4	250	2	T37101	probable sigma fac
306	33	62.3	605	2	T15291	sphingomyelin phos	379	32	60.4	255	2	I54307	MHC HLA-A30JS heav
307	33	62.3	605	2	S06398	alpha-globulin typ	380	32	60.4	259	2	D96673	hypothetical prote
308	33	62.3	615	2	D83838	asparagine synthet	381	32	60.4	261	2	G47116	trifoliotoxin resis
309	33	62.3	619	2	C70669	probable acyl-CoA	382	32	60.4	261	2	F96722	hypothetical prote
310	33	62.3	626	2	B70749	probable acyl-CoA	383	32	60.4	263	2	T48607	probable transcrip
311	33	62.3	628	1	A40802	protein-tyrosine k	384	32	60.4	265	2	T07395	myb-related transc
312	33	62.3	657	1	TVEFWA	transforming prote	385	32	60.4	265	2	H96777	hypothetical prote
313	33	62.3	660	2	F98020	hypothetical prote	386	32	60.4	270	1	HLHU28	MHC class I histoc
314	33	62.3	668	2	T05803	hypothetical prote	387	32	60.4	273	1	HLHUAM	MHC class I histoc
315	33	62.3	719	2	S76766	hypothetical prote	388	32	60.4	273	1	HLHU69	MHC class I histoc
316	33	62.3	813	2	G81698	leucyl-tRNA synthe	389	32	60.4	273	1	I38509	MHC class I histoc
317	33	62.3	895	1	FAFPAA	alpha-actinin - fr	390	32	60.4	274	1	HLHU32	MHC class I histoc
318	33	62.3	895	2	T13414	probable alpha-act	391	32	60.4	274	1	I68774	MHC HLA-B39 chain
319	33	62.3	924	2	T13413	probable alpha-act	392	32	60.4	274	2	I54463	MHC HLA-B38 chain
320	33	62.3	984	2	T00326	hypothetical prote	393	32	60.4	274	2	AG1306	D-alanyl-D-alanine
321	33	62.3	1032	1	G7BP74	baseplate protein	394	32	60.4	274	2	S24439	class I histocompa



541	32	60.4	363	2	JH0542	class I histocompa	614	32	60.4	477	2	D85984	RNA polymerase sig
542	32	60.4	363	2	S07113	class I histocompa	615	32	60.4	477	2	A98139	RNA polymerase sig
543	32	60.4	363	2	S03537	class I histocompa	616	32	60.4	477	2	A41026	regulatory protein
544	32	60.4	364	2	A35997	MHC class I histoc	617	32	60.4	477	2	B75170	hypothetical prote
545	32	60.4	364	2	S03535	class I histocompa	618	32	60.4	482	2	G96616	hypothetical prote
546	32	60.4	364	2	I46604	MHC PD14 transplan	619	32	60.4	487	2	R82065	RNA polymerase sig
547	32	60.4	364	2	D35997	MHC class I histoc	620	32	60.4	493	2	A96197	hypothetical prote
548	32	60.4	365	1	HLHUA2	MHC class I histoc	621	32	60.4	493	2	A13089	conserved hypothet
549	32	60.4	365	2	S16769	MHC class I histoc	622	32	60.4	502	2	S00720	transcription init
550	32	60.4	365	2	I38443	gene HLA-A-0203 pr	623	32	60.4	506	2	S23866	probable DNA topoi
551	32	60.4	365	2	A45847	MHC class I histoc	624	32	60.4	507	2	G01614	zinc finger protei
552	32	60.4	365	2	I61902	MHC class I histoc	625	32	60.4	513	1	S43941	protein kinase DUN
553	32	60.4	365	2	I38441	gene HLA-A-6802 pr	626	32	60.4	520	2	T08399	hypothetical prote
554	32	60.4	365	2	I37542	MHC class I histoc	627	32	60.4	524	2	A31318	glucose transpor
555	32	60.4	365	2	I37470	HLA-A*0210 - human	628	32	60.4	524	2	C69297	acetyl-CoA decarbo
556	32	60.4	365	2	I84487	MHC HLA-A cell sur	629	32	60.4	526	2	AF3570	nuclein-binding per
557	32	60.4	365	2	I84448	MHC class I histoc	630	32	60.4	527	2	T04329	importin alpha - t
558	32	60.4	365	2	I56053	class I histocompa	631	32	60.4	532	2	T52102	probable nuclear t
559	32	60.4	365	2	JH0534	class I histocompa	632	32	60.4	532	2	T52268	importin alpha lva
560	32	60.4	365	2	S01171	class I histocompa	633	32	60.4	535	2	T52098	probable nuclear t
561	32	60.4	365	2	I36961	MHC class I protei	634	32	60.4	536	2	G64752	xylian 1,4-beta-xy
562	32	60.4	365	2	I84432	MHC class I histoc	635	32	60.4	540	2	B87350	hypothetical prote
563	32	60.4	365	2	JL0135	MHC class I histoc	636	32	60.4	540	2	G71348	probable apolipop
564	32	60.4	365	2	I72170	MHC class I histoc	637	32	60.4	553	2	S75892	probable glycerol-
565	32	60.4	365	2	I37476	MHC class I histoc	638	32	60.4	561	2	A55235	riophy protein 2
566	32	60.4	365	2	A47636	MHC class I histoc	639	32	60.4	566	2	C44461	l-type voltage-dep
567	32	60.4	365	2	I83063	HLA-A*0210 - human	640	32	60.4	597	2	I52859	calcium channel pr
568	32	60.4	365	2	I56039	HLA-A*030.3 precurso	641	32	60.4	597	2	S18304	glutathione-regula
569	32	60.4	365	2	I61856	MHC class I histoc	642	32	60.4	601	2	AH1003	translation elonga
570	32	60.4	365	2	I37478	MHC class I histoc	643	32	60.4	611	2	S38162	glutathionylapemi
571	32	60.4	365	2	I37477	MHC class I histoc	644	32	60.4	619	2	A91113	glutathionylapemi
572	32	60.4	365	2	S77963	MHC class I histoc	645	32	60.4	619	2	A85958	glutathionylapemi
573	32	60.4	365	2	I38436	MHC class I histoc	646	32	60.4	619	2	A57538	glutathionylapemi
574	32	60.4	365	2	I37483	HLA-Aw34.2 antigen	647	32	60.4	631	2	T00925	hypothetical prote
575	32	60.4	365	2	I38610	MHC class I histoc	648	32	60.4	632	2	T46020	hypothetical prote
576	32	60.4	365	2	I38519	MHC class I histoc	649	32	60.4	633	2	D72284	oligopeptide ABC t
577	32	60.4	365	2	I34416	HLA-Aw24 protein -	650	32	60.4	666	2	D87243	conserved integral
578	32	60.4	365	2	I72171	HLA-Aw33.1, HLA-Aw	651	32	60.4	680	4	I38491	nucleophosmin/anap
579	32	60.4	365	2	I38518	HLA-A*0102 allele	652	32	60.4	685	2	AF0850	hypothetical prote
580	32	60.4	365	2	I37482	MHC class I histoc	653	32	60.4	690	2	A42161	CGMP-gated cation
581	32	60.4	365	2	I61857	MHC HLA-A2-4a chai	654	32	60.4	721	2	T40945	hypothetical prote
582	32	60.4	365	2	I38442	gene HLA-A-0205 pr	655	32	60.4	727	2	A71069	hypothetical prote
583	32	60.4	365	2	I57814	MHC class I-alpha	656	32	60.4	733	1	VH1WEB	hypothetical prote
584	32	60.4	365	2	I54493	MHC class I histoc	657	32	60.4	793	2	JC5831	nucleocapsid prote
585	32	60.4	365	2	I46603	MHC PD14a transpla	658	32	60.4	807	1	WMAD15	kinesin-related pr
586	32	60.4	368	1	HLMSKD	MHC class I histoc	659	32	60.4	810	2	A97852	late 100K protein
587	32	60.4	370	1	HLHUA3	MHC class I histoc	660	32	60.4	811	2	T43175	virB4 protein prec
588	32	60.4	374	2	H71091	hypothetical prote	661	32	60.4	879	2	C90879	armadillo protein
589	32	60.4	374	2	T02021	hypothetical prote	662	32	60.4	879	2	H64888	membrane protein y
590	32	60.4	376	2	S32820	alloantigen F - ra	663	32	60.4	879	2	G85739	hypothetical prote
591	32	60.4	379	2	S46711	hypothetical prote	664	32	60.4	880	2	C72521	hypothetical prote
592	32	60.4	380	2	B70076	aminoacylase homol	665	32	60.4	885	2	A25817	nonstructural prot
593	32	60.4	398	2	AC3322	membrane-bound lyt	666	32	60.4	1048	2	T31653	hypothetical prote
594	32	60.4	401	2	G84160	glucose-1-phosphat	667	32	60.4	1084	2	T15616	hypothetical prote
595	32	60.4	410	1	DEPSXA	3-methyl-2-oxobuta	668	32	60.4	1108	2	A48508	cyclic-nucleotide
596	32	60.4	418	2	D75283	hypothetical prote	669	32	60.4	1113	2	T47381	hypothetical prote
597	32	60.4	427	2	A84667	probable MYB fami	670	32	60.4	1148	2	S51855	hypothetical prote
598	32	60.4	428	2	B81531	conserved hypothet	671	32	60.4	1150	2	T41260	hypothetical prote
599	32	60.4	429	2	AH0630	4-hydroxyphenylace	672	32	60.4	1175	2	D85089	hypothetical prote
600	32	60.4	432	2	D72008	CR850 hypothetical	673	32	60.4	1191	2	S76414	beta transducin-li
601	32	60.4	432	2	E86616	CR850 hypothetical	674	32	60.4	1198	2	E86402	hypothetical prote
602	32	60.4	432	2	C87581	integrase/recombin	675	32	60.4	1201	2	F86386	hypothetical prote
603	32	60.4	437	2	F69396	acyl-CoA dehydroge	676	32	60.4	1260	2	A72603	probable nitrate r
604	32	60.4	453	2	A97431	alpha-glucosidase-b	677	32	60.4	1285	2	H85041	hypothetical prote
605	32	60.4	453	2	A82649	hypothetical prote	678	32	60.4	1305	2	H96559	hypothetical prote
606	32	60.4	455	2	C84133	glutamine syntheta	679	32	60.4	1314	2	T47331	hypothetical prote
607	32	60.4	461	2	T39889	protein kinase - f	680	32	60.4	1472	2	A84470	hypothetical prote
608	32	60.4	462	2	A57120	small nuclear ribo	681	32	60.4	1485	1	ISZPT2	DNA copolysomase
609	32	60.4	470	2	T31465	cell cycle protein	682	32	60.4	1589	2	T13826	translation initia
610	32	60.4	473	2	H71044	hypothetical prote	683	32	60.4	1756	2	T02599	hypothetical prote
611	32	60.4	476	2	S64231	hypothetical prote	684	32	60.4	2024	2	A54103	centrosome autoph
612	32	60.4	477	2	AG0905	RNA polymerase sig	685	32	60.4	2124	2	T28658	polyketide synthas
613	32	60.4	477	2	A35695	transcription init	686	32	60.4	2311	1	TVCHSR	kinase-related pro

687	32	60.4	2706	2	T28155	variant-specific s	760	31	58.5	338	2	S75196	hypothetical prote
688	32	60.4	3573	2	S23070	erythronolide synt	761	31	58.5	338	2	A53290	oligopeptide trans
689	31.5	59.4	892	1	S42228	replication licens	762	31	58.5	338	2	A86855	oligopeptide ABC t
690	31	58.5	28	2	F46522	t-cell receptor et	763	31	58.5	339	2	H75283	phenylalanine-tRNA
691	31	58.5	61	2	T03587	isocitrate dehydro	764	31	58.5	339	2	I56071	MHC class I histoc
692	31	58.5	63	2	A83899	hypothetical prote	765	31	58.5	339	2	T29405	hypothetical prote
693	31	58.5	74	2	F96670	hypothetical prote	766	31	58.5	339	2	AG0165	L-allo-threonine a
694	31	58.5	86	2	A2441	hypothetical prote	767	31	58.5	340	2	S11143	class I histocoma
695	31	58.5	115	2	E84512	probable MYB famil	768	31	58.5	341	2	AI1039	phage integrase [i
696	31	58.5	126	2	A82302	conserved hypochet	769	31	58.5	342	1	HLHUC4	MHC class I histoc
697	31	58.5	130	2	H71415	hypothetical prote	770	31	58.5	345	2	S07114	MHC class I histoc
698	31	58.5	136	1	C69411	conserved hypochet	771	31	58.5	348	2	I68749	MHC class I lympho
699	31	58.5	161	2	AB2054	hypothetical prote	772	31	58.5	348	2	S29990	histocompatibility
700	31	58.5	166	2	I69005	hypothetical prote	773	31	58.5	352	2	T20729	hypothetical prote
701	31	58.5	166	2	I69005	histocompatibility	774	31	58.5	354	1	VGB567	glycoprotein D pre
702	31	58.5	173	2	T04975	carbonate dehydrat	775	31	58.5	354	2	I54551	histocompatibility
703	31	58.5	181	2	I79640	MHC cell surface a	776	31	58.5	354	2	I48848	TL antigen - mouse
704	31	58.5	182	2	A49411	human leukocyte an	777	31	58.5	354	2	I48848	probable membrane-
705	31	58.5	182	2	A89026	protein F13A2.5 [i	778	31	58.5	356	2	D95925	class I histocoma
706	31	58.5	187	2	H72392	hypothetical prote	779	31	58.5	357	2	S11139	probable ABC trans
707	31	58.5	194	2	H23357	proteinase - bovin	780	31	58.5	359	2	F95406	protein-tyrosine k
708	31	58.5	201	2	T33593	hypothetical prote	781	31	58.5	359	2	A48073	MHC class I histoc
709	31	58.5	206	2	I37529	HLA-Cw7 - human (f	782	31	58.5	361	2	B25132	MHC class I histoc
710	31	58.5	206	2	I37528	HLA-Cw1 - human (f	783	31	58.5	361	2	I48851	TL antigen - mouse
711	31	58.5	213	2	B27898	beta-crystallin B3	784	31	58.5	362	2	I56130	HLA-B*5401 - human
712	31	58.5	219	2	A70314	deoxyribose-phosph	785	31	58.5	362	2	A60384	MHC class I histoc
713	31	58.5	221	2	A82202	hypothetical prote	786	31	58.5	362	2	A45845	MHC class I histoc
714	31	58.5	222	1	BFBO	folate-binding pro	787	31	58.5	362	2	JOH291	class I histocoma
715	31	58.5	225	2	H90735	dethiobiotin synth	788	31	58.5	362	2	JOH292	class I histocoma
716	31	58.5	225	2	A85586	dethiobiotin synth	789	31	58.5	365	2	I72218	class I histocoma
717	31	58.5	226	2	A70436	hypothetical prote	790	31	58.5	365	2	JOH544	class I histocoma
718	31	58.5	229	2	C97047	conserved hypochet	791	31	58.5	366	2	JOH545	class I histocoma
719	31	58.5	237	2	T28070	hypothetical prote	792	31	58.5	366	2	JOH546	class I histocoma
720	31	58.5	248	2	C72632	hypothetical prote	793	31	58.5	366	2	JOH547	MHC class I histoc
721	31	58.5	251	2	F70412	dihydroorotate deh	794	31	58.5	366	2	I37526	HLA-C alpha chain
722	31	58.5	251	2	S20455	pqqC protein - Kle	795	31	58.5	366	2	I37078	lymphocyte antigen
723	31	58.5	254	2	A10600	tRNA hydroxylase [	796	31	58.5	366	2	I81232	MHC class I histoc
724	31	58.5	256	2	H93585	conserved hypochet	797	31	58.5	366	2	I37544	lymphocyte antigen
725	31	58.5	257	2	T12092	G-box-binding prot	798	31	58.5	366	2	I81231	lymphocyte antigen
726	31	58.5	258	2	T00278	conserved hypochet	799	31	58.5	366	2	I54430	MHC class I histoc
727	31	58.5	259	2	B71823	udp-n-acetylenolpy	800	31	58.5	366	2	JOH526	MHC class I histoc
728	31	58.5	261	2	T29076	hypothetical prote	801	31	58.5	366	2	I61866	MHC class I histoc
729	31	58.5	270	2	S24361	miaE protein - Sal	802	31	58.5	366	2	I37523	MHC class I histoc
730	31	58.5	274	2	S03807	cytochrome-c oxida	803	31	58.5	366	2	I72113	MHC histocompatibi
731	31	58.5	274	2	D86300	hypothetical prote	804	31	58.5	366	2	S42823	MHC class I histoc
732	31	58.5	280	2	C72569	phenylethanolamine	805	31	58.5	366	2	I59822	lymphocyte antigen
733	31	58.5	282	1	A28171	hypothetical prote	806	31	58.5	366	2	I38507	MHC class I histoc
734	31	58.5	283	2	H82979	hypothetical prote	807	31	58.5	366	2	I37527	MHC class I histoc
735	31	58.5	287	2	H83618	malonate decarboxy	808	31	58.5	366	2	I37135	MHC class I histoc
736	31	58.5	297	2	B44781	troponin T, cardia	809	31	58.5	366	2	I56034	gene HLA-C protein
737	31	58.5	297	2	H84186	hypothetical prote	810	31	58.5	366	2	A60369	MHC class I histoc
738	31	58.5	298	2	S44994	class I histocoma	811	31	58.5	366	2	I38505	MHC class I histoc
739	31	58.5	299	2	S30443	troponin T - rat	812	31	58.5	366	2	B37028	MHC class I histoc
740	31	58.5	302	1	TPCHC	troponin T, cardia	813	31	58.5	367	2	AF3224	monooxygenase Acu5
741	31	58.5	302	2	AH0550	hypothetical ROK-f	814	31	58.5	371	1	WNBEY0	dUTP diphosphatase
742	31	58.5	303	2	A86443	probable major int	815	31	58.5	372	2	A25148	thymus leukemia an
743	31	58.5	308	2	G83104	probable ferredoxi	816	31	58.5	373	2	A55718	interleukin-2 rece
744	31	58.5	308	2	D69429	hypothetical prote	817	31	58.5	375	2	H84666	Probable MYB famil
745	31	58.5	312	2	T49764	hypothetical prote	818	31	58.5	376	2	G70301	N-acetylmurichine
746	31	58.5	313	2	I36958	MHC ChIA chain - c	819	31	58.5	377	2	B64703	conserved hypochet
747	31	58.5	313	2	I46049	MHC class I antige	820	31	58.5	384	2	A25132	MHC class I histoc
748	31	58.5	314	2	H82115	probable adenine-s	821	31	58.5	384	2	I54499	MHC thymus leukemi
749	31	58.5	315	2	F98295	hypothetical prote	822	31	58.5	385	2	T02640	hypothetical prote
750	31	58.5	316	2	S58719	probable membrane	823	31	58.5	387	2	A33497	prophage G-Box bin
751	31	58.5	316	2	C37028	MHC class I histoc	824	31	58.5	387	2	H86445	hypothetical prote
752	31	58.5	321	1	S45338	myb-related protei	825	31	58.5	387	2	AE2253	trRNA CCA-adding en
753	31	58.5	321	2	B69130	replication factor	826	31	58.5	393	2	AI1312	trRNA CCA-adding en
754	31	58.5	325	2	I54449	MHC class I HLA-Cx	827	31	58.5	393	2	AI1684	hypothetical prote
755	31	58.5	328	2	H75445	conserved hypochet	828	31	58.5	398	2	S40752	hypothetical prote
756	31	58.5	333	2	AF1924	succinate dehydrog	829	31	58.5	399	2	E86348	hypothetical prote
757	31	58.5	335	2	A40038	MHC class I histoc	830	31	58.5	400	2	AE9924	hypothetical prote
758	31	58.5	338	2	D70382	phenylalanine-tRNA	831	31	58.5	401	2	F90446	n-carbamoyl-L-amin
759	31	58.5	338	2	A39953	MHC class I histoc	832	31	58.5	401	2	E84757	hypothetical prote

833	31	58.5	408	2	F86729	30S ribosomal prot
834	31	58.5	408	2	C70796	hypothetical prote
835	31	58.5	418	2	B83734	hypothetical prote
836	31	58.5	421	2	G95308	probable ABC sugar
837	31	58.5	422	2	A31154	D-tagatose-bisphos
838	31	58.5	433	2	A70465	probable GTP bindi
839	31	58.5	437	2	T16477	hypothetical prote
840	31	58.5	441	2	S83346	malate dehydrogena
841	31	58.5	445	2	T30604	hypothetical prote
842	31	58.5	455	1	JQ0507	adenosylmethionine
843	31	58.5	456	2	B83750	gluconate permease
844	31	58.5	461	2	T05773	protein kinase hom
845	31	58.5	463	2	T09243	dnak-type molecula
846	31	58.5	466	2	A95355	probable inner-mem
847	31	58.5	476	2	G70175	aminoacyl-histidin
848	31	58.5	491	2	A59199	hybrid cluster (4F
849	31	58.5	507	2	T08337	hypothetical prote
850	31	58.5	555	2	T01391	WD-repeat protein
851	31	58.5	559	2	G86238	protein T1024.13
852	31	58.5	560	2	I59302	brain specific Na+
853	31	58.5	561	2	H69755	oligo-1,6-glucosid
854	31	58.5	588	1	FWCNA8	alpha-globulin B p
855	31	58.5	593	2	A80046	probable N-acetylm
856	31	58.5	607	2	T03023	calcium-dependent
857	31	58.5	608	2	C89760	two-component sens
858	31	58.5	613	2	I39295	X-linked PEST-cont
859	31	58.5	615	2	AF1848	threonyl-tRNA synt
860	31	58.5	618	2	AC0884	glutathionylpermi
861	31	58.5	621	2	T48646	phytoene dehydroge
862	31	58.5	625	2	B41172	dna protein - Haem
863	31	58.5	625	2	T02033	calcium/calmodulin
864	31	58.5	626	2	H82266	1-deoxyxylulose-5-
865	31	58.5	673	2	T00328	hypothetical prote
866	31	58.5	754	1	BABOH	peptide-aspartate
867	31	58.5	757	2	E97230	trehalose/maltose
868	31	58.5	777	2	G69310	penicillin G acyla
869	31	58.5	788	2	I51530	integrin beta-3 su
870	31	58.5	879	2	PC1225	protein-tyrosine k
871	31	58.5	883	2	S49126	brevican precursor
872	31	58.5	899	2	A35895	androgen receptor
873	31	58.5	902	2	B40494	androgen receptor
874	31	58.5	904	1	T10067	replication licens
875	31	58.5	958	2	T02741	probable ligand-ga
876	31	58.5	961	2	AD0548	puative autotransp
877	31	58.5	980	2	S71090	peroxisome biogene
878	31	58.5	981	2	T05505	hypothetical prote
879	31	58.5	1014	2	C83990	beta-galactosidase
880	31	58.5	1028	2	A45388	protein-tyrosine k
881	31	58.5	1034	2	A49425	beta-galactosidase
882	31	58.5	1037	2	A56594	Na+/K+-exchanging
883	31	58.5	1038	1	S03632	Na+/K+-exchanging
884	31	58.5	1038	2	JT0663	ras GTPase-activat
885	31	58.5	1042	2	G64514	type I restriction
886	31	58.5	1044	2	S01966	GTPase-activating
887	31	58.5	1047	2	A40121	GTPase-activating
888	31	58.5	1052	2	JC4200	protein-tyrosine k
889	31	58.5	1052	2	I53012	focal adhesin kin
890	31	58.5	1052	2	A46166	protein-tyrosine k
891	31	58.5	1068	2	I51670	focal adhesin kin
892	31	58.5	1076	2	B96682	protein F1E22.14 [
893	31	58.5	1081	2	JC5944	protein-tyrosine k
894	31	58.5	1085	2	JC7736	C3G protein, long
895	31	58.5	1086	2	S76044	hypothetical prote
896	31	58.5	1148	2	D82091	exodeoxyribonuclea
897	31	58.5	1154	2	T48829	related to GREBP c
898	31	58.5	1181	2	A43346	1-phosphatidylinos
899	31	58.5	1197	2	I39613	pyruvate (flavodox
900	31	58.5	1199	2	AD2156	pyruvate-flavodoxi
901	31	58.5	1208	2	T27822	hypothetical prote
902	31	58.5	1280	2	T51500	hypothetical prote
903	31	58.5	1291	2	T13389	hypothetical prote
904	31	58.5	1307	2	T35944	probable beta-gala
905	31	58.5	1502	2	S53602	carbamoyl-phosphat

GNWVS5	1	1525	58.5	31	906	genome polyprotein
B90924	2	1538	58.5	31	907	probable ATP-depen
F85772	2	1538	58.5	31	908	ATP-dependent heli
G64922	2	1538	58.5	31	909	probable ATP-depen
T30200	2	1621	58.5	31	910	protein-tyrosine k
T21432	2	1711	58.5	31	911	hypothetical prote
T21861	2	1877	58.5	31	912	hypothetical prote
T18399	2	2042	58.5	31	913	variant-specific s
T00093	2	2055	58.5	31	914	hypothetical prote
S38480	2	2115	58.5	31	915	nonstructural prot
MNWRN	1	2205	58.5	31	916	nonstructural poly
JB0271	2	2388	58.5	31	917	beta spectrin, bet
S47008	2	2515	58.5	31	918	tenascin-like prot
A86216	2	2658	58.5	31	919	protein T23G18.2 [
T08841	2	3005	58.5	31	920	polypeptide - dour
T18501	2	3394	58.5	31	921	hypothetical prote
T34513	2	3507	58.5	31	922	hypothetical prote
B96695	2	5138	58.5	31	923	hypothetical prote
B96514	2	5138	58.5	31	924	hypothetical prote
D75391	2	526	57.5	30.5	925	AlGP-related prote
URRTAP	1	976	57.5	30.5	926	peptidylglycine mo
G96904	2	1544	57.5	30.5	927	DNA segregation AT
AH3366	2	73	56.6	30	928	nitroreductase fam
JQ1429	2	75	56.6	30	929	hypothetical 8.1K
T38245	2	110	56.6	30	930	hypothetical prote
E25387	2	115	56.6	30	931	hypothetical prote
H72386	2	116	56.6	30	932	mazG-related prote
C81005	2	118	56.6	30	933	hypothetical prote
B82026	2	118	56.6	30	934	hypothetical prote
A81007	2	118	56.6	30	935	hypothetical prote
T49358	2	122	56.6	30	936	related to glycine
B83532	2	130	56.6	30	937	hypothetical prote
D69843	1	131	56.6	30	938	conserved hypothet
F70373	2	138	56.6	30	939	hypothetical prote
G84036	2	138	56.6	30	940	hypothetical prote
AH2458	2	144	56.6	30	941	hypothetical prote
S76050	2	147	56.6	30	942	hypothetical prote
G90736	2	150	56.6	30	943	hypothetical prote
H85586	2	150	56.6	30	944	molybdopterin bios
S31883	2	150	56.6	30	945	molybdopterin bios
AG1153	2	150	56.6	30	946	PTS system, fructo
B71119	2	152	56.6	30	947	probable aspartate
S75561	2	153	56.6	30	948	hypothetical prote
T15379	2	155	56.6	30	949	hypothetical prote
D75069	2	158	56.6	30	950	hypothetical prote
T18780	2	160	56.6	30	951	hypothetical prote
D95299	2	163	56.6	30	952	conserved hypothet
A83262	2	164	56.6	30	953	hypothetical prote
T29244	2	165	56.6	30	954	hypothetical prote
T52480	2	168	56.6	30	955	cytochrome-c oxida
C90386	2	175	56.6	30	956	conserved hypothet
S54778	2	177	56.6	30	957	NR-13 protein - qu
S03635	2	189	56.6	30	958	calcyphosine - dog
C86564	2	199	56.6	30	959	Ct471 hypothetical
F72060	2	199	56.6	30	960	conserved hypothet
AC0676	2	202	56.6	30	961	hydrogenase 1 matu
S20586	2	203	56.6	30	962	DNA-directed RNA p
G96959	2	204	56.6	30	963	hypothetical prote
J80399	2	209	56.6	30	964	ribosomal protein
D87635	2	210	56.6	30	965	transcription regu
D84565	2	213	56.6	30	966	probable protein k
D97119	2	216	56.6	30	967	amidase from nicot
C81099	2	221	56.6	30	968	hypothetical prote
C81842	2	221	56.6	30	969	hypothetical prote
H71136	2	221	56.6	30	970	hypothetical prote
G75078	2	222	56.6	30	971	hypothetical prote
I59479	2	223	56.6	30	972	serum amyloid P -
AE1650	2	226	56.6	30	973	hypothetical prote
AF1589	2	226	56.6	30	974	hypothetical prote
H83078	2	229	56.6	30	975	hypothetical prote
A45814	2	231	56.6	30	976	female protein pre
T08291	2	231	56.6	30	977	hypothetical prote
B82987	2	232	56.6	30	978	probable hydrolase

979	30	56.6	235	2	H85564	hypothetical prote
980	30	56.6	235	2	C90714	hypothetical prote
981	30	56.6	235	2	C64799	hypothetical prote
982	30	56.6	235	2	D71808	hypothetical prote
983	30	56.6	237	1	D69136	anaerobic ribonuc
984	30	56.6	237	1	JC5660	hepatoma-derived g
985	30	56.6	238	2	A71220	hypothetical prote
986	30	56.6	241	2	A53014	chloride conductan
987	30	56.6	245	2	AG2203	glucose inhibited
988	30	56.6	247	2	H70432	ABC transporter -
989	30	56.6	247	2	T16061	hypothetical prote
990	30	56.6	248	2	C90461	hypothetical prote
991	30	56.6	251	2	B40969	folate-binding pro
992	30	56.6	255	2	A33417	folate-binding pro
993	30	56.6	255	2	A40969	folate-binding pro
994	30	56.6	256	1	RTMST	thyroliiberin precu
995	30	56.6	256	2	S74354	hypothetical prote
996	30	56.6	256	2	T05854	hypothetical prote
997	30	56.6	256	2	H69747	protein kinase hom
998	30	56.6	257	2	A45753	folate-binding pro
999	30	56.6	258	2	T13591	tail fiber adhesin
1000	30	56.6	268	2	T18971	hypothetical prote
RESULT 1						
A60506 big gastrin - North American opossum						
N/Contains: gastrin						
C/Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)						
C/Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004						
C/Accession: A60506						
R/Shinomura, Y.; Eng, J.; Rattan, S.C.; Yalow, R.S.						
Comp. Biochem. Physiol. B 96, 239-242, 1990						
A/Title: Opossum (Didelphis virginiana) "little" and "big" gastrins.						
A/Reference number: A60506; MUID:90298616; PMID:2361360						
A/Accession: A60506						
A/Molecule type: protein						
A/Residues: 1-33 <SH>						
A/Cross-references: UNIPROT:P33713; UNIPARC:UPI000012B0F1						
C/Superfamily: gastrin						
C/Keywords: amidated carboxyl end; hormone; pyroglutamic acid; sulfoprotein						
F;1-33/Product: big gastrin #status experimental <WATB>						
F;18-33/Product: gastrin #status experimental <WATL>						
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental						
F;28/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental						
F;33/Modified site: amidated carboxyl end (Phe) #status experimental						
Query Match 94.3%; Score 50; DB 2; Length 33;						
Best Local Similarity 88.9%; Pred. No. 0.034;						
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;						
Qy	1	EGPWLEEEE	9			
		:				
Db	18	QGPWLEEE	26			
RESULT 2						
GMHUB gastrin precursor [validated] - human						
N/Contains: big gastrin; cryptagastrin; gastrin; gastrin-17						
C/Species: Homo sapiens (man)						
C/Date: 24-Apr-1984 #sequence revision 30-Jun-1987 #text_change 09-Jul-2004						
C/Accession: A93997; A93497; A94473; A93152; A91628; A18854; A40869; A32487; B32487; C32						
R/Ito, R.; Sato, K.; Helmer, T.; Jay, G.; Agarwal, K.						
Proc. Natl. Acad. Sci. U.S.A. 81, 4662-4666, 1984						
A/Title: Structural analysis of the gene encoding human gastrin: the large intron contain						
A/Reference number: A93997; MUID:84272693; PMID:6087340						
A/Accession: A93997						
A/Molecule type: DNA						
A/Residues: 1-101 <I>O>						

A/Cross-references: UNIPROT:P01350; UNIPARC:UPI000012B0F4; GB:K01254; GB:J00147; NID:g18  
R/Kato, K.; Hayaishi, Y.; Takahashi, Y.; Himeno, S.; Matsubara, K.  
Nucleic Acids Res. 11, 8197-8203, 1983  
A/Title: Molecular cloning of the human gastrin gene.  
A/Reference number: A93497; MUID:84169471; PMID:6324077  
A/Accession: A93497  
A/Molecule type: DNA  
A/Residues: 1-101 <KAT>  
A/Cross-references: UNIPARC:UPI000012B0F4; GB:X00183; NID:g31648; PIDN:CAA25005.1; PID:g  
R/Harris, J.I.; Kenner, E.W.  
unpublished results, cited by Gregory, R.A., and Tracy, H.J., in Gastrointestinal Hormon  
A/Reference number: A94473  
A/Accession: A94473  
A/Molecule type: protein  
A/Residues: 59-64, 'H' 66, 'S' 68-92 <HAR>  
A/Cross-references: UNIPARC:UPI0000173595  
A/Experimental source: gastrinoma tissue  
R/Bentley, P.H.; Kenner, G.W.; Sheppard, R.C.  
Nature 209, 583-585, 1966  
A/Title: Human gastrin isolation, structure and synthesis.  
A/Reference number: A93152; MUID:67021327; PMID:5921183  
A/Accession: A93152  
A/Molecule type: protein  
A/Residues: 76-92 <BEN>  
A/Cross-references: UNIPARC:UPI000014A9F1  
A/Note: gastrin comprises the carboxyl-terminal 17 residues of big gastrin  
R/Gregory, R.A.; Tracy, H.J.; Agarwal, K.L.; Groseman, M.I.  
Gut 10, 603-608, 1969  
A/Title: Aminoacid constitution of two gastrins isolated from Zollinger-Ellison tumour t  
A/Reference number: A91628; MUID:69298172; PMID:5822140  
A/Accession: A91628  
A/Molecule type: protein  
A/Residues: 76-92 <GRE>  
A/Cross-references: UNIPARC:UPI000014A9F1  
A/Note: the gastrin was isolated from human Zollinger-Ellison pancreatic tumor  
R/Wiborg, O.; Berglund, L.; Boel, E.; Norris, F.; Norris, K.; Rehfeld, J.F.; Marcker, K.  
Proc. Natl. Acad. Sci. U.S.A. 81, 1067-1069, 1984  
A/Title: Structure of a human gastrin gene.  
A/Reference number: A18854; MUID:84144842; PMID:6322186  
A/Accession: A18854  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-101 <WIB>  
A/Cross-references: UNIPARC:UPI000012B0F4; GB:K01254; GB:J00147; NID:g182987; PIDN:AA859  
R/Huebner, V.D.; Jiang, R.; Lee, T.D.; Legesse, K.; Walshe, J.H.; Shively, J.E.; Chew, P.  
J. Biol. Chem. 266, 12223-12227, 1991  
A/Title: Purification and structural characterization of progastrin-derived peptides fro  
A/Reference number: A40869; MUID:91286236; PMID:2061307  
A/Accession: A40869  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 22-51 <HUE>  
A/Cross-references: UNIPARC:UPI0000173596  
R/Higashimoto, Y.; Himeno, S.; Shinomura, Y.; Nagao, K.; Tamura, T.; Tarui, S.  
Biochem. Biophys. Res. Commun. 160, 1364-1370, 1989  
A/Title: Purification and structural determination of urinary NH-2-terminal big gastrin  
A/Reference number: A32487; MUID:89273602; PMID:2730647  
A/Accession: A32487  
A/Molecule type: protein  
A/Residues: 59-67 <HI2>  
A/Cross-references: UNIPARC:UPI000014A9EF  
A/Experimental source: urine  
A/Note: this urinary fragment of big gastrin was designated peak Ia  
A/Accession: B32487  
A/Molecule type: protein  
A/Residues: 59-66 <HI3>  
A/Cross-references: UNIPARC:UPI0000173597  
A/Experimental source: urine  
A/Note: this urinary fragment of big gastrin was designated peak Ib  
A/Accession: C32487  
A/Molecule type: protein  
A/Residues: 59-68 <HI4>  
A/Cross-references: UNIPARC:UPI0000173598

A;Experimental source: urine  
A;Note: This urinary fragment of big gastrin was designated peak II  
F;Higashimoto, Y.; Shinomura, Y.; Nagao, K.; Yasunaga, Y.; Tamura, T.; Tarui, S.  
Biochem. Biophys. Res. Commun. 172, 1392-1399, 1990  
A;Title: Purification of N-terminal hexapeptide of big gastrin from human urine.  
A;Reference number: A36249; MUID:91059586; PMID:2244919  
A;Accession: A36249  
A;Molecule type: protein  
A;Residues: 59-64 <HG>  
A;Cross-references: UNIPARC:UPI0000173599  
A;Note: This urinary fragment of big gastrin was designated peak III  
R;Boel, E.; Vuust, J.; Norris, P.; Norris, K.; Wind, A.; Rehfeld, J.F.; Marcker, K.A.  
Proc. Natl. Acad. Sci. U.S.A. 80, 2866-2869, 1983  
A;Title: Molecular cloning of human gastrin cDNA: evidence for evolution of gastrin by g  
A;Reference number: I37408; MUID:83221503; PMID:6574456  
A;Accession: I37408  
A;Molecule type: mRNA  
A;Residues: 1-101 <RES>  
A;Cross-references: UNIPARC:UPI00001280F4; EMBL:V00511; NID:g31654; PIDN:CAA23769.1; PID  
R;Rehfeld, J.F.; Johnsen, A.H.  
Eur. J. Biochem. 223, 765-773, 1994  
A;Title: Identification of gastrin component I as gastrin-71. The largest possible bloac  
A;Reference number: S48183; MUID:94333379; PMID:8055952  
A;Accession: S48183  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 22-40 <REH>  
A;Cross-references: UNIPARC:UPI000017359A  
R;Kariya, Y.; Kato, K.; Hayashizaki, Y.; Himeno, S.; Tarui, S.; Matabara, K.  
Gene 50, 345-352, 1986  
A;Title: Expression of human gastrin gene in normal and gastrinoma tissues.  
A;Reference number: I54006; MUID:87219893; PMID:3034736  
A;Accession: I54006  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-101 <KAR>  
A;Cross-references: UNIPARC:UPI00001280F4; GB:M15958; NID:g182990; PIDN:AAA52520.1; PID:  
R;Rehfeld, J.F.; Hansen, C.B.; Johnsen, A.H.  
EMBO J. 14, 389-396, 1995  
A;Title: Post-poly(Glu) cleavage and degradation modified by O-sulfated tyrosine: a nove  
A;Reference number: S54350; MUID:95137019; PMID:7530658  
A;Accession: S54350  
A;Molecule type: protein  
A;Residues: 76-92 <REW>  
A;Cross-references: UNIPARC:UPI000014A9F1  
A;Note: Gastrin-6 isolated from gastric mucosa and blood is fully active; sulfation of i  
A;Genetics:  
A;Gene: GDB:GAS  
A;Cross-references: GDB:119261; OMIM:137250  
A;Map position: 17q-17q  
A;Introns: 71/1  
C;Superfamily: gastrin  
C;Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-56/Product: cryptogastrin (amino-terminal propeptide) #status experimental <PRO>  
F;59-92/Product: big gastrin #status experimental <BGN>  
F;76-92/Product: gastrin #status experimental <SGN>  
F;87-92/Product: gastrin-6 #status experimental <GN6>  
F;59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #link BGN #status  
F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #link SGN #status  
F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 94.3%; Score 50; DB 1; Length 101;  
Best Local Similarity 88.9%; Pred. No. 0.12;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 EGPWLEEEE 9  
Db 76 QGPWLEEEE 84

RESULT 3

CMCT  
Gastrin precursor [validated] - cat  
N;Contains: big gastrin (Gastrin-34); gastrin  
C;Species: Felis silvestris catus (domestic cat)  
C;Date: 13-Jun-1983 #sequence revision 02-Jun-1994 #text\_change 09-Jul-2004  
C;Accession: S14401; A01621; A61074  
R;Kim, S.J.; Uhm, K.N.; Kang, Y.K.; Yoo, O.J.  
DNA Seq. 1, 181-187, 1991  
A;Title: Bovine and feline gastrin cDNA sequences and the amino acid and nucleotide sequ  
A;Reference number: S14400; MUID:92127058; PMID:1773057  
A;Accession: S14401  
A;Molecule type: mRNA  
A;Residues: 1-104 <KM>  
A;Cross-references: UNIPROT:P01354; UNIPARC:UPI00001280F2; EMBL:X16582; NID:g1099; PIDN:  
R;Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.  
J. Am. Chem. Soc. 91, 3096-3097, 1969  
A;Title: Feline gastrin. An example of peptide sequence analysis by mass spectrometry.  
A;Reference number: A01621; MUID:69206035; PMID:5784957  
A;Accession: A01621  
A;Molecule type: protein  
A;Residues: 76-92 <AGA>  
A;Cross-references: UNIPARC:UPI00001735A3  
R;Eng, J.; Du, B.H.; Johnson, G.F.; Kanakamedala, S.; Samuel, S.; Raufman, J.P.; Straus,  
Regul. Pept. 37, 9-13, 1992  
A;Title: Cat gastrinoma and the sequence of cat gastrins.  
A;Reference number: A61074; MUID:92262853; PMID:1585019  
A;Accession: A61074  
A;Molecule type: protein  
A;Residues: 59-92 <ENG>  
A;Cross-references: UNIPARC:UPI00001735A4  
C;Superfamily: gastrin  
C;Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;59-92/Product: big gastrin #status experimental <BMAT>  
F;76-92/Product: gastrin #status experimental <MAT>  
F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen  
F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 94.3%; Score 50; DB 1; Length 104;  
Best Local Similarity 88.9%; Pred. No. 0.13;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 EGPWLEEEE 9  
Db 76 QGPWLEEEE 84

RESULT 4

A60071  
Gastrin - rhesus macaque  
C;Species: Macaca mulatta (rhesus macaque)  
C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 09-Jul-2004  
C;Accession: A60071  
Regul. Pept. 32, 39-45, 1991  
A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences.  
A;Reference number: A60071; MUID:91164506; PMID:2003150  
A;Accession: A60071  
A;Molecule type: protein  
A;Residues: 1-17 <YUA>  
A;Cross-references: UNIPROT:P33714; UNIPARC:UPI00001280F5  
C;Superfamily: gastrin  
C;Keywords: amidated carboxyl end; hormone; intestine; pyroglutamic acid; sulfoprotein  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;12/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
F;17/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 90.6%; Score 48; DB 2; Length 17;  
Best Local Similarity 77.8%; Pred. No. 0.035;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 EGPWLEEEE 9

Db 1 QGPMWEEEE 9

RESULT 5

GMDG

gastrin precursor [validated] - dog

N/Contains: big gastrin; gastrin

C/Species: Canis lupus familiaris (dog)

C/Date: 13-Jun-1993 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004

C/Accession: B61053; J50425; A01620; B60070

R/Gantz, I.; Takeuchi, T.; Yamada, T.

Digestion 46, 99-104, 1990

A/Title: Cloning of canine gastrin cDNA's encoding variant amino acid sequences.

A/Reference number: A61053; MUID:91085716; PMID:2252079

A/Accession: B61053

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-104 <GAN>

A/Cross-references: UNIPROT:P01353; UNIPARC:UPI0000012B0ED

A/Accession: A61053

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-84, 'T', '86-104 <GA2>

A/Cross-references: UNIPARC:UPI0000017359E

A/Note: it is unclear whether the sequence difference results from polymorphism, multiple peptides 7, 689-693, 1986

R/Bonato, C.; Eng, J.; Holmes, J.D.; Miedel, M.; Pan, Y.C.E.; Yalow, R.S.

A/Title: Sequences of gastrins purified from a single antrum of dog and of goat.

A/Reference number: JS0425; MUID:87016557; PMID:3763441

A/Accession: JS0425

A/Molecule type: protein

A/Residues: 59-92 <BON>

A/Cross-references: UNIPARC:UPI0000017359F

A/Experimental source: antral mucosa

A/Note: about 10% of gastrin is sulfated

R/Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.

Experientia 25, 346-348, 1969

A/Title: Structure and synthesis of canine gastrin.

A/Reference number: A01620; MUID:69253357; PMID:5799207

A/Accession: A01620

A/Molecule type: protein

A/Residues: 76-82, 'A', '84, 'E', '86-92 <AGA>

A/Cross-references: UNIPARC:UPI000001735A0

R/Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.

Regul. Pept. 25, 223-233, 1989

A/Title: The constitution and properties of phosphorylated and unphosphorylated C-termin

A/Reference number: A60070; MUID:89331947; PMID:2756156

A/Accession: B60070

A/Molecule type: protein

A/Residues: 96-104 <DES>

A/Cross-references: UNIPARC:UPI000001735A1

C/Comment: Big gastrin constitutes only about 5% of antral gastrin.

C/Superfamily: gastrin

C/Keywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic acid; F;1-21/Domain: signal sequence #status predicted <SIG>

F;59-92/Product: big gastrin #status experimental <MAT>

F;76-92/Product: gastrin #status experimental <NAL>

F;59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen

F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen

F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental

F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

F;96/Binding site: phosphate (Ser) (covalent) (partial) #status experimental

Query Match 90.6%; Score 48; DB 1; Length 104;

Best Local Similarity 77.8%; Pred. No. 0.28;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEEE 9

Db 76 QGPMWEEEE 84

RESULT 6

GMPGB

gastrin precursor [validated] - pig

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 17-Dec-1982 #sequence\_revision 17-Dec-1982 #text\_change 09-Jul-2004

C/Accession: A93903; B94473; A93148; I46622; A60070; A01618

R/Yoo, O.J.; Powell, C.T.; Agarwal, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1049-1053, 1982

A/Title: Molecular cloning and nucleotide sequence of full-length cDNA coding for porcine

A/Reference number: A93903; MUID:82174533; PMID:6951161

A/Accession: A93903

A/Molecule type: mRNA

A/Residues: 1-104 <YOO>

A/Cross-references: UNIPROT:P01351; UNIPARC:UPI0000012B0F6; GB:V01303; GB:J00651; NID:g18

R/Harris, J.I.; Kenner, E.W.

unpublished results, cited by Gregory, R.A., and Tracy, H.J., in Gastrointestinal Hormon

A/Reference number: A94473

A/Accession: B94473

A/Molecule type: protein

A/Residues: 59-64, 'HPP', '68-92 <HAR>

A/Cross-references: UNIPARC:UPI0000017359B

A/Note: Tyr-87 is sulfated in two-thirds of the molecules

R/Gregory, H.; Hardy, P.M.; Jones, D.S.; Kenner, G.W.; Sheppard, R.C.

Nature 204, 931-933, 1964

A/Title: The antral hormone gastrin.

A/Reference number: A93148

A/Accession: A93148

A/Molecule type: protein

A/Residues: 76-92 <GRE>

A/Cross-references: UNIPARC:UPI0000017359C

R/Anderson, J.C.; Barton, M.A.; Gregory, R.A.; Hardy, P.M.; Kenner, G.W.; MacLeod, J.K.;

Nature 204, 933-934, 1964

A/Reference number: A93149

A/Contents: annotation; synthesis

R/Agarwal, K.L.; Noyes, B.E.

Ann. N. Y. Acad. Sci. 343, 433-442, 1980

A/Title: Studies on gastrin mRNA structure using an oligonucleotide probe.

A/Reference number: I46622; MUID:80240380; PMID:6930858

A/Accession: I46622

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 56-82 <AGA>

A/Cross-references: UNIPARC:UPI0000016C6EA; GB:M25036; NID:g164626; PIDN:AAA31111.1; PID:

R/Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.

Regul. Pept. 25, 223-233, 1989

A/Title: The constitution and properties of phosphorylated and unphosphorylated C-termin

A/Reference number: A60070; MUID:89331947; PMID:2756156

A/Accession: A60070

A/Status: preliminary

A/Molecule type: protein

A/Residues: 97-104 <DES>

A/Cross-references: UNIPARC:UPI0000017359D

C/Superfamily: gastrin

C/Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-56/Domain: amino-terminal propeptide #status predicted <PRO>

F;59-92/Product: big gastrin #status experimental <BGN>

F;76-92/Product: gastrin #status experimental <SGN>

F;59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen

F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen

F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental

F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

F;96/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 90.6%; Score 48; DB 1; Length 104;

Best Local Similarity 77.8%; Pred. No. 0.28;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEEE 9

Db 76 QGPMWEEEE 84

## RESULT 7

GMSH  
 gastrin - sheep  
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C;Date: 13-Jun-1983 #sequence\_revision 13-Jun-1983 #text\_change 20-Mar-1998  
 C;Accession: A01619  
 R;Agarwal, K.L.; Beacham, J.; Bentley, P.H.; Gregory, R.A.; Kenner, G.W.; Sheppard, R.C.  
 Nature 219, 614-615, 1988  
 A;Title: Isolation, structure and synthesis of ovine and bovine gastrins.  
 A;Reference number: A01619; MUID:68357500; PMID:5665711  
 A;Accession: A01619  
 A;Molecule type: protein  
 A;Residues: 1-17 <AGA>  
 A;Cross-references: UNIPARC:UPI00001735A2  
 C;Superfamily: gastrin  
 C;Keywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic acid;  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;12/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
 F;17/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 88.7%; Score 47; DB 1; Length 17;  
 Best Local Similarity 77.8%; Pred. No. 0.052;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
 :||:||||  
 Db 1 QGPWVEEEE 9

## RESULT 8

JS0426  
 big gastrin - goat  
 N;Contents: gastrin  
 C;Species: Capra aegagrus hircus (domestic goat)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
 C;Accession: JS0426  
 R;Bonato, C.; Eng, J.; Hulmes, J.D.; Miedel, M.; Pan, Y.C.E.; Yalow, R.S.  
 Peptides 7, 689-693, 1986  
 A;Title: Sequences of gastrins purified from a single antrum of dog and of goat.  
 A;Reference number: JS0425; MUID:87016557; PMID:3763441  
 A;Accession: JS0426  
 A;Molecule type: protein  
 A;Residues: 1-34 <BON>  
 A;Cross-references: UNIPROT:P04564; UNIPARC:UPI000012B0EE  
 A;Experimental source: antrum  
 A;Note: about 90% of gastrin is sulfated  
 C;Superfamily: gastrin  
 C;Keywords: amidated carboxyl end; hormone; pancreas; pyroglutamic acid; secretagogue;  
 F;1-34/Product: big gastrin #status experimental <BGS>  
 F;18-34/Product: gastrin #status experimental <GSN>  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;18/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen  
 F;29/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
 F;34/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 88.7%; Score 47; DB 2; Length 34;  
 Best Local Similarity 77.8%; Pred. No. 0.12;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
 :||:||||  
 Db 18 QGPWVEEEE 26

## RESULT 9

GMO  
 gastrin precursor [validated] - bovine  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 31-Dec-1991 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
 C;Accession: S14400; A01609; B01619; A01619  
 R;Kim, S.J.; Uhm, K.N.; Kang, Y.K.; Yoo, O.J.  
 DNA Seq. 1, 181-187, 1991

A;Title: Bovine and feline gastrin cDNA sequences and the amino acid and nucleotide sequ  
 A;Reference number: S14400; MUID:92127058; PMID:1773057  
 A;Accession: S14400  
 A;Molecule type: mRNA  
 A;Residues: 1-104 <KIM>  
 A;Cross-references: UNIPROT:P01352; UNIPARC:UPI000012B0EC; EMBL:X16581; NID:G648; PIDN:C  
 R;Lund, T.; Olsen, J.; Rehfeld, J.F.  
 Mol. Endocrinol. 3, 1585-1588, 1989  
 A;Title: Cloning and sequencing of the bovine gastrin gene.  
 A;Reference number: A41409; MUID:90114160; PMID:2608050  
 A;Accession: A41409  
 A;Molecule type: DNA  
 A;Residues: 1-31, 'L', 33-36, 'R', 38-47, 'T', 49-73, 'N', 75-80, 'G', 82-95, 'M', 97-98, 'G', 100-104  
 A;Cross-references: UNIPARC:UPI000016C312; GB:M1657; NID:G163079; PIDN:AAA30537.1; PID:  
 R;Agarwal, K.L.; Beacham, J.; Bentley, P.H.; Gregory, R.A.; Kenner, G.W.; Sheppard, R.C.  
 Nature 219, 614-615, 1988  
 A;Title: Isolation, structure and synthesis of ovine and bovine gastrins.  
 A;Reference number: A01619; MUID:68357500; PMID:5665711  
 A;Accession: B01619  
 A;Molecule type: protein  
 A;Residues: 76-92 <AGA>  
 A;Cross-references: UNIPARC:UPI00001735A2  
 C;Genetics:  
 A;Introns: 71/1  
 C;Superfamily: gastrin  
 C;Keywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic acid;  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;59-92/Product: big gastrin #status predicted <BGN>  
 F;76-92/Product: gastrin #status experimental <SGN>  
 F;59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
 F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen  
 F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
 F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 88.7%; Score 47; DB 1; Length 104;  
 Best Local Similarity 77.8%; Pred. No. 0.41;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
 :||:||||  
 Db 76 QGPWVEEEE 84

## RESULT 10

T46166  
 MYB27 protein - Arabidopsis thaliana  
 N;Alternate names: protein T4D2.130  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 31-Dec-2004  
 C;Accession: T46166  
 R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;  
 submitted to the Protein Sequence Database, December 1999  
 A;Reference number: Z23025  
 A;Accession: T46166  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-238 <NYA>  
 A;Cross-references: UNIPROT:Q9SCP1; UNIPARC:UPI000000CSAE; EMBL:AL132958  
 A;Experimental source: cultivar Columbia; BAC clone T4D2  
 C;Genetics:  
 A;Map position: 3  
 A;Introns: 42/1; 85/2; 119/1  
 A;Note: T4D2.130  
 C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 84.9%; Score 45; DB 2; Length 238;  
 Best Local Similarity 87.5%; Pred. No. 2.3;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEEEE 9  
 :||:||||  
 Db 12 GPWLEBED 19

A:Residues: 1-370 <BUL> A:Cross-references: UNIPARC:UPI0000165FD3; GB:U67525; GB:L77117; NID:g2826325; PIDN:AA899 C:Genetics: A:Map position: REV738679-737567 C:Superfamily: yeast deoxyhypusine synthase C:Keywords: hypusine biosynthesis; NAD; oxidoreductase; transferase		A:Residues: 1-370 <BUL> A:Cross-references: UNIPARC:UPI0000165FD3; GB:U67525; GB:L77117; NID:g2826325; PIDN:AA899 C:Genetics: A:Map position: REV738679-737567 C:Superfamily: yeast deoxyhypusine synthase C:Keywords: hypusine biosynthesis; NAD; oxidoreductase; transferase	
Query Match 79.2%; Score 42; DB 2; Length 370; Best Local Similarity 75.0%; Pred. No. 12; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;		Query Match 79.2%; Score 42; DB 2; Length 370; Best Local Similarity 75.0%; Pred. No. 12; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
QY 1 EGPWLEEE 8      :	Db 54 EGPWLEDD 61	QY 1 EGPWLEEE 8      :	Db 54 EGPWLEDD 61
RESULT 14 C91080 hypothetical protein ECs3611 [imported] - Escherichia coli (strain O157:H7, substrain RN C:Species: Escherichia coli C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 C:Accession: C91080 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gasaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom A:Reference number: A99629; MUID:21156231; PMID:11258796 A:Accession: C91080 A:Status: preliminary A:Molecule type: DNA A:Residues: 1-248 <HAY> A:Cross-references: UNIPROT:Q8X4R9; UNIPARC:UPI00000D0D8A; GB:BA000007; PIDN:BA837034.1; A:Experimental source: strain O157:H7, substrain RMD 050952 C:Genetics: A:Gene: ECs3611		RESULT 15 D85925 hypothetical protein Z4066 [imported] - Escherichia coli (strain O157:H7, substrain EDL9 C:Species: Escherichia coli C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C:Accession: D85925 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouis, K.; Apodaca, Nature 409, 529-533, 2001 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A:Reference number: A85480; MUID:21074935; PMID:11206551 A:Accession: D85925 A:Status: preliminary A:Molecule type: DNA A:Residues: 1-248 <STO> A:Cross-references: UNIPROT:Q8X4R9; UNIPARC:UPI00000D0D8A; GB:AE005174; NID:gl2517214; A:Experimental source: strain O157:H7, substrain EDL933 C:Genetics: A:Gene: Z4066	
Query Match 77.4%; Score 41; DB 2; Length 248; Best Local Similarity 66.7%; Pred. No. 12; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;		Query Match 77.4%; Score 41; DB 2; Length 248; Best Local Similarity 66.7%; Pred. No. 12; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	
QY 1 EGPWLEEE 9 :    :	Db 234 QGPWLSKEE 242	QY 1 EGPWLEEE 9 :    :	Db 234 QGPWLSKEE 242
A:Residues: 1-335 <KAW> A:Cross-references: UNIPROT:Q9V0N5; UNIPARC:UPI00001293BA; GB:AJ248285; GB:AL096836; NID A:Experimental source: strain Orsay C:Genetics: A:Gene: dyl1; PAB0511 C:Superfamily: yeast deoxyhypusine synthase C:Keywords: hypusine biosynthesis; oxidoreductase; transferase		A:Residues: 1-335 <KAW> A:Cross-references: UNIPROT:Q9V0N5; UNIPARC:UPI00001293BA; GB:AJ248285; GB:AL096836; NID A:Experimental source: strain Orsay C:Genetics: A:Gene: dyl1; PAB0511 C:Superfamily: yeast deoxyhypusine synthase C:Keywords: hypusine biosynthesis; oxidoreductase; transferase	
Query Match 81.1%; Score 43; DB 2; Length 335; Best Local Similarity 77.8%; Pred. No. 7.4; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		Query Match 81.1%; Score 43; DB 2; Length 335; Best Local Similarity 77.8%; Pred. No. 7.4; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY 1 EGPWLEEE 9      :	Db 20 EGPWLEDEVE 28	QY 1 EGPWLEEE 9      :	Db 20 EGPWLEDEVE 28
RESULT 13 F64401 deoxyhypusine synthase (EC 2.5.1.146) MJ0814 [similarity] - Methanococcus jannaschii C:Species: Methanococcus jannaschii C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Nov-2001 C:Accession: F64401 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, ; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A:Reference number: A64300; MUID:96337999; PMID:8688087 A:Accession: F64401 A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA		RESULT 13 F64401 deoxyhypusine synthase (EC 2.5.1.146) MJ0814 [similarity] - Methanococcus jannaschii C:Species: Methanococcus jannaschii C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Nov-2001 C:Accession: F64401 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, ; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A:Reference number: A64300; MUID:96337999; PMID:8688087 A:Accession: F64401 A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA	

## RESULT 16

QJ2390  
MYB transcription factor (Atmyb2) [imported] - Arabidopsis thaliana  
N/Alternate names: myb-related protein 2; ATMYB2 protein  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 31-Dec-2004  
C/Accession: JQ2390; B84912  
R/Urao, T.; Yamaguchi-Shinozaki, K.; Urao, S.; Shinozaki, K.  
Plant Cell 5, 1529-1539, 1993  
A/Title: An arabidopsis myb homolog is induced by dehydration stress and its gene product  
A/Reference number: JQ2390; MUID:94146551; PMID:8312738  
A/Accession: JQ2390  
A/Molecule type: mRNA  
A/Residues: 1-273 <RA>  
A/Cross-references: UNIPROT:Q39028; UNIPARC:UPI00000A4CE9; DBJ:D14712; NID:9455462; PID  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: B84912  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-273 <STO>  
A/Cross-references: UNIPARC:UPI00000A4CE9; GB:AE002093; NID:92275197; PIDN:AAB63819.1; C  
C/Comment: The expression of the gene encoding for this protein is induced by dehydratic

C/Genetics:  
A/Gene: Atmyb2; At2g47190  
A/Map position: 2  
A/Introns: 53/1; 96/2  
C/Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology  
C/Keywords: DNA binding; duplication  
P/17-69/Domain: myb DNA-binding repeat homology <MYB1>  
F/70-120/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 77.4%; Score 41; DB 1; Length 273;  
Best Local Similarity 66.7%; Pred. No. 13;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
:|||||:  
Db 22 KGPWTEED 30

## RESULT 17

T09758  
myb-related protein - upland cotton  
N/Alternate names: MYB-like DNA-binding domain protein  
C/Species: Gossypium hirsutum (upland cotton)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 31-Dec-2004  
C/Accession: T09758  
R/Jogurtio, L.L.; Zhang, J.; Wilkins, T.A.  
submitted to the EMBL Data Library, November 1997  
A/Description: Structure and expression of six classes of myb-domain genes in allotetrap  
A/Reference number: Z16842  
A/Accession: T09758  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-293 <LOG>  
A/Cross-references: UNIPROT:O49020; UNIPARC:UPI00000A0E11; EMBL:AF034133; NID:g2921337;  
A/Experimental source: cultivar Acala SJ-2; ovule  
C/Genetics:  
A/Note: CmY-N  
C/Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology  
C/Keywords: DNA binding; transcription regulation  
F/70-119/Domain: myb DNA-binding repeat homology <MYB>

Query Match 77.4%; Score 41; DB 2; Length 293;  
Best Local Similarity 66.7%; Pred. No. 14;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
:|||||:  
Db 22 KGPWTEED 30

## RESULT 18

CMGPB  
big gastrin [validated] - guinea pig  
N/Contains: gastrin  
C/Species: Cavia porcellus (guinea pig)  
C/Date: 30-Sep-1987 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
C/Accession: A26089  
R/Bonato, C.; Eng, J.; Pan, Y.C.E.; Miedel, M.; Hulmes, J.D.; Yalow, R.S.  
Life Sci. 39, 959-964, 1986  
A/Title: Guinea pig 33-amino acid gastrin.  
A/Reference number: A26089; MUID:86309993; PMID:3747718  
A/Accession: A26089  
A/Molecule type: protein  
A/Residues: 1-33 <BON>  
A/Cross-references: UNIPROT:P06885; UNIPARC:UPI000012B0EF  
C/Comment: Big gastrin constitutes only about 5% of antral gastrin.  
C/Superfamily: gastrin  
C/Keywords: amidated carboxyl end; hormone; pyroglutamic acid  
F/1-33/Product: big gastrin #status experimental <BGN>  
F/18-33/Product: gastrin #status experimental <SGN>  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F/33/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 75.5%; Score 40; DB 1; Length 33;  
Best Local Similarity 75.0%; Pred. No. 1.7;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8  
:|||||:  
Db 18 QGPWAEED 25

## RESULT 19

B29541  
big gastrin - Chinchilla brevicaudata  
C/Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata  
C/Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 09-Jul-2004  
C/Accession: B29541  
R/Shinomura, Y.; Eng, J.; Yalow, R.S.  
Biochem. Biophys. Res. Commun. 143, 7-14, 1987  
A/Title: Chinchilla "big" and "little" gastrins.  
A/Reference number: A90130; MUID:87156784; PMID:3827930  
A/Accession: B29541  
A/Molecule type: protein  
A/Residues: 1-33 <SHI>  
A/Cross-references: UNIPROT:P10034; UNIPARC:UPI000012B0F0  
C/Superfamily: gastrin

Query Match 75.5%; Score 40; DB 2; Length 33;  
Best Local Similarity 75.0%; Pred. No. 1.7;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8  
:|||||:  
Db 18 QGPWAEED 25

## RESULT 20

S20350  
napin nla - rape  
C/Species: Brassica napus (rape)  
C/Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 31-Dec-2004  
C/Accession: S20350; S20351  
R/Monsalve, R.I.; Lopez-Otin, C.; Villalba, M.; Rodriguez, R.  
FEBS Lett. 295, 207-210, 1991  
A/Title: A new distinct group of 2 S albumins from rapeseed. Amino acid sequence of two  
A/Reference number: S20350; MUID:92111741; PMID:1765156

A;Accession: S20350  
A;Molecule type: protein  
A;Residues: 1-110 <MON>  
A;Cross-references: UNIPROT:P24565; UNIPARC:UPI00000124EBF  
C;Superfamily: Alpha amylase inhibitor  
C;Keywords: pyroglutamic acid; seed; storage protein  
F;1-31/Product: napin small chain #status experimental <SMA>  
F;32-110/Product: napin large chain #status experimental <LAR>  
F;32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental

Query Match 75.5%; Score 40; DB 2; Length 110;  
Best Local Similarity 75.0%; Pred. No. 6.8;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 8  
||||| |  
Db 37 EGPWLREQ 44

RESULT 21  
JQ0961  
myb-related protein 315 - garden snapdragon  
C;Species: Antirrhinum majus (garden snapdragon)  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 31-Dec-2004  
C;Accession: JQ0961  
R;Jackson, D.; Culianez-Macia, F.; Prescott, A.G.; Roberts, K.; Martin, C.  
Plant Cell 3, 115-125, 1991  
A;Title: Expression patterns of myb genes from Antirrhinum flowers.  
A;Reference number: JQ0956; MUID:93005689; PMID:1840903  
A;Accession: JQ0961  
A;Molecule type: mRNA  
A;Residues: 1-268 <JAC>  
A;Cross-references: UNIPROT:P81394; UNIPARC:UPI000000ABAE8  
A;Experimental source: strain J1:522  
C;Comment: The gene encoding for this protein is expressed in all plant organs.  
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology  
C;Keywords: DNA binding; duplication; nucleus; transcription regulation  
F;9-61/Domain: myb DNA-binding repeat homology <MYB1>  
F;62-112/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 75.5%; Score 40; DB 1; Length 268;  
Best Local Similarity 75.0%; Pred. No. 19;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GPWLEEEE 9  
||| |||  
Db 15 GPWTEED 22

RESULT 22  
A71448  
probable MYB transcription factor - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
A;Variety: columbia  
C;Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 31-Dec-2004  
C;Accession: A71448  
R;Bavan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirks  
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giel  
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.  
Nature 391, 485-488, 1998  
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech  
erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; And  
C.; Chalwatzis, N.  
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal  
A;Reference number: A71400; MUID:98121113; PMID:9461215  
A;Accession: A71448  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-745 <BEV>  
A;Cross-references: UNIPROT:O23618; UNIPARC:UPI000000A9853; GB:Z97344; NID:g2245126; PID:  
C;Genetics:  
A;Map position: 4COP9-4G3845  
F;63-113/Domain: myb DNA-binding repeat homology <MYB>

Query Match 75.5%; Score 40; DB 2; Length 745;  
Best Local Similarity 66.7%; Pred. No. 60;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9  
||||| |  
Db 15 KGPWLPEED 23

## RESULT 23

C35878  
class I major histocompatibility antigen B6-8 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 12-Oct-1990 #sequence\_revision 13-Jan-1993 #text\_change 09-Jul-2004  
C;Accession: C35878  
R;Ito, K.; Van Kaer, L.; Bonneville, M.; Hsu, S.; Murphy, D.B.; Tonegawa, S.  
Cell 62, 549-561, 1990  
A;Title: Recognition of the product of a novel MHC TL region gene (27(b)) by a mouse gam  
A;Reference number: A35878; MUID:90335964; PMID:2379238  
A;Accession: C35878  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-204 <ITO>  
A;Cross-references: UNIPROT:Q31205; UNIPARC:UPI000008A93F; GB:M35246; NID:g199661; PIDN:  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 73.6%; Score 39; DB 2; Length 204;  
Best Local Similarity 85.7%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEEE 9  
||||| |  
Db 75 PWLEQEE 81

## RESULT 24

A49885  
MHC class I histocompatibility antigen T10(b) alpha chain precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: A49885  
R;Schild, H.; Mavaddat, N.; Litzenberger, C.; Ehrlich, E.W.; Davis, M.M.; Bluestone, J.A.  
Cell 76, 29-37, 1994  
A;Title: The nature of major histocompatibility complex recognition by gammadelta T cell  
A;Reference number: A49885; MUID:94116064; PMID:8287478  
A;Accession: A49885  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-377 <SCH>  
A;Cross-references: UNIPROT:Q8WLM9; UNIPROT:Q31206; UNIPARC:UPI0000176F6C  
C;Genetics:  
A;Gene: T10  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F;206-271/Domain: immunoglobulin homology <IMM>

Query Match 73.6%; Score 39; DB 2; Length 377;  
Best Local Similarity 85.7%; Pred. No. 41;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEEE 9  
||||| |  
Db 73 PWLEQEE 79

## RESULT 25

A35878  
class I major histocompatibility antigen PCC3-4/27 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 12-Oct-1990 #sequence\_revision 12-Oct-1990 #text\_change 09-Jul-2004  
C;Accession: A35878  
R;Ito, K.; Van Kaer, L.; Bonneville, M.; Hsu, S.; Murphy, D.B.; Tonegawa, S.  
Cell 62, 549-561, 1990

```

A:Title: Recognition of the product of a novel MHC TL region gene (27(b)) by a mouse gam
A:Reference number: A35878; MUID:90335964; PMID:2379238
A:Accession: B35878
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-379 <ITO>
A:Cross-references: UNIPROT:Q31208; UNIPARC:UPI0000028345; GB:M35243; NID:g199667; PIDN:
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:208-273/Domain: immunoglobulin homology <IMM>

Query Match      73.6%; Score 39; DB 2; Length 379;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PWLEEEE 9
Db      75 PWLEQEE 81

RESULT 26
B35878
Class I major histocompatibility antigen BALB-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 12-Oct-1990 #sequence_revision 13-Jan-1993 #text_change 09-Jul-2004
C:Accession: B35878
R:Ito, K.; Van Kaer, L.; Bonneville, M.; Hsu, S.; Murphy, D.B.; Tonegawa, S.
Cell 62, 549-561, 1990
A:Title: Recognition of the product of a novel MHC TL region gene (27(b)) by a mouse gam
A:Reference number: A35878; MUID:90335964; PMID:2379238
A:Accession: B35878
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-379 <ITO>
A:Cross-references: UNIPROT:Q31208; UNIPARC:UPI0000028345; GB:M35243; NID:g199667; PIDN:
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:208-273/Domain: immunoglobulin homology <IMM>

Query Match      73.6%; Score 39; DB 2; Length 379;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PWLEEEE 9
Db      75 PWLEQEE 81

RESULT 27
B35878
Class I major histocompatibility antigen PCC3-24 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 09-Jul-2004
C:Accession: B35878
R:Ito, K.; Van Kaer, L.; Bonneville, M.; Hsu, S.; Murphy, D.B.; Tonegawa, S.
Cell 62, 549-561, 1990
A:Title: Recognition of the product of a novel MHC TL region gene (27(b)) by a mouse gam
A:Reference number: A35878; MUID:90335964; PMID:2379238
A:Accession: B35878
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-406 <ITO>
A:Cross-references: UNIPROT:Q31206; UNIPARC:UPI0000028342; GB:M35244; NID:g199663; PIDN:
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:208-273/Domain: immunoglobulin homology <IMM>

Query Match      73.6%; Score 39; DB 2; Length 406;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PWLEEEE 9
Db      75 PWLEQEE 81
```

```

RESULT 28
S11246
LAG-3 protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000
C:Accession: S11246
R:Triebel, F.; Jitsukawa, S.; Baixeras, E.; Roman-Roman, S.; Genevee, C.; Viegas-Pequign
J. Exp. Med. 171, 1393-1405, 1990
A:Title: LAG-3, a novel lymphocyte activation gene closely related to CD4.
A:Reference number: S11246; MUID:90237736; PMID:1692078
A:Accession: S11246
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-498 <TRI>
A:Cross-references: UNIPARC:UPI000016D72E; EMBL:X51985
A:Note: the author translated the codon CCA for residue 388 as Arg
C:Genetics:
A:Gene: GDB:LAG3
A:Cross-references: GDB:127449; OMIM:153337
A:Map position: 12p13.3-12p13.3
C:Superfamily: human LAG-3 protein
C:Keywords: transmembrane protein

Query Match      73.6%; Score 39; DB 2; Length 498;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GPWLEEEE 9
Db      395 GPWLEAQE 402

RESULT 29
T00808
Hypothetical protein At2g41520 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T32G6.4
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00808; G84842
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crösbey, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, November 1997
A:Description: Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence.
A:Reference number: Z14163
A:Accession: T00808
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-960 <ROU>
A:Cross-references: UNIPROT:O22214; UNIPARC:UPI000009D5DC; EMBL:AC002510; NID:g2618683;
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84842
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-960 <STO>
A:Cross-references: UNIPARC:UPI000009D5DC; GB:AE002093; NID:g2618687; PIDN:AAB84334.1; G
C:Genetics:
A:Gene: T32G6.4; At2g41520
A:Map position: 2
A:Introns: 95/1; 557/2; 637/2; 680/3; 731/3; 800/3; 878/2; 904/3

Query Match      73.6%; Score 39; DB 2; Length 960;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EGPWLEE 7
Db      915 EGPWLKE 921
```

## RESULT 30

T51666  
Myb-related transcription factor MYB59 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 31-Dec-2004  
C;Accession: T51666  
R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Paz-Ares, J.; Weishaar, B.  
Plant J. 16, 263-276, 1998  
A;Title: Towards functional characterisation of the members of the R2R3-MYB gene family  
A;Reference number: Z14349; MUID:9839469; PMID:9839469  
A;Accession: T51666  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-234 <KRA>  
A;Cross-references: UNIPROT:O50069; UNIPARC:UPI00000A332A; EMBL:AF062894; PIDN:AAC83616  
A;Experimental source: cultivar Columbia  
C;Genetics:  
A;Gene: MYB59  
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology  
C;Keywords: transcription factor

Query Match 71.7%; Score 38; DB 2; Length 234;  
Best Local Similarity 55.6%; Pred. No. 35; Indels 1; Gaps 0;  
Matches 5; Conservative 3; Mismatches 0;

Qy 1 EGPWLEEEE 9  
:|||||:  
Db 10 KGPWTEQED 18

## RESULT 31

T49254  
Myb DNA binding protein-like - Arabidopsis thaliana  
N;Alternate names: protein F12M12.100  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 31-Dec-2004  
C;Accession: T49254  
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseid, M.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, May 2000  
A;Reference number: 225020  
A;Accession: T49254  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-256 <JOR>  
A;Cross-references: UNIPROT:Q9LX82; UNIPARC:UPI00000A84DD; EMBL:AL355775; GSPDB:GN000061;  
A;Experimental source: cultivar Columbia; BAC clone F12M12  
C;Genetics:  
A;Gene: ATSP:F12M12.100  
A;Map position: 3  
A;Introns: 40/1; 83/2  
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 71.7%; Score 38; DB 2; Length 256;  
Best Local Similarity 55.6%; Pred. No. 39; Indels 1; Gaps 0;  
Matches 5; Conservative 3; Mismatches 0;

Qy 1 EGPWLEEEE 9  
:|||||:  
Db 9 KGPWTEQED 17

## RESULT 32

T03850  
myb-related protein myb1. TMV-inducible - common tobacco  
C;Species: Nicotiana tabacum (common tobacco)  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 31-Dec-2004  
C;Accession: T03850  
R;Yang, Y.; Kleesig, D.F.  
Proc. Natl. Acad. Sci. U.S.A. 93, 14972-14977, 1996  
A;Title: Isolation and characterization of a tobacco mosaic virus-inducible myb oncogene  
A;Reference number: Z15119; MUID:97121500; PMID:8962166

A;Accession: T03850  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-278 <YAN>  
A;Cross-references: UNIPROT:P93391; UNIPARC:UPI00000F9F2; EMBL:U72762; NID:gl732246; P11  
A;Experimental source: strain Xanthi nc  
C;Genetics:  
A;Gene: myb1  
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology  
C;Keywords: DNA binding; transcription regulation  
F;9-61/Domain: myb DNA-binding repeat homology <MYB1>  
F;62-112/Domain: myb DNA-binding repeat homology <MYB>

Query Match 71.7%; Score 38; DB 2; Length 278;  
Best Local Similarity 55.6%; Pred. No. 43; Indels 1; Gaps 0;  
Matches 5; Conservative 3; Mismatches 0;

Qy 1 EGPWLEEEE 9  
:|||||:  
Db 14 KGPWIPBED 22

## RESULT 33

T51509  
probable transcription factor (MYB9) - Arabidopsis thaliana  
N;Alternate names: protein F5E19.110  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 31-Dec-2004  
C;Accession: T51509  
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mewes, H.W.; submitted to the Protein Sequence Database, August 2000  
A;Reference number: Z25394  
A;Accession: T51509  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-325 <SAT>  
A;Cross-references: UNIPROT:Q9LFE1; UNIPARC:UPI00000A6D3; EMBL:AL391147  
A;Experimental source: cultivar Columbia; BAC clone F5E19  
C;Genetics:  
A;Map position: 5  
A;Introns: 88/2  
A;Note: F5E19.110  
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 71.7%; Score 38; DB 2; Length 325;  
Best Local Similarity 55.6%; Pred. No. 51; Indels 1; Gaps 0;  
Matches 5; Conservative 3; Mismatches 0;

Qy 1 EGPWLEEEE 9  
:|||||:  
Db 14 KGPWTEQED 22

## RESULT 34

D82158  
N-acetylglucosamine-6-phosphate deacetylase VC1783 [imported] - Vibrio cholerae (strain  
C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: D82158  
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A;Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301  
A;Accession: D82158  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-378 <HEI>  
A;Cross-references: UNIPROT:Q9KR60; UNIPARC:UPI00000C30E5; GB:AE004255; GB:AE003852; NID  
A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VC1783

A:Map position: 1

Query Match 71.7%; Score 38; DB 2; Length 378;  
Best Local Similarity 66.7%; Pred. No. 61;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
|||||  
Db 130 EGPWLNPEK 138

RESULT 35

T48253  
myb-like protein - Arabidopsis thaliana  
N:Alternate names: protein T1E22.80  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: T48253  
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, March 2000  
A:Reference number: Z24489  
A:Accession: T48253  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-529 <BEV>  
A:Cross-references: UNIPROT:Q9L293; UNIPARC:UPI00000A0F8C; EMBL:AL162874  
A:Experimental source: cultivar Columbia; BAC clone T1E22  
C:Genetics:  
A:Map position: 5  
A:Introns: 46/2; 63/3; 83/1; 114/3; 149/2; 192/2  
A:Note: T1E22.80

Query Match 71.7%; Score 38; DB 2; Length 529;  
Best Local Similarity 55.6%; Pred. No. 89;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
|||||  
Db 108 KGPWTQBED 116

RESULT 36

T26149  
hypothetical protein W04D2.1b - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T26149  
R:Lennard, N.  
submitted to the EMBL Data Library, June 1996  
A:Reference number: Z20161  
A:Accession: T26149  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-894 <WIL>  
A:Cross-references: UNIPROT:Q9XVU8; UNIPARC:UPI00000611FF; EMBL:Z75552; PIDN:CAA99944.1;  
A:Experimental source: clone W04D2  
C:Genetics:  
A:Gene: CESP:W04D2.1b  
A:Map position: 5  
A:Introns: 41/3; 149/1; 232/1; 259/3; 290/3; 633/1; 777/2; 845/3  
C:Superfamily: alpha-actinin; alpha-actinin actin-binding domain homology; calmodulin re  
C:Keywords: EF hand

Query Match 71.7%; Score 38; DB 2; Length 894;  
Best Local Similarity 85.7%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPWLEEE 8  
|||||  
Db 649 GPWLEEE 655

RESULT 37

A48403

alpha-actinin - Caenorhabditis elegans (fragment)  
C:Species: Caenorhabditis elegans  
C:Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A48403  
R:Barstead, R.J.; Kleiman, L.; Waterston, R.H.  
Cell Motil. Cytoskeleton 20, 69-78, 1991  
A:Title: Cloning, sequencing, and mapping of an alpha-actinin gene from the nematode *Caenorhabditis elegans*  
A:Reference number: A48403; MUID:92097210; PMID:1758579  
A:Accession: A48403  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-910 <BAR>  
A:Cross-references: UNIPROT:Q9TXC0; UNIPARC:UPI000007F56C  
A:Note: sequence extracted from NCBI Backbone (NCBI:73003)  
C:Superfamily: alpha-actinin; alpha-actinin actin-binding domain homology; calmodulin re  
C:Keywords: actin binding; EF hand  
F:26-237/Domain: alpha-actinin actin-binding domain homology <ACT>  
F:294-405/Domain: spectrin/dystrophin repeat homology <SP1>  
F:414-520/Domain: spectrin/dystrophin repeat homology <SP2>  
F:529-642/Domain: spectrin/dystrophin repeat homology <SP3>  
F:768-799/Domain: calmodulin repeat homology <EF1>  
F:808-840/Domain: calmodulin repeat homology <EF2>

Query Match 71.7%; Score 38; DB 2; Length 910;  
Best Local Similarity 85.7%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPWLEEE 8  
|||||  
Db 665 GPWLEEE 671

RESULT 38

T26147  
hypothetical protein W04D2.1a - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T26147  
R:Lennard, N.  
submitted to the EMBL Data Library, June 1996  
A:Reference number: Z20161  
A:Accession: T26147  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-920 <WIL>  
A:Cross-references: UNIPROT:Q23158; UNIPARC:UPI00000611FD; EMBL:Z75552; PIDN:CAA99941.1;  
A:Experimental source: clone W04D2  
C:Genetics:  
A:Gene: CESP:W04D2.1a  
A:Map position: 5  
A:Introns: 41/3; 149/1; 232/1; 285/3; 316/3; 659/1; 803/2; 871/3  
C:Superfamily: alpha-actinin; alpha-actinin actin-binding domain homology; calmodulin re  
C:Keywords: EF hand

Query Match 71.7%; Score 38; DB 2; Length 920;  
Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPWLEEE 8  
|||||  
Db 675 GPWLEEE 681

RESULT 39

T41135  
hypothetical protein SPC1795.08c - fission yeast (*Schizosaccharomyces pombe*)  
C:Species: *Schizosaccharomyces pombe*  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T41135  
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, D.  
submitted to the EMBL Data Library, April 1998  
A:Reference number: Z21971

A;Accession: T41135  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-985 <LYN>  
A;Cross-references: UNIPROT:O59773; UNIPARC:UPI000006AD2B; EMBL:AL022598; PIDN:CAA18643.  
A;Experimental source: strain 972h-; cosmid c1795  
C;Genetics:  
A;Gene: SPDB:SPCC1795.08c  
A;Map position: 3  
A;Introns: 3/3; 97/2

Query Match 71.7%; Score 38; DB 2; Length 985;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
DB 709 EAPWLPEED 717  
|||||

RESULT 40  
T09070  
probable tenascin X - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: T09070  
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sg  
submitted to the EMBL Data Library, October 1997  
A;Description: Sequence of the mouse major histocompatibility locus class III region.  
A;Reference number: Z16543  
A;Accession: T09070  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-4006 <ROW>  
A;Cross-references: UNIPROT:O35452; UNIPARC:UPI000002A159; EMBL:AF030001; NID:G2564945;  
C;Genetics:  
A;Gene: TNX  
A;Map position: 17  
A;Introns: 124/1; 735/1; 773/3; 826/1; 914/1; 1037/1; 1135/1; 1232/1; 1329/1; 1440/1; 15  
019/1; 3115/1; 3208/1; 3302/1; 3405/1; 3517/1; 3558/1; 3606/1; 3646/1; 3694/1; 3737/3; 3  
C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin ty  
C;Keywords: extracellular matrix  
F;422-448/Domain: EGF homology <EGF>  
F;826-906/Domain: fibronectin type III repeat homology <3FR>  
F;3789-3997/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 71.7%; Score 38; DB 2; Length 4006;  
Best Local Similarity 75.0%; Pred. No. 8.9e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8  
DB 986 EGPWAHEE 993  
|||||

RESULT 41  
S26636  
napin n1b - rape  
C;Species: Brassica napus (rape)  
C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 31-Dec-2004  
C;Accession: S26636  
R;Monsaive, R.I.; Lopez-Otin, C.; Villalba, M.; Rodriguez, R.  
FEBS Lett. 295, 207-210, 1991  
A;Title: A new distinct group of 2 S albumins from rapeseed. Amino acid sequence of two  
A;Reference number: S20350; MUID:92111741; PMID:1765156  
A;Accession: S26636  
A;Molecule type: protein  
A;Residues: 1-106 <MON>  
A;Cross-references: UNIPROT:P24565; UNIPARC:UPI00001763E6  
C;Superfamily: Alpha amylase inhibitor  
C;Keywords: pyroglutamic acid; seed; storage protein  
F;1-31/Product: napin small chain #status experimental <SMA>  
F;32-106/Product: napin large chain #status experimental <LAR>

F;32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment

F;32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment

Query Match 69.8%; Score 37; DB 2; Length 106;  
Best Local Similarity 62.5%; Pred. No. 21;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8  
DB 37 QGPWLREQ 44  
|||||

RESULT 42  
G69355  
MJ0653 homolog AF0847 - Archaeoglobus fulgidus  
N;Alternate names: inosine-monophosphate dehydrogenase (guaB-1) homolog [mismomer]  
C;Species: Archaeoglobus fulgidus  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: G69355  
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,  
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
A;Reference number: A69250; MUID:98049343; PMID:9389475  
A;Accession: G69355  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-189 <KLE>  
A;Cross-references: UNIPROT:O29411; UNIPARC:UPI0000056F4F; GB:AE001045; GB:AE000782; NID  
C;Superfamily: conserved hypothetical protein MJ0653; CBS homology  
C;Keywords: duplication  
F;79-127/Domain: CBS homology <CBS>

Query Match 69.8%; Score 37; DB 1; Length 189;  
Best Local Similarity 77.8%; Pred. No. 41;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
DB 148 EGPVIEEE 156  
|||||

RESULT 43  
F69335  
conserved hypothetical protein AF0686 - Archaeoglobus fulgidus  
C;Species: Archaeoglobus fulgidus  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: F69335  
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
A;Reference number: A69250; MUID:98049343; PMID:9389475  
A;Accession: F69335  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-222 <KLE>  
A;Cross-references: UNIPROT:O29571; UNIPARC:UPI0000056FF7; GB:AE001057; GB:AE000782; NID  
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF0686

Query Match 69.8%; Score 37; DB 2; Length 222;  
Best Local Similarity 66.7%; Pred. No. 49;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
DB 119 EKPWVEEE 127  
|||||

```
RESULT 44
A37766
SEC14 protein - yeast (Kluyveromyces marxianus var. lactis)
C;Species: Kluyveromyces marxianus var. lactis, Candida spharctica
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A37766
R;Salama, S.R.; Cleves, A.E.; Malehorn, D.B.; Whitters, E.A.; Bankaitis, V.A.
J. Bacteriol. 172, 4510-4521, 1990
A;Title: Cloning and characterization of Kluyveromyces lactis SEC14, a gene whose product
A;Reference number: A37766; MUID:90330560; PMID:2198263
A;Accession: A37766
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-301 <SAL>
A;Cross-references: UNIPROT:P24859; UNIPARC:UPI0000135588
C;Superfamily: cellular retinaldehyde-binding protein; cellular retinaldehyde-binding pr
F;57-264/Domain: cellular retinaldehyde-binding protein homology <CRB>

Query Match 69.8%; Score 37; DB 1; Length 301;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GPWLEEE 8
Db 281 GPWREEE 287

RESULT 45
T45859
R2R3-MYB transcription factor - Arabidopsis thaliana
N;Alternate names: protein F3A4.140
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Dec-2004
C;Accession: T45859
R;Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23007
A;Accession: T45859
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <BAR>
A;Cross-references: UNIPROT:Q9SN12; UNIPARC:UPI00000A3C92; EMBL:AL132978
A;Experimental source: cultivar Columbia; BAC clone F3A4
C;Genetics:
A;Map position: 3
A;Note: F3A4.140
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 69.8%; Score 37; DB 2; Length 301;
Best Local Similarity 55.6%; Pred. No. 69;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 6 KGPWSQED 14

RESULT 46
S71285
myb-related protein, 33.2K - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 31-Dec-2004
C;Accession: S71285
R;Kirik, V.; Baumlein, H.
submitted to the EMBL Data Library, September 1995
A;Description: Characterization of two cDNAs encoding MYB-related proteins in Arabidopsi
A;Reference number: S71285
A;Accession: S71285
A;Molecule type: mRNA
A;Residues: 1-304 <KIR>
A;Cross-references: UNIPROT:Q39155; UNIPARC:UPI000009D1EE; EMBL:Z54137; NID:gl263096; PI
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
```

C;Keywords: DNA binding; duplication  
F;1-52/Domain: myb DNA-binding repeat homology <MYB1>  
F;53-103/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 69.8%; Score 37; DB 1; Length 304;  
Best Local Similarity 55.6%; Pred. No. 70;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9  
Db 6 KGPWSQED 14

RESULT 47  
A87443  
GTP-binding protein Era [imported] - Caulobacter crescentus  
C;Species: Caulobacter crescentus  
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 31-Dec-2004  
C;Accession: A87443  
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A;Title: Complete Genome Sequence of Caulobacter crescentus.  
A;Reference number: A87249; MUID:21173698; PMID:11259647  
A;Accession: A87443  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-333 <STO>  
A;Cross-references: UNIPARC:UPI0000165C04; GB:AE005673; NID:gl13422951; PIDN:AAK23541.1;  
C;Genetics:  
A;Gene: CC1562  
C;Superfamily: GTP-binding protein era homolog, bacteria type; translation elongation fa

Query Match 69.8%; Score 37; DB 2; Length 333;  
Best Local Similarity 66.7%; Pred. No. 78;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9  
Db 207 EGPWLYPED 215

RESULT 48  
S11198  
transforming protein myb (clone Mbm-2) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 21-Nov-1993 #sequence\_revision 24-Jul-1997 #text\_change 09-Jul-2004  
C;Accession: S11198  
R;Westin, E.H.; Gorse, K.M.; Clarke, M.F.  
Oncogene 5, 1117-1124, 1990  
A;Title: Alternative splicing of the human c-myb gene.  
A;Reference number: S11197; MUID:90363543; PMID:2202948  
A;Accession: S11198  
A;Molecule type: mRNA  
A;Residues: 1-348 <WES>  
A;Cross-references: UNIPROT:Q14025; UNIPARC:UPI000006FD14; EMBL:X52126; NID:g29990; PIDN  
A;Experimental source: clone Mbm-2  
C;Superfamily: myb transforming protein; myb DNA-binding repeat homology  
C;Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcription re  
F;36-87/Domain: myb DNA-binding repeat homology <MYB1>  
F;88-139/Domain: myb DNA-binding repeat homology <MYB2>  
F;140-190/Domain: myb DNA-binding repeat homology <MYB3>

Query Match 69.8%; Score 37; DB 2; Length 348;  
Best Local Similarity 55.6%; Pred. No. 82;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9  
Db 93 KGPWTKED 101

RESULT 49  
S18198  
class I histocompatibility antigen Gogo-A4 alpha chain - gorilla (fragment)  
C:Species: Gorilla gorilla (gorilla)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S18198  
R:Watkins, D.I.; Chen, Z.W.; Garber, T.L.; Hughes, A.L.; Letvin, N.L.  
Immunogenetics 34, 185-191, 1991  
A:Title: Segmental exchange between MHC class I genes in a higher primate: recombination  
A:Reference number: S18197; MUID:91372865; PMID:1894312  
A:Accession: S18198  
A>Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-357 <WAT>  
A:Cross-references: UNIPROT:O78205; UNIPARC:UPI00000897DE; EMBL:X54376; NID:G22891; PIDN  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F:212-277/Domain: immunoglobulin homology <IMM>

Query Match 69.8%; Score 37; DB 2; Length 357;  
Best Local Similarity 71.4%; Pred. No. 84;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEEE 9  
||:|:|  
Db 66 PWIEQEE 72

RESULT 50  
JH0535  
class I histocompatibility antigen Gogo-A0201 heavy chain precursor - lowland gorilla  
C:Species: Gorilla gorilla (lowland gorilla)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: JH0535  
R:Lawlor, D.A.; Warren, E.; Taylor, P.; Farham, P.  
J. Exp. Med. 174, 1491-1509, 1991  
A:Title: Gorilla class I major histocompatibility complex alleles: comparison to human a  
A:Reference number: JH0534; MUID:92078860; PMID:1744581  
A:Accession: JH0535  
A:Molecule type: DNA  
A:Residues: 1-365 <LAW>  
A:Cross-references: UNIPROT:P30376; UNIPARC:UPI0000124E23; EMBL:X60259; NID:G22855; PIDN  
A:Experimental source: EBV-transformed B cell  
C:Genetics:  
A:Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1; 365/1  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C:Keywords: transmembrane protein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-365/Product: class I histocompatibility antigen heavy chain, Gogo-A0201 #status pre  
F:25-114/Domain: alpha-1 <AL1>  
F:115-206/Domain: alpha-2 <AL2>  
F:207-298/Domain: alpha-3 <AL3>  
F:220-285/Domain: immunoglobulin homology <IMM>  
F:299-365/Domain: intracellular #status predicted <INT>

Query Match 69.8%; Score 37; DB 2; Length 365;  
Best Local Similarity 71.4%; Pred. No. 86;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEEE 9  
||:|:|  
Db 74 PWIEQEE 80

Search completed: January 3, 2006, 09:11:28  
Job time : 18.4286 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:06 ; Search time 92.1429 Seconds  
(without alignments)  
68.912 Million cell updates/sec

Title: US-10-759-832-7  
Perfect score: 53  
Sequence: 1 BGPWLEEE 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Uniprot 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	94.3	33	1 GAST_DIDMA	P31713 didelphis m
2	50	94.3	101	1 GAST_HUMAN	P01350 homo sapien
3	50	94.3	104	1 GAST_FELCA	P01354 felis silve
4	48	90.6	17	1 GAST_MACMU	P31714 macaca mula
5	48	90.6	104	1 GAST_CANFA	P01353 canis famil
6	48	90.6	104	1 GAST_PIG	P01351 sus scrofa
7	47	88.7	34	1 GAST_CAPIH	P04564 capra hircu
8	47	88.7	104	1 GAST_BOVIN	P01352 bos taurus
9	47	88.7	104	1 GAST_SHEEP	O02886 ovis aries
10	46	86.8	107	1 GAST_HORSE	P55885 equus cabal
11	45	84.9	238	2 Q9SCF1_ARATH	Q9scp1 arabidopsis
12	43	81.1	335	1 DHYS_PYRAB	Q9v0n5 pyrococcus
13	42	79.2	330	1 DHYS_METJA	Q58224 methanococc
14	42	79.2	472	1 ZIMS_HUMAN	Q96pe6 homo sapien
15	42	79.2	472	2 Q6NTE1_HUMAN	Q6nce1 homo sapien
16	42	79.2	1103	2 Q4S209_TETNG	Q4sz09 tetraodon n
17	41	77.4	83	2 Q8LKG4_LOLPR	Q8lkg4 lolium pere
18	41	77.4	160	2 Q8S415_MAIZE	Q8s415 zea mays (m
19	41	77.4	248	2 Q8XR49_ECO57	Q8xr49 escherichia
20	41	77.4	273	2 Q941F8_ARATH	Q941f8 arabidopsis
21	41	77.4	273	2 Q941F6_ARATH	Q941f6 arabidopsis
22	41	77.4	273	2 Q941F9_ARATH	Q941f9 arabidopsis
23	41	77.4	273	2 Q39028_ARATH	Q39028 arabidopsis
24	41	77.4	273	2 Q93V20_ARATH	Q93v20 arabidopsis
25	41	77.4	273	2 Q93V46_ARATH	Q93v46 arabidopsis
26	41	77.4	286	2 Q8H257_9ROSI	Q8h257 gossypioide
27	41	77.4	287	2 Q8H261_GOSHI	Q8h261 gossypium h
28	41	77.4	287	2 Q8H260_GOSHI	Q8h260 gossypium h
29	41	77.4	287	2 Q8H259_9ROSI	Q8h259 gossypium r
30	41	77.4	287	2 Q8H258_9ROSI	Q8h258 gossypium h
31	41	77.4	293	2 Q49020_GOSHI	Q49020 gossypium h

32	41	77.4	293	2 Q94JN4_GOSHI	Q94jn4 gossypium h
33	41	77.4	293	2 Q94JN5_GOSHI	Q94jn5 gossypium h
34	41	77.4	340	2 Q7F9M1_ORYSA	Q7f9m1 oryza sativ
35	41	77.4	652	2 Q72IA2_THET2	Q72ia2 thermus the
36	41	77.4	652	2 Q5SHY6_THET8	Q5shy6 thermus the
37	41	77.4	1424	2 QSRGAB_BRARE	Q59a8 brachydanio
38	40	75.5	33	1 GAST_CAVPO	P06885 cavia porce
39	40	75.5	33	1 GAST_CHIBR	P10034 chinchilla
40	40	75.5	110	1 28SI_BRANA	P24565 brassica na
41	40	75.5	129	2 Q7XKD8_ORYSA	Q7xkd8 oryza sativ
42	40	75.5	268	2 P81394_ANTMA	P81394 antirrhinum
43	40	75.5	269	2 Q8C5S5_MOUSE	Q8c5s5 mus musculu
44	40	75.5	310	2 Q9FJP2_ARATH	Q9fjp2 arabidopsis
45	40	75.5	311	2 Q4IRA3_GIBZE	Q4ira3 gibberella
46	40	75.5	311	2 Q8VE83_MOUSE	Q8ve83 mus musculu
47	40	75.5	311	2 Q9COD5_MOUSE	Q9cgd5 m mus muscu
48	40	75.5	316	2 Q4LGN3_9BURK	Q4lgn3 burkholderi
49	40	75.5	319	2 Q8CCQ4_MOUSE	Q8ccq4 mus musculu
50	40	75.5	349	2 Q9SPG8_ARATH	Q9spg8 arabidopsis
51	40	75.5	360	2 Q8GWP0_ARATH	Q8gwp0 arabidopsis
52	40	75.5	423	2 Q52IQ5_CHICK	Q52iq5 gallus gall
53	40	75.5	423	2 Q55PP9_CRYNE	Q55pp9 cryptococcu
54	40	75.5	423	2 Q5KDQ8_CRYNE	Q5kdq9 cryptococcu
55	40	75.5	527	2 Q4ZSF0_PSESY	Q4zsf0 pseudomonas
56	40	75.5	527	2 Q880Y9_PSESM	Q880y9 pseudomonas
57	40	75.5	577	2 Q86X18_HUMAN	Q86x18 homo sapien
58	40	75.5	618	2 Q52L14_XENLA	Q52l14 xenopus lae
59	40	75.5	685	2 Q66JB6_XENTR	Q66jb6 xenopus tro
60	40	75.5	745	2 Q23618_ARATH	Q23618 arabidopsis
61	40	75.5	754	2 Q4RX16_TETNG	Q4rx16 tetraodon n
62	40	75.5	834	2 Q8ZT18_PYRAE	Q8zt18 pyrobaculum
63	39	73.6	181	2 Q85065_9BROM	Q85065 peanut stun
64	39	73.6	204	2 Q31205_MOUSE	Q31205 mus musculu
65	39	73.6	298	2 Q5JMA5_ORYSA	Q5jma5 oryza sativ
66	39	73.6	344	2 Q9BCZ1_MOUSE	Q9bcz1 mus musculu
67	39	73.6	377	2 Q8WLM9_MOUSE	Q8wlm9 mus musculu
68	39	73.6	378	2 Q8D611_VIEBV	Q8d611 vibrio vuln
69	39	73.6	378	2 Q7MD30_VIEBV	Q7md30 vibrio vuln
70	39	73.6	379	2 Q31208_MOUSE	Q31208 mus musculu
71	39	73.6	379	2 Q31615_MOUSE	Q31615 mus musculu
72	39	73.6	379	2 Q861Q6_MOUSE	Q861q6 mus musculu
73	39	73.6	406	2 Q31206_MOUSE	Q31206 mus musculu
74	39	73.6	490	2 Q6EQ30_ORYSA	Q6eq30 oryza sativ
75	39	73.6	525	1 LAG3_HUMAN	P18627 homo sapien
76	39	73.6	551	2 Q8GME7_STRGL	Q8gme7 streptomyce
77	39	73.6	561	2 Q56WX1_ARATH	Q56wx1 arabidopsis
78	39	73.6	589	2 Q5W47_9TRYP	Q57w47 trypanosoma
79	39	73.6	618	2 Q5PMP6_SALPA	Q5pmp6 salmonella
80	39	73.6	749	2 Q8T3S1_DROME	Q8t3s1 drosophila
81	39	73.6	816	2 Q9VNV0_DROME	Q9vnv0 drosophila
82	39	73.6	930	1 ATS5_HUMAN	Q9una0 homo sapien
83	39	73.6	930	2 Q521V4_HUMAN	Q521v4 homo sapien
84	39	73.6	960	2 Q22214_ARATH	Q22214 arabidopsis
85	39	73.6	1043	2 Q6AFN4_LEIXX	Q6afn4 leifeonia x
86	39	73.6	1108	2 Q8W4F7_ARATH	Q8w4f7 arabidopsis
87	39	73.6	1474	2 Q4SE63_TETNG	Q4se63 tetraodon n
88	39	73.6	1480	2 Q9GQ04_HUMAN	Q9gq04 homo sapien
89	39	73.6	1753	2 Q87NM8_PSESM	Q87nm8 pseudomonas
90	39	73.6	3384	2 Q4SSG3_TETNG	Q4seg3 tetraodon n
91	38	71.7	85	2 Q4JL84_ARATH	Q4jlr4 arabidopsis
92	38	71.7	120	2 Q5GZH4_XANOR	Q5gzh4 xanthomonas
93	38	71.7	135	2 Q5QT29_ORYSA	Q5qt29 oryza sativ
94	38	71.7	153	2 Q4GSV6_BRARE	Q4gsv6 brachydanio
95	38	71.7	157	2 Q8S416_MAIZE	Q8s416 zea mays (m
96	38	71.7	196	2 Q4G5V4_BRARE	Q4gsv4 brachydanio
97	38	71.7	220	2 Q9FM28_HUMAN	Q9fm28 homo sapien
98	38	71.7	221	2 Q6FEV3_ORYSA	Q6fev3 oryza sativ
99	38	71.7	225	2 Q4TGS1_ORYSA	Q4tgs1 oryza sativ
100	38	71.7	235	2 Q4GSV3_BRARE	Q4gsv3 brachydanio
101	38	71.7	234	2 Q50069_ARATH	Q50069 arabidopsis
102	38	71.7	235	2 Q9FN86_ARATH	Q9fn86 arabidopsis
103	38	71.7	237	2 Q5JNK6_ORYSA	Q5jnk6 oryza sativ
104	38	71.7	242	2 Q4JL76_ORYSA	Q4jl76 oryza sativ

105	38	71.7	242	2	Q5NK12	ORYSA	Q5nk12	oryza sativ	178	37	69.8	305	2	Q7NRM4	CHRYVO	Q7nrm4	chromobacte
106	38	71.7	248	2	Q57K14	SALCH	Q57k14	salmonella	179	37	69.8	307	2	Q84PP3	LOTJA	Q84pp3	lotus japon
107	38	71.7	248	2	Q8ZMF0	SALTY	Q8zmf0	salmonella	180	37	69.8	313	2	Q8PA53	XENLA	Q8pa53	xenopus lae
108	38	71.7	249	2	Q4GSV2	BRARE	Q4gsv2	brachydanio	181	37	69.8	316	1	ERA	CAUCR	P50071	caulobacter
109	38	71.7	256	2	Q94IG1	ARAGE	Q94ig1	arabis gemm	182	37	69.8	336	1	DHYS	PYRFU	Q5jey0	pyrococcus
110	38	71.7	256	2	Q9LX82	ARATH	Q9lx82	arabidopsis	183	37	69.8	337	1	DHYS	PYRKO	Q6mcy6	parachlamyd
111	38	71.7	276	2	Q56UT4	ORYSA	Q56ut4	oryza sativ	184	37	69.8	339	2	Q6MCT6	PARUMI	Q84lp8	boea crassi
112	38	71.7	278	2	P93391	TOBAC	P93391	nicotiana t	185	37	69.8	340	2	Q84LP8	9LAMI	Q708e6	homo sapien
113	38	71.7	284	2	Q72GE7	THET2	Q72ge7	thermus the	186	37	69.8	347	2	Q708B6	HUMAN	Q14025	homo sapien
114	38	71.7	284	2	Q5SM40	THET8	Q5sm40	thermus the	187	37	69.8	348	2	Q14025	HUMAN	Q8msu6	drosofila
115	38	71.7	315	2	Q5SN44	CRYNE	Q5sn44	cryptococcu	188	37	69.8	349	2	Q8MSU6	DROME	Q30896	homo sapien
116	38	71.7	315	2	Q5KBH3	CRYNE	Q5kbh3	cryptococcu	189	37	69.8	350	2	Q708B8	HUMAN	Q30896	pithecia pi
117	38	71.7	317	2	Q5TB66	VIBCH	Q5tb66	vibrio chol	190	37	69.8	355	2	Q30896	PITPI	Q78205	gorilla gor
118	38	71.7	318	2	Q9X5F7	ZYMMO	Q9x5f7	zymomonas m	191	37	69.8	357	1	1A02	GORGO	P30376	gorilla gor
119	38	71.7	325	2	Q9LFEI	ARATH	Q9lfei	arabidopsis	192	37	69.8	365	1	1A03	GORGO	P30377	gorilla gor
120	38	71.7	325	2	Q6R054	ARATH	Q6r054	arabidopsis	193	37	69.8	365	1	1A04	GORGO	Q30178	gorilla gor
121	38	71.7	369	1	Q51LX7	MAGGR	Q51lx7	magnaporthe	194	37	69.8	365	1	1A04	HUMAN	Q95h89	homo sapien
122	38	71.7	369	1	3HSU7	HUMAN	Q9lh2f3	homo sapien	195	37	69.8	365	1	1A80	HUMAN	Q95h89	pan troglod
123	38	71.7	371	2	Q4UV90	XANCP	Q4uv90	xanthomonas	196	37	69.8	365	2	Q95H89	PANTR	Q95h89	pan troglod
124	38	71.7	371	2	Q8P8U1	XANCP	Q8p8u1	xanthomonas	197	37	69.8	365	2	Q95H89	PANTR	Q95h88	pan troglod
125	38	71.7	371	2	Q8PKU8	XANCP	Q8pku8	xanthomonas	198	37	69.8	365	2	Q95H88	PANTR	Q4sn48	arabidopsis
126	38	71.7	378	2	Q9KR60	VIBCH	Q9kr60	vibrio chol	199	37	69.8	367	2	Q04192	ARATH	Q04192	tetraodon n
127	38	71.7	378	2	Q4GSV5	BRARE	Q4gsv5	brachydanio	200	37	69.8	379	2	Q90787	CHICK	P01104	avian myelo
128	38	71.7	432	2	Q7S835	NEUCR	Q7s835	neurospora	201	37	69.8	382	1	MYB	AVIMB	Q88bq6	pseudomonas
129	38	71.7	439	2	Q5CAG7	ORYSA	Q5cag7	oryza sativ	202	37	69.8	388	2	Q88BQ6	PSESM	Q88bq6	pseudomonas
130	38	71.7	499	2	Q5QT31	ORYSA	Q5qt31	oryza sativ	203	37	69.8	388	2	Q88BQ6	PSESM	Q88bq6	pseudomonas
131	38	71.7	507	2	Q883D0	PSESM	Q883d0	pseudomonas	204	37	69.8	394	2	Q5BKU0	XENTR	Q5bk10	xenopus tro
132	38	71.7	529	2	Q9LZ93	ARATH	Q9l293	arabidopsis	205	37	69.8	395	2	Q4SAQ7	TETNG	Q9v0g5	pyrococcus
133	38	71.7	530	2	Q7X9I3	9ROSI	Q7x9i3	populus tre	206	37	69.8	398	2	Q9V0G5	PYRAB	Q9v0g5	pyrococcus
134	38	71.7	548	2	Q94FL8	ARATH	Q94fl8	arabidopsis	207	37	69.8	402	2	Q708B5	HUMAN	Q708b5	homo sapien
135	38	71.7	548	2	Q6R032	ARATH	Q6r032	arabidopsis	208	37	69.8	403	2	Q4WVJ3	ASPFU	Q4wvj3	aspergillus
136	38	71.7	584	2	Q5N9U1	ORYSA	Q5n9u1	oryza sativ	209	37	69.8	436	2	Q8MPH5	OXYTR	Q8mph5	oxytricha t
137	38	71.7	669	2	Q5SGK3	DICDI	Q5sgk3	dicyosteli	210	37	69.8	436	2	Q8MPH7	OXYTR	Q8mph7	oxytricha t
138	38	71.7	704	2	Q7X6U9	ORYSA	Q7x6u9	oryza sativ	211	37	69.8	439	2	Q4NIB9	9NICC	Q4nib9	archobacte
139	38	71.7	818	2	Q4GSV7	BRARE	Q4gsv7	brachydanio	212	37	69.8	439	2	Q8BTV4	MOUSE	Q8btv4	mus musculu
140	38	71.7	894	2	Q60LN1	CAEBR	Q60ln1	caenorhabdi	213	37	69.8	441	2	Q84TW8	ORYSA	Q84tw8	oryza sativ
141	38	71.7	894	2	Q9XVU8	CAEBL	Q9xvu8	caenorhabdi	214	37	69.8	449	2	Q708E3	HUMAN	Q708e3	homo sapien
142	38	71.7	910	2	Q9TXC0	CAEBL	Q9xc0	caenorhabdi	215	37	69.8	455	2	Q4SR32	TETNG	Q4sr32	tetraodon n
143	38	71.7	920	2	Q23158	CAEBL	Q23158	caenorhabdi	216	37	69.8	467	2	Q4T411	TETNG	Q4t411	tetraodon n
144	38	71.7	985	2	Q59773	SCHPO	Q59773	schizosacch	217	37	69.8	525	2	Q4RR94	TETNG	Q4rr94	tetraodon n
145	38	71.7	991	2	Q7RTR0	HUMAN	Q7rtr0	homo sapien	218	37	69.8	528	1	LAD1	MOUSE	P57016	mus musculu
146	38	71.7	1264	2	Q615L7	ORYSA	Q615l7	oryza sativ	219	37	69.8	528	2	Q8R3D5	MOUSE	Q8r3d5	mus musculu
147	38	71.7	1291	2	Q93H21	STRAW	Q93h21	strepcomyce	220	37	69.8	554	2	Q7ZXI0	XENLA	Q7zx10	xenopus lae
148	38	71.7	1406	2	Q35452	MOUSE	Q35452	mus musculu	221	37	69.8	555	2	Q28080	BOVIN	Q28080	bos taurus
149	38	71.7	4114	2	Q54796	MOUSE	Q54796	mus musculu	222	37	69.8	566	2	Q5KSM4	9ACTO	Q5ksm4	strepcomyce
150	37.5	70.8	1054	2	Q5AWH5	EMENI	Q5awh5	aspergillus	223	37	69.8	572	2	Q6C2X4	YARLI	Q6c2x4	yarrowia li
151	37	69.8	75	2	Q8RGW2	FUSNN	Q8rgw2	fusobacteri	224	37	69.8	575	2	Q15693	TOXGO	Q15693	toxoplasma
152	37	69.8	107	2	Q5VNH8	ORYSA	Q5vnh8	oryza sativ	225	37	69.8	590	2	Q76629	ORYLA	Q76629	brachydanio
153	37	69.8	128	2	Q6LC31	MOUSE	Q6lc31	mus musculu	226	37	69.8	592	2	Q76629	ORYLA	Q76629	brachydanio
154	37	69.8	160	2	Q4SY81	TETNG	Q4sy81	tetraodon n	227	37	69.8	593	2	Q61928	MOUSE	Q61928	mus musculu
155	37	69.8	167	2	Q821H7	STRAW	Q821h7	strepcomyce	228	37	69.8	602	2	Q8T079	DROME	Q8t079	drosofila
156	37	69.8	181	2	Q95409	9PRIM	Q95409	gorilla gor	229	37	69.8	612	2	Q708E1	HUMAN	Q708e1	homo sapien
157	37	69.8	189	2	Q29411	ARCHAEOGLOB	Q29411	archaeoglob	230	37	69.8	624	1	MYB	XENLA	Q6drh7	brachydanio
158	37	69.8	191	2	Q7XJ11	QUERO	Q7xj11	quercus rob	231	37	69.8	633	2	Q6DRH7	BRARE	Q6drh7	brachydanio
159	37	69.8	191	2	P97753	9MURI	P97753	mus sp. gag	232	37	69.8	633	2	Q4KMF7	BRARE	Q4kmf7	brachydanio
160	37	69.8	204	2	Q5WHH4	BAGSK	Q5whh4	bacillus cl	233	37	69.8	636	1	MYB	MOUSE	P06876	mus musculu
161	37	69.8	207	2	Q5Z450	ORYSA	Q5z450	oryza sativ	234	37	69.8	637	2	Q708E7	HUMAN	Q708e7	homo sapien
162	37	69.8	215	2	Q5ZM07	CHICK	Q5zm07	gallus gall	235	37	69.8	640	1	MYB	BOVIN	P46200	bos taurus
163	37	69.8	216	2	Q4SQY5	TETNG	Q4sqy5	tetraodon n	236	37	69.8	640	1	MYB	HUMAN	Q708e9	homo sapien
164	37	69.8	220	2	Q5FN08	GLUOX	Q5fn08	gluconobact	237	37	69.8	640	1	MYB	CHICK	P01103	gallus gall
165	37	69.8	222	1	Y686	ARCTU	Q29571	archaeoglob	238	37	69.8	641	1	MYB	CHICK	Q6pba4	brachydanio
166	37	69.8	232	2	Q6PK80	CANGA	Q6fk80	candida gla	239	37	69.8	641	2	Q6PBA4	BRARE	Q6pba4	brachydanio
167	37	69.8	247	2	Q729F4	DESVH	Q729f4	desulfovibr	240	37	69.8	648	2	Q61421	MOUSE	Q61421	mus musculu
168	37	69.8	254	2	Q9LDD3	ADIRA	Q9ldd3	adiantum ra	241	37	69.8	659	2	Q70AC3	HUMAN	Q70ac3	homo sapien
169	37	69.8	267	2	Q5THS6	HUMAN	Q5ths6	homo sapien	242	37	69.8	678	2	Q708J0	HUMAN	Q708j0	homo sapien
170	37	69.8	276	2	Q5THS5	HUMAN	Q5ths5	homo sapien	243	37	69.8	686	1	MYBB	CHICK	Q03237	gallus gall
171	37	69.8	277	2	Q7NPI0	GLOVI	Q7np10	gloeobacter	244	37	69.8	686	2	Q7KNF3	DROME	Q7knf3	drosofila
172	37	69.8	299	2	Q5KV07	GROKA	Q5kv07	geobacillus	245	37	69.8	690	2	Q5THS4	HUMAN	Q5ths4	homo sapien
173	37	69.8	301	1	SEC14	KJULA	P24859	kluyveromyc	246	37	69.8	690	2	Q8IHC2	DROME	Q8ihc2	drosofila
174	37	69.8	301	2	Q9SN12	ARATH	Q9sn12	arabidopsis	247	37	69.8	691	2	Q9V9D1	DROME	Q9v9d1	drosofila
175	37	69.8	303	2	Q82EM3	STRAW	Q82em3	strepcomyce	248	37	69.8	697	2	Q8SR10	ENCCU	Q8sr10	encephalico
176	37	69.8	304	2	Q39155	ARATH	Q39155	arabidopsis	249	37	69.8	700	1	MYBB	HUMAN	P10244	homo sapien
177	37	69.8	304	2	Q49745	ARATH	Q49745	arabidopsis	250	37	69.8	700	2	Q53F07	HUMAN	Q53f07	homo sapien

251	37	69.8	700	2	Q5F3N6_CHICK	Q5f3n6 gallus gall	324	36	67.9	346	2	Q4S2D7_TETNG	Q4s2d7 tetraodon n
252	37	69.8	704	1	MYBB_MOUSE	P48972 mus musculus	325	36	67.9	350	2	Q8LBF0_ARATH	Q8lbf0 arabidopsis
253	37	69.8	715	2	Q619Z6_MOUSE	Q61926 mus musculus	326	36	67.9	350	2	Q9LDR8_ARATH	Q9ldr8 arabidopsis
254	37	69.8	726	2	Q708E2_HUMAN	Q708e2 homo sapien	327	36	67.9	352	2	Q65409_ARATH	Q65409 arabidopsis
255	37	69.8	728	1	BAP1_MOUSE	Q99p37 mus musculus	328	36	67.9	355	1	NUDM_MOUSE	Q99lc3 mus musculus
256	37	69.8	728	1	MYBA_XENLA	Q05935 xenopus lae	329	36	67.9	355	2	Q80WE0_RAT	Q80we0 rattus norv
257	37	69.8	729	1	BAP1_HUMAN	Q92560 homo sapien	330	36	67.9	355	2	Q561S0_RAT	Q561s0 rattus norv
258	37	69.8	743	1	MYBB_XENLA	P52551 xenopus lae	331	36	67.9	358	2	Q31012_SAGFU	Q31012 saginus fu
259	37	69.8	746	2	Q4SFC3_TETNG	Q48fc3 tetraodon n	332	36	67.9	361	2	Q9PD62_ENTFC	Q9fd62 enterococc
260	37	69.8	748	2	Q6NRE6_XENLA	Q6nre6 xenopus lae	333	36	67.9	361	2	Q617A3_MACFA	Q617a3 macaca fasc
261	37	69.8	751	1	MYBA_MOUSE	P51960 mus musculus	334	36	67.9	365	2	Q64QT9_BACFR	Q64qt9 bacteroides
262	37	69.8	752	1	MYBA_HUMAN	P10243 homo sapien	335	36	67.9	378	2	Q5LAF3_BACFR	Q5laf3 bacteroides
263	37	69.8	752	2	Q8BU17_MOUSE	Q8bu17 mus musculus	336	36	67.9	379	2	Q42575_ARATH	Q42575 arabidopsis
264	37	69.8	757	1	MYBA_CHICK	P52550 gallus gall	337	36	67.9	439	2	Q7QAT3_ANOGA	Q7qat3 anopheles g
265	37	69.8	759	2	Q4VBE3_XENTR	Q4vbe3 xenopus tro	338	36	67.9	443	2	Q5NZF4_AZOSE	Q5nzf4 azoarcus sp
266	37	69.8	761	2	Q708E4_HUMAN	Q708e4 homo sapien	339	36	67.9	496	2	Q9SR26_ARATH	Q9sr26 arabidopsis
267	37	69.8	814	2	Q4WN48_ASPPU	Q4wn48 aspergillus	340	36	67.9	505	2	Q9ACC4_ARATH	Q9acc4 arabidopsis
268	37	69.8	827	2	Q8BHX2_MOUSE	Q8bhx2 mus musculus	341	36	67.9	505	2	Q9M655_ARATH	Q9m652 arabidopsis
269	37	69.8	827	2	Q54HP1_DICDI	Q54hp1 dictyosteli	342	36	67.9	506	2	Q8H1P9_ARATH	Q8h1p9 arabidopsis
270	37	69.8	909	2	Q9LYE0_ARATH	Q9lye0 arabidopsis	343	36	67.9	520	2	Q6CCC4_YARLI	Q6ccc4 yarrowia li
271	37	69.8	952	2	Q94FL9_ARATH	Q94fl9 arabidopsis	344	36	67.9	530	2	Q922Q2_MOUSE	Q922q2 mus musculu
272	37	69.8	961	2	Q6CJC3_KJULA	Q6cjc3 kluyveromyc	345	36	67.9	535	2	Q92VK0_RHIME	Q92vk0 rhizobium m
273	37	69.8	1133	2	Q67M84_SYMT	Q67m84 symbiobacte	346	36	67.9	544	2	Q94382_SCHPO	Q94382 schizosacch
274	37	69.8	1401	2	Q5KJY6_MOUSE	Q5kjiy6 mus musculus	347	36	67.9	570	2	Q41IB5_GIBZE	Q41ib5 gibberella
275	37	69.8	1424	2	Q5KJY6_MOUSE	Q5kjiy6 mus musculus	348	36	67.9	588	2	Q948S4_TOBAC	Q948s4 nicotiana t
276	37	69.8	1424	2	Q7TNC6_MOUSE	Q7tnc6 mus musculus	349	36	67.9	607	2	Q9MAN8_ARATH	Q9man8 arabidopsis
277	37	69.8	1550	2	Q886T4_PSESM	Q886t4 pseudomonas	350	36	67.9	636	2	Q6NUI8_HUMAN	Q6nui8 homo sapien
278	37	69.8	1984	2	Q886T4_PSESM	Q886t4 pseudomonas	351	36	67.9	637	2	Q5WS85_LEGPL	Q5ws85 legionella
279	37	69.8	42	2	Q9LE12_9TRAC	Q9le12 equisetum s	352	36	67.9	637	2	Q5X0Z9_LEGPA	Q5x0z9 legionella
280	37	69.8	42	2	Q9LE80_ADIRA	Q9le80 adiantum ra	353	36	67.9	637	2	Q5X0Z9_LEGPA	Q5x0z9 legionella
281	37	69.8	42	2	Q9LE87_MARPO	Q9le87 marchantia	354	36	67.9	646	1	TERM_ADE40	Q52rj3 legionella
282	37	69.8	42	2	Q9LE84_ADIRA	Q9le84 adiantum ra	355	36	67.9	666	2	Q95XG8_CAEEL	Q95xg8 human adeno
283	37	69.8	42	2	Q9LE27_9TRAC	Q9le27 lycopodium	356	36	67.9	666	2	Q95XG8_CAEEL	Q95xg8 caenorhabdi
284	37	69.8	91	2	Q9LE26_PSIINU	Q9le26 psirotum nu	357	36	67.9	679	2	Q9C2N1_NEUCR	Q9c2n1 neurospora
285	37	69.8	96	1	Q9LE26_PSIINU	Q9le26 psirotum nu	358	36	67.9	680	2	Q9CD84_MYCLE	Q9cd84 mycobacteri
286	37	69.8	99	2	Q6ZF12_ORYSA	Q6zfi2 oryza sativ	359	36	67.9	683	1	ZN510_HUMAN	Q9y2h8 homo sapien
287	37	69.8	99	1	PER3_PLEBO	P46036 plectonema	360	36	67.9	683	2	Q6BYR0_DEBHA	Q6byr0 debaryomyce
288	37	69.8	99	1	RRP3_GUITH	Q91e88 secale cere	361	36	67.9	683	2	Q5SZP5_HUMAN	Q5szp5 homo sapien
289	37	69.8	111	2	Q9H3I5_HUMAN	Q9h3i5 homo sapien	362	36	67.9	691	2	Q5KFT1_CRYNE	Q5kft1 cryptococcu
290	37	69.8	134	2	Q5SZP4_HUMAN	Q5szp4 homo sapien	363	36	67.9	691	2	Q8VY21_ARATH	Q8vy21 arabidopsis
291	37	69.8	135	2	Q6FSL6_CANGA	Q6fsl6 candida gla	364	36	67.9	694	2	Q5SQD6_CRYNE	Q5sqd6 cryptococcu
292	37	69.8	138	2	Q9H4Z7_HUMAN	Q9h4z7 homo sapien	365	36	67.9	715	2	Q6S528_ARATH	Q6s528 arabidopsis
293	37	69.8	178	2	Q5JRK3_HUMAN	Q5jrk3 homo sapien	366	36	67.9	735	2	Q5B638_EMENI	Q5b638 aspergillus
294	37	69.8	179	2	Q5E7X1_VIBP1	Q5e7x1 vibrio fisc	367	36	67.9	762	2	Q4WJ47_ASPPU	Q4w47 aspergillus
295	37	69.8	181	2	Q63RT7_BURPS	Q63rt7 burkholderi	368	36	67.9	776	2	Q9S7G7_ARATH	Q9s7g7 arabidopsis
296	37	69.8	185	2	Q32435_BACSU	Q32435 bacillus su	369	36	67.9	810	1	ZN33A_HUMAN	Q06730 homo sapien
297	37	69.8	189	1	Y2536_VIBCH	Q9kp43 vibrio chol	370	36	67.9	812	2	Q5VZ86_HUMAN	Q5vz86 homo sapien
298	37	69.8	197	2	Q9LE47_HORVU	Q9le47 hordeum vul	371	36	67.9	821	1	EBN3_EBV	P12977 epstein-bar
299	37	69.8	203	2	Q9HXG2_PSEAE	Q9hxg2 pseudomonas	372	36	67.9	834	1	ZNFA1_HUMAN	P51814 homo sapien
300	37	69.8	204	2	Q5AT17_EMENI	Q5at17 aspergillus	373	36	67.9	865	2	V2A_PSVJ	P28727 peanut stun
301	37	69.8	226	1	YODN_BACSU	Q34414 bacillus su	374	36	67.9	865	2	Q723C9_HUMAN	Q723c9 homo sapien
302	37	69.8	226	2	Q65IE3_BACLD	Q65ie3 bacillus su	375	36	67.9	869	2	Q8NB57_HUMAN	Q8nb57 homo sapien
303	37	69.8	241	2	Q5F4Y3_NEIG1	Q5f4y3 neisseria g	376	36	67.9	907	2	Q69021_HUMAN	Q69021 human harpe
304	37	69.8	241	2	Q9JW64_NEIMA	Q9jw64 neisseria m	377	36	67.9	921	2	Q6CFI8_YARLI	Q6cfi8 yarrowia li
305	37	69.8	241	2	Q9JX08_NEIMB	Q9jx08 neisseria m	378	36	67.9	925	2	Q69138_9GAMA	Q69138 human herpe
306	37	69.8	250	2	Q5QT30_ORYSA	Q5qt30 oryza sativ	379	36	67.9	944	2	Q8AZJ8_9GAMA	Q8azj8 human herpe
307	37	69.8	253	2	Q7U4A8_SYNFX	Q7u4a8 synechococc	380	36	67.9	958	2	Q5N7Y8_ORYSA	Q5n7y8 oryza sativ
308	37	69.8	273	2	Q6P6W6_RAT	Q6p6w6 rattus norv	381	36	67.9	972	2	Q8ND50_HUMAN	Q8nd50 homo sapien
309	37	69.8	278	2	Q4ZY96_PSESY	Q4zy96 pseudomonas	382	36	67.9	982	2	Q8B0T1_9REOV	Q8b0t1 epizootic h
310	37	69.8	285	2	Q82A78_STRAW	Q82a78 streptomyce	383	36	67.9	982	2	Q8B0T4_9REOV	Q8b0t4 epizootic h
311	37	69.8	307	2	Q82FJ8_STRAW	Q82fj8 streptomyce	384	36	67.9	982	2	Q8B0T7_9REOV	Q8b0t7 epizootic h
312	37	69.8	314	2	Q00658_EMENI	Q00658 emeritella	385	36	67.9	982	2	Q8B0U1_9REOV	Q8b0u1 epizootic h
313	37	69.8	314	2	Q5BG01_EMENI	Q5bg01 aspergillus	386	36	67.9	994	2	Q53EL9_HUMAN	Q53el9 homo sapien
314	37	69.8	314	2	Q4WK99_ASPPU	Q4wk99 aspergillus	387	36	67.9	994	2	Q5QT32_ORYSA	Q5qt32 oryza sativ
315	37	69.8	315	2	Q860F6_MACNE	Q860f6 macaca neme	388	36	67.9	1042	2	Q948S5_TOBAC	Q948s5 nicotiana t
316	37	69.8	315	2	Q860F6_MACNE	Q860f6 macaca neme	389	36	67.9	1106	2	Q6XDB6_RAT	Q6xdb6 rattus norv
317	37	69.8	317	2	Q752K6_ASHGO	Q752k6 ashbya goss	390	36	67.9	1344	2	Q4QDT8_LEIMA	Q4qdt8 leishmania
318	37	69.8	317	2	Q75LP7_ORYSA	Q75lp7 oryza sativ	391	36	67.9	1421	2	Q84ZR6_ORYSA	Q84zr6 oryza sativ
319	37	69.8	319	2	Q98Z13_RHIVI	Q98z13 human immun	392	36	67.9	1513	2	Q5LFX2_SILPO	Q5lfx2 silicibacte
320	37	69.8	320	2	Q8A6K8_BACTN	Q8a6k8 bacteroides	393	36	67.9	1568	2	Q95785_HUMAN	Q95785 homo sapien
321	37	69.8	330	2	Q52038_HALSA	Q52038 halobacteri	394	36	67.9	3391	2	Q9WDA2_9FLAV	Q9wda2 dengue viru
322	37	69.8	331	2	O82281_ARATH	O82281 arabidopsis	395	36	67.9	3391	2	Q9WDA4_9FLAV	Q9wda4 dengue viru
323	37	69.8	331	2	O8LAY6_ARATH	O8lay6 arabidopsis							
324	37	69.8	333	2	O6NK64_CORDI	O6nk64 corynebacte							
325	37	69.8	338	2	Q6F2D7_SOLDE	Q6f2d7 solanum dem							

397	35.5	67.0	285	2	Q92XC9_RHIME	Q92xc9 rhizobium m	470	35	66.0	269	2	Q6QAD8_ARATH	Q6qad8 arabidopsis
398	35.5	67.0	286	2	Q6W2G0_RHISN	Q6w2g0 rhizobium s	471	35	66.0	272	2	Q9XIUS_SOYBN	Q9xius glycine max
399	35	66.0	49	2	Q42024_ARATH	Q42024 arabidopsis	472	35	66.0	273	2	Q94IF7_ARATH	Q94if7 arabidopsis
400	35	66.0	63	2	Q8S436_SORBI	Q8s436 sorghum bic	473	35	66.0	274	2	Q40173_LYCES	Q40173 lycopersico
401	35	66.0	63	2	Q8S434_SORBI	Q8s434 sorghum bic	474	35	66.0	274	2	Q92AF3_LISIN	Q92af3 listeria in
402	35	66.0	63	2	Q8S435_SORBI	Q8s435 sorghum bic	475	35	66.0	275	2	Q9XIUS_SOYBN	Q9xius glycine max
403	35	66.0	64	2	Q8S439_SORBI	Q8s439 sorghum bic	476	35	66.0	277	2	Q9SLT1_TOBAC	Q9slt1 nicotiana t
404	35	66.0	64	2	Q8S437_SORBI	Q8s437 sorghum bic	477	35	66.0	277	2	Q7V7S8_PROMM	Q7v7s8 prochloroco
405	35	66.0	83	2	Q628J2_ORYSA	Q628j2 oryza sativ	478	35	66.0	278	2	Q497S9_ARATH	Q497s9 arabidopsis
406	35	66.0	84	2	Q63QV4_BURPDI	Q63qv4 burkholderi	479	35	66.0	279	2	Q04110_ORYSA	Q04110 oryza sativ
407	35	66.0	87	2	Q8S443_SORBI	Q8s443 sorghum bic	480	35	66.0	279	2	Q6ES55_ORYSA	Q6es55 oryza sativ
408	35	66.0	87	2	Q8S445_SORBI	Q8s445 sorghum bic	481	35	66.0	280	2	Q8S629_ORYSA	Q8s629 oryza sativ
409	35	66.0	87	2	Q8S419_ORYSA	Q8s419 oryza sativ	482	35	66.0	280	2	Q9SBG0_ARATH	Q9sbg0 arabidopsis
410	35	66.0	87	2	Q8S428_ORYSA	Q8s428 oryza sativ	483	35	66.0	280	2	Q02993_PTHY	Q02993 petunia hyb
411	35	66.0	87	2	Q8S433_SORBI	Q8s433 sorghum bic	484	35	66.0	280	2	Q8GYE5_ARATH	Q8gye5 arabidopsis
412	35	66.0	88	2	Q8S423_ORYSA	Q8s423 oryza sativ	485	35	66.0	281	2	Q9SLT0_TOBAC	Q9slt0 nicotiana t
413	35	66.0	88	2	Q8S430_ORYSA	Q8s430 oryza sativ	486	35	66.0	281	2	Q9SLT7_TOBAC	Q9slt7 nicotiana t
414	35	66.0	110	2	Q69QB1_ORYSA	Q69qb1 oryza sativ	487	35	66.0	282	2	Q9C7U7_ARATH	Q9c7u7 arabidopsis
415	35	66.0	114	2	Q8RXA1_ORYSA	Q8rxa1 oryza sativ	488	35	66.0	282	2	Q9M0J5_ARATH	Q9m0j5 arabidopsis
416	35	66.0	117	2	Q83JQ0_ENTFA	Q83jq0 enterococu	489	35	66.0	286	2	Q4N714_THEPA	Q4n714 theileria p
417	35	66.0	136	2	Q62D26_ORYSA	Q62d26 oryza sativ	490	35	66.0	286	2	Q9SPG1_ARATH	Q9spg1 arabidopsis
418	35	66.0	136	2	Q92986_ARATH	Q92986 arabidopsis	491	35	66.0	286	2	Q6R075_ARATH	Q6r075 arabidopsis
419	35	66.0	146	2	Q67UQ5_ORYSA	Q67uq5 oryza sativ	492	35	66.0	287	2	Q9FRQ8_ARATH	Q9frq8 arabidopsis
420	35	66.0	147	2	Q6F2C8_SOLDE	Q6f2c8 solanum dem	493	35	66.0	288	2	Q5ATK3_EMENI	Q5atk3 aspergillus
421	35	66.0	147	2	Q5SK03_THET8	Q5sk03 thermus the	494	35	66.0	292	2	Q82WT4_NITEU	Q82wt4 nitrosomona
422	35	66.0	147	2	Q72K65_THET2	Q72k65 thermus the	495	35	66.0	294	1	Q0O1_PETHY	Q0oex6 petunia hyb
423	35	66.0	150	2	Q8S325_ORYSA	Q8s325 oryza sativ	496	35	66.0	294	2	Q9E855_BRAJA	Q9e855 bradyrhizob
424	35	66.0	152	2	Q8S400_ORYSA	Q8s400 oryza sativ	497	35	66.0	295	2	Q609Q0_METCA	Q609q0 methylococc
425	35	66.0	152	2	Q7X8X3_ORYSA	Q7x8x3 oryza sativ	498	35	66.0	296	2	Q5M832_RAT	Q5m832 rattus norv
426	35	66.0	157	2	Q6QD72_NICBE	Q6qd72 nicotiana b	499	35	66.0	299	2	Q9HHH0_HALSA	Q9hhh0 halobacteri
427	35	66.0	158	1	ATLE_AGRAE	Q6wy08 agrocycbe ae	500	35	66.0	299	2	Q9M2D9_ARATH	Q9m2d9 arabidopsis
428	35	66.0	158	2	Q8DEJ5_VIBVU	Q8dej5 vibrio vuln	501	35	66.0	300	2	Q6H7S0_ORYSA	Q6h7s0 oryza sativ
429	35	66.0	158	2	Q7MNV5_VIBVY	Q7mnv5 vibrio vuln	502	35	66.0	300	2	Q9KY91_STRCO	Q9ky91 streptomyce
430	35	66.0	159	2	Q8S401_ORYSA	Q8s401 oryza sativ	503	35	66.0	301	2	Q82IA7_STRAW	Q82ia7 streptomyce
431	35	66.0	162	2	Q8S327_ORYSA	Q8s327 oryza sativ	504	35	66.0	307	2	Q9W389_ORYSA	Q9w389 oryza sativ
432	35	66.0	165	2	Q7VPH7_GALSE	Q7vph7 galago sene	505	35	66.0	309	2	Q9H0P2_ORYSA	Q9h0p2 oryza sativ
433	35	66.0	167	2	Q6EP51_ORYSA	Q6ep51 oryza sativ	506	35	66.0	309	2	Q9ATD4_GOSHI	Q9atd4 gossypium h
434	35	66.0	177	2	Q7YPK1_AOTVO	Q7ypk1 aotus vocif	507	35	66.0	309	2	Q84N19_ORYSA	Q84n19 oryza sativ
435	35	66.0	184	2	Q8S3Y8_SORBI	Q8s3y8 sorghum bic	508	35	66.0	310	1	TRXB_RICCN	Q92102 rickettsia
436	35	66.0	191	2	Q9L9J6_BRAJA	Q9l9j6 bradyrhizob	509	35	66.0	310	1	TRXB_RICPR	Q9rd97 rickettsia
437	35	66.0	198	2	Q8VDX0_MOUSE	Q8vdx0 mus musculu	510	35	66.0	310	2	Q7PBX6_RICSI	Q7pbx6 rickettsia
438	35	66.0	204	2	Q8S3Y5_SORBI	Q8s3y5 sorghum bic	511	35	66.0	310	2	Q4ULP1_RICFE	Q4ulp1 rickettsia
439	35	66.0	204	2	Q8S3Y1_ORYSA	Q8s3y1 oryza sativ	512	35	66.0	310	2	Q68WT3_RICTY	Q68wt3 rickettsia
440	35	66.0	204	2	Q8S3Y2_ORYSA	Q8s3y2 oryza sativ	513	35	66.0	311	2	Q04109_ORYSA	Q04109 oryza sativ
441	35	66.0	206	2	Q5G361_9HIV1	Q5g361 human immun	514	35	66.0	311	2	P81392_ANTMA	P81392 antirrhinum
442	35	66.0	208	2	Q8SU10_ENCCU	Q8su10 encephalito	515	35	66.0	316	2	Q6F260_BARQU	Q6f260 bartonella
443	35	66.0	208	2	Q621Y5_ORYSA	Q621y5 oryza sativ	516	35	66.0	317	2	Q6G2N0_BARHE	Q6g2n0 bacillus ha
444	35	66.0	208	2	Q8S402_ORYSA	Q8s402 oryza sativ	517	35	66.0	317	2	Q9KEH0_BACHD	Q9keh0 bacillus ha
445	35	66.0	210	2	Q52VK7_9HIV1	Q52vk7 human immun	518	35	66.0	318	2	Q5Z637_ORYSA	Q5z637 oryza sativ
446	35	66.0	212	2	Q8S3Y4_ORYSA	Q8s3y4 oryza sativ	519	35	66.0	319	2	Q6R043_ARATH	Q6r043 arabidopsis
447	35	66.0	213	2	Q91041_9HIV1	Q91041 human immun	520	35	66.0	319	2	Q9SPG6_ARATH	Q9spg6 arabidopsis
448	35	66.0	215	2	Q94721_SCHPO	Q94721 schizosacch	521	35	66.0	319	2	Q9PMK1_ORYSA	Q9pmk1 oryza sativ
449	35	66.0	218	1	UNG_FOWPV	P21968 fowlpox vir	522	35	66.0	321	2	Q69M01_ORYSA	Q69m01 oryza sativ
450	35	66.0	218	2	Q70H89_FOWPV	P21968 fowlpox vir	523	35	66.0	321	2	Q9LDI5_ARATH	Q9ldi5 arabidopsis
451	35	66.0	223	2	Q9RNZ6_ZYMMO	Q9rnz6 zymomonas m	524	35	66.0	321	2	Q6N2H5_RHOPA	Q6n2h5 rhodopseudo
452	35	66.0	228	2	Q6AEL8_LEIXX	Q6ael8 leifsonia x	525	35	66.0	321	2	Q9NDO9_BRAJA	Q9ndq9 bradyrhizob
453	35	66.0	230	2	Q67231_AQUAE	Q67231 aquifex aeo	526	35	66.0	322	2	Q67VZ4_ORYSA	Q67vz4 oryza sativ
454	35	66.0	233	2	Q62WF3_HUMAN	Q62wf3 homo sapien	527	35	66.0	323	2	Q9SBG3_ARATH	Q9sbg3 arabidopsis
455	35	66.0	238	2	Q8TMG2_METAC	Q8tmg2 methanosarc	528	35	66.0	323	2	Q8LBF8_ARATH	Q8lbf8 arabidopsis
456	35	66.0	239	2	Q8PS81_METMA	Q8ps81 methanosarc	529	35	66.0	324	2	Q9SCU7_ARATH	Q9scu7 arabidopsis
457	35	66.0	248	2	Q84L54_ANTAD	Q84l54 anthurium a	530	35	66.0	324	2	Q6R077_ARATH	Q6r077 arabidopsis
458	35	66.0	257	1	LIIVG_ARCFU	Q28981 archaeoglob	531	35	66.0	324	2	Q9M0Y5_ARATH	Q9m0y5 arabidopsis
459	35	66.0	257	1	MYB4_ORYSA	Q7xbh4 oryza sativ	532	35	66.0	324	2	Q5FUM1_GLUOX	Q5fum1 gluconobact
460	35	66.0	258	2	Q4NFZ0_9MITCC	Q4nfz0 arthrobacte	533	35	66.0	324	2	Q98IS9_RHILO	Q98is9 rhizobium l
461	35	66.0	261	2	Q7BYE9_ORYSA	Q7bye9 oryza sativ	534	35	66.0	326	2	Q9LXFI_ARATH	Q9lxfi arabidopsis
462	35	66.0	261	2	Q6R074_ARATH	Q6r074 arabidopsis	535	35	66.0	329	2	Q4TM41_98PHN	Q4tm41 erythrobact
463	35	66.0	261	2	Q9T0G9_ARATH	Q9t0g9 arabidopsis	536	35	66.0	330	2	Q9CA52_ARATH	Q9ca52 arabidopsis
464	35	66.0	261	2	Q8D600_BRAJA	Q8d600 bradyrhizob	537	35	66.0	332	2	Q42467_ARATH	Q42467 arabidopsis
465	35	66.0	264	2	Q8TWN0_METMA	Q8twn0 mechanopyru	538	35	66.0	332	2	Q6W175_RHISN	Q6w175 rhizobium s
466	35	66.0	264	2	Q9XIUS_SOYBN	Q9xius glycine max	539	35	66.0	333	2	Q9SN78_ARATH	Q9sn78 arabidopsis
467	35	66.0	264	2	Q9S7E3_SOYBN	Q9s7e3 glycine max	540	35	66.0	335	2	Q9ZTC1_ARATH	Q9ztc1 arabidopsis
468	35	66.0	267	2	Q652E6_ORYSA	Q652e6 oryza sativ	541	35	66.0	336	2	Q84PP4_LOTJA	Q84pp4 lotus japon
469	35	66.0	269	2	Q9LK14_ARATH	Q9lk14 arabidopsis	542	35	66.0	337	2	Q5TTF9_ANOGA	Q5ttf9 anopheles g

543	35	66.0	340	2	Q6V0J2_PINTA	Q6v0j2 pinus taeda	616	35	66.0	506	2	Q9KBL6_BACHD	Q9kbl6 bacillus ha
544	35	66.0	341	2	Q7E198_ORYSA	Q7e198 oryza sativ	617	35	66.0	507	2	Q9LSJ3_ARATH	Q9lsj3 arabidopsis
545	35	66.0	342	2	Q8TUV9_METKA	Q8tuv9 methanopyru	618	35	66.0	509	2	Q9AN21_BRAJA	Q9an21 bradyrhizob
546	35	66.0	343	1	NUDM_BOVIN	P34942 bos taurus	619	35	66.0	517	2	Q96GD8_HUMAN	Q96gd8 homo sapien
547	35	66.0	343	2	Q92RY6_ARATH	Q92ry6 arabidopsis	620	35	66.0	517	2	Q61PJ9_HUMAN	Q61pj9 homo sapien
548	35	66.0	343	2	Q84PP2_SOYBN	Q84pp2 glycine max	621	35	66.0	517	2	Q5RE20_PONPY	Q5re20 pongo pygma
549	35	66.0	345	2	Q7XUV5_ORYSA	Q7xuv5 oryza sativ	622	35	66.0	518	2	Q669T2_HUMAN	Q669t2 homo sapien
550	35	66.0	345	2	Q6R098_ARATH	Q6r098 arabidopsis	623	35	66.0	518	2	Q89TH4_BRAJA	Q89th4 bradyrhizob
551	35	66.0	345	2	Q91E63_ARATH	Q91e63 arabidopsis	624	35	66.0	519	2	Q55V69_CRYNE	Q55v69 cryptococcu
552	35	66.0	347	2	Q40175_LYCES	Q40175 lycopersico	625	35	66.0	529	2	Q7D9P8_MYCTU	Q7d9p8 mycobacteri
553	35	66.0	348	2	Q84PP5_LOTJA	Q84pp5 lotus japon	626	35	66.0	529	2	Q06394_MYCTU	Q06394 mycobacteri
554	35	66.0	351	2	Q9SPG0_ARATH	Q9spg0 arabidopsis	627	35	66.0	529	2	Q7U1U6_MYCBO	Q7u1u6 mycobacteri
555	35	66.0	351	2	Q5SKU3_CHICK	Q5sku3 gallus gall	628	35	66.0	530	2	Q63HQ8_HUMAN	Q63hq8 homo sapien
556	35	66.0	352	2	Q6R036_ARATH	Q6r036 arabidopsis	629	35	66.0	530	2	Q8NA64_HUMAN	Q8na64 ustilago ma
557	35	66.0	352	2	Q5PXA4_ANTMA	Q5pxa4 antirrhinum	630	35	66.0	547	2	Q4PB73_USTMA	Q4pb73 bacillus sp
558	35	66.0	357	2	Q6ZDR4_ORYSA	Q6zdr4 oryza sativ	631	35	66.0	552	2	Q8RR56_9BACI	Q8rr56 bacillus sp
559	35	66.0	357	2	Q8GUAI_ORYSA	Q8guai oryza sativ	632	35	66.0	552	2	Q8GRP8_LEIMA	Q8grp8 leishmania
560	35	66.0	364	2	Q6QXB7_9CAUD	Q6qxb7 clostridium	633	35	66.0	562	2	Q75GX3_ORYSA	Q75gx3 oryza sativ
561	35	66.0	365	2	Q9S9Z2_ARATH	Q9s9z2 arabidopsis	634	35	66.0	569	2	Q5FYB1_HUMAN	Q5fyb1 homo sapien
562	35	66.0	367	2	Q84U53_9ASPA	Q84u53 dendrobium	635	35	66.0	569	2	Q4NC86_9MICC	Q4nc86 arthrobacte
563	35	66.0	368	2	Q04141_ORYSA	Q04141 oryza sativ	636	35	66.0	576	2	Q9BRG2_HUMAN	Q9brg2 homo sapien
564	35	66.0	368	2	Q6Z414_ORYSA	Q6z414 oryza sativ	637	35	66.0	576	2	Q9Y2X4_HUMAN	Q9y2x4 homo sapien
565	35	66.0	368	2	Q50141_9VIRU	Q50141 acidianus r	638	35	66.0	580	2	Q5RGE9_BRARE	Q5rge9 brachydanio
566	35	66.0	372	2	Q4WHR4_ASPPU	Q4whr4 aspergillus	639	35	66.0	583	2	Q8MSN6_DROME	Q8msn6 drosophila
567	35	66.0	375	2	Q5B311_EMENI	Q5b311 aspergillus	640	35	66.0	583	2	Q9VUC9_DROME	Q9vuc9 drosophila
568	35	66.0	376	2	Q9GJ00_MACFA	Q9gjo0 macaca fasc	641	35	66.0	617	2	Q5R9R8_PONPY	Q5r9r8 pongo pygma
569	35	66.0	377	2	Q6N060_HUMAN	Q6n060 homo sapien	642	35	66.0	627	2	Q74489_SINY3	Q74489 synchocyst
570	35	66.0	377	2	Q6Z699_ORYSA	Q6z699 oryza sativ	643	35	66.0	635	2	Q6DG03_BRARE	Q6dg03 brachydanio
571	35	66.0	377	2	Q7VDZ1_PROMA	Q7vdz1 prochloroco	644	35	66.0	646	2	Q6FGJ5_CANGA	Q6fgj5 candida gla
572	35	66.0	377	2	Q8CIY2_MOUSE	Q8ciy2 mus musculu	645	35	66.0	652	2	Q8DG22_VIBVU	Q8dg22 vibrio vuln
573	35	66.0	382	2	Q04488_ARATH	Q04488 arabidopsis	646	35	66.0	652	2	Q7MMH2_VIBVU	Q7mmh2 vibrio vuln
574	35	66.0	387	1	PATB_BACSU	Q08432 bacillus eu	647	35	66.0	681	2	Q4SLS5_TETNG	Q4sls5 tetraodon n
575	35	66.0	389	1	ZFY119_MOUSE	Q9daz9 mus musculu	648	35	66.0	686	2	Q5MCW4_HUMAN	Q5mcw4 homo sapien
576	35	66.0	389	2	Q4WXW6_ASPPU	Q4wxw6 aspergillus	649	35	66.0	689	2	O01719_STRPU	O01719 strongyloce
577	35	66.0	395	2	Q582R5_9TRYP	Q582r5 trypanosoma	650	35	66.0	690	2	Q711N7_FASHE	Q711n7 fasciola he
578	35	66.0	395	2	Q99BH4_9PABN	Q99bh4 newcastle d	651	35	66.0	712	2	Q895W0_CLOTE	Q895w0 clostridum
579	35	66.0	396	2	Q6T2Z6_SOYBN	Q6t2z6 glycine max	652	35	66.0	712	2	Q4UIJ5_THEAN	Q4uij5 theileria a
580	35	66.0	397	2	Q7LYW0_THELI	Q7lyw0 thermococu	653	35	66.0	714	2	Q8V7G0_9VIRU	Q8v7g0 torque teno
581	35	66.0	397	2	Q9HHD3_9EURY	Q9hd3 thermococu	654	35	66.0	745	2	Q6GNF6_XENLA	Q6gnf6 xenopus lae
582	35	66.0	400	2	Q5Z3P9_MAGGR	Q5z3p9 magnaporthe	655	35	66.0	760	2	Q61S13_HUMAN	Q61s13 homo sapien
583	35	66.0	400	2	Q4H8Y7_9DETO	Q4h8y7 deinococcus	656	35	66.0	760	2	Q9Y222_HUMAN	Q9y222 homo sapien
584	35	66.0	400	2	Q5XG07_XENLA	Q5xg07 xenopus lae	657	35	66.0	761	2	P70413_MOUSE	P70413 mus musculu
585	35	66.0	401	2	Q59044_PYRHO	Q59044 pyrococcus	658	35	66.0	776	2	Q8CE22_MOUSE	Q8ce22 mus musculu
586	35	66.0	408	1	ASSY_METKA	Q60x7 methylococc	659	35	66.0	776	2	Q9LDX5_ARATH	Q9ldx5 arabidopsis
587	35	66.0	410	2	Q80VR8_MOUSE	Q80vr8 mus musculu	660	35	66.0	790	2	Q96M89_HUMAN	Q96m89 homo sapien
588	35	66.0	411	2	Q6AYC3_RAT	Q6ayc3 rattus norv	661	35	66.0	792	2	Q67LX9_SYTH	Q67lx9 symbiobacte
589	35	66.0	411	2	Q6P8K5_MOUSE	Q6p8k5 mus musculu	662	35	66.0	803	2	Q17493_CABEL	Q17493 caenorhabdi
590	35	66.0	414	2	Q4Q495_LEIMA	Q4q495 leishmania	663	35	66.0	810	2	Q9ZCG4_RICPR	Q9zcg4 rickettsia
591	35	66.0	415	2	Q89045_RAT	Q89045 rattus norv	664	35	66.0	829	2	Q9MAX2_9ROSI	Q9max2 croton subl
592	35	66.0	417	1	PR11_MOUSE	P20664 mus musculu	665	35	66.0	859	2	Q5XH98_XENTR	Q5xh98 xenopus tro
593	35	66.0	417	2	Q4WB58_ASPPU	Q4wb58 aspergillus	666	35	66.0	887	2	Q6VTJ3_XENLA	Q6vtj3 xenopus lae
594	35	66.0	417	2	Q5FW94_MOUSE	Q5fw94 m dna prima	667	35	66.0	893	2	Q9H0L3_HUMAN	Q9h0l3 homo sapien
595	35	66.0	420	1	PR11_HUMAN	P49642 homo sapien	668	35	66.0	893	2	Q8IYMO_HUMAN	Q8iym0 homo sapien
596	35	66.0	420	2	Q53F98_HUMAN	Q53f98 homo sapien	669	35	66.0	952	2	Q84UP7_ORYSA	Q84up7 oryza sativ
597	35	66.0	421	1	MYB2_PHYPA	P80073 physcomitre	670	35	66.0	970	2	Q51YM6_MAGGR	Q51ym6 magnaporthe
598	35	66.0	421	2	Q02952_PETHY	Q02952 petunia hyb	671	35	66.0	1016	2	Q7ULE2_RHOBA	Q7ule2 rhodospirell
599	35	66.0	421	2	Q7M984_WOLSU	Q7m984 wolinnella s	672	35	66.0	1043	1	SYI_THET8	SYI thet8
600	35	66.0	426	2	Q4Q153_LEIMA	Q4q153 leishmania	673	35	66.0	1059	1	POL2_DROME	POL2 drome
601	35	66.0	426	2	Q4WJ26_ASPPU	Q4wj26 aspergillus	674	35	66.0	1067	2	Q7ZJR6_THET2	Q7zjr6 thermus the
602	35	66.0	454	2	Q8CA56_MOUSE	Q8ca56 mus musculu	675	35	66.0	1109	2	Q41PR7_GIBZE	Q41pr7 gibbrella
603	35	66.0	455	2	Q51P63_ENTHI	Q51p63 entamoeba h	676	35	66.0	1115	2	Q4IE52_GIBZE	Q4ie52 gibbrella
604	35	66.0	456	2	Q9L215_ARATH	Q9l215 arabidopsis	677	35	66.0	1141	2	Q7RVH6_NEUCR	Q7rvh6 neurospora
605	35	66.0	459	2	Q8YPAB_ANASP	Q8ypab anabaena sp	678	35	66.0	1202	2	Q7V5H6_PROMM	Q7v5h6 prochloroco
606	35	66.0	460	2	Q53JU2_ORYSA	Q53ju2 oryza sativ	679	35	66.0	1239	2	Q55138_SYNG	Q55138 synchocyst
607	35	66.0	461	2	Q9ZRG9_ORYSA	Q9zrg9 oryza sativ	680	35	66.0	1333	2	Q4TCA3_TETNG	Q4tca3 tetraodon n
608	35	66.0	468	2	Q7U7N7_SYNPX	Q7u7n7 synchococc	681	35	66.0	1383	2	Q6C913_YARLI	Q6c913 yarrowia li
609	35	66.0	470	2	Q8C0S0_MOUSE	Q8c0s0 mus musculu	682	35	66.0	1426	2	Q5RE74_PONPY	Q5re74 pongo pygma
610	35	66.0	480	2	Q4WNU5_ASPPU	Q4wnu5 aspergillus	683	35	66.0	1440	1	URPB1_HUMAN	URpb1 homo sapien
611	35	66.0	482	2	Q94FN0_LOTJA	Q94fn0 lotus japon	684	35	66.0	1479	2	Q6Z9Z3_MOUSE	Q6z9z3 mus musculu
612	35	66.0	486	2	Q96S80_HUMAN	Q96s80 homo sapien	685	35	66.0	1509	2	Q8S6P1_ORYSA	Q8s6p1 oryza sativ
613	35	66.0	489	2	Q69LK8_ORYSA	Q69lk8 oryza sativ	686	35	66.0	1510	2	Q570Z6_MOUSE	Q570z6 mus musculu
614	35	66.0	500	2	Q6N950_RHOBA	Q6n950 rhodopseudo	687	35	66.0	1672	2	Q6BSQ2_DEBHA	Q6bsq2 debaryomyce
615	35	66.0	506	2	Q8TCP7_HUMAN	Q8tcp7 homo sapien	688	35	66.0				

689	35	66.0	1809	2	Q8MP02_PERAM	Q8mp02 periplaneta	762	34	64.2	219	2	Q64H90_ANTMA	Q64h90 antirrhinum
690	35	66.0	1820	1	STAR9_HUMAN	Q9p2p6 homo sapien	763	34	64.2	220	2	Q6K033_9BILA	Q6k033 cephalodell
691	35	66.0	2147	2	Q6XHB0_DICDI	Q6xb0 dictyosteli	764	34	64.2	220	2	Q7XZD3_RAPSA	Q7xzd3 rapanus ea
692	35	66.0	2147	2	Q54WS5_DICDI	Q54ws5 dictyosteli	765	34	64.2	223	2	Q8F726_LEPIN	Q8f726 leptospira
693	35	66.0	3036	2	Q4PAT2_DICDI	Q4pat2 ustilago ma	766	34	64.2	226	1	MYB21_ARATH	Q91k95 arabidopsis
694	35	66.0	3434	2	Q4VIX4_9FLAV	Q4vix4 alfuy virus	767	34	64.2	231	2	Q72NL0_LEPIC	Q72nl0 leptospira
695	35	66.0	5105	2	Q7PJQ9_ANOGA	Q7pjq9 anopheles g	768	34	64.2	232	2	Q5DAL6_SCHJA	Q5dal6 schistosoma
696	35	66.0	5105	2	Q7PMK5_ANOGA	Q7pmk5 anopheles g	769	34	64.2	232	2	Q8PRW0_METMA	Q8prw0 methanosarc
697	35	66.0	6193	2	Q8KSQ0_STRCP	Q8ksq0 streptomyce	770	34	64.2	235	2	Q4IH23_GIBZE	Q4ih29 gibberella
698	34.5	65.1	815	2	Q92ND3_RHIZE	Q92nd3 rhizobium m	771	34	64.2	236	2	Q7YR3_NEUCR	Q7yr3 neurospora
699	34	64.2	50	2	Q8S414_MAIZE	Q8s414 zea mays (m	772	34	64.2	239	2	Q9LTV4_ARATH	Q9ltv4 arabidopsis
700	34	64.2	73	2	Q74EW1_GEOSL	Q74ew1 geobacter s	773	34	64.2	245	2	Q681D0_ARATH	Q681d0 arabidopsis
701	34	64.2	76	2	Q6UNA9_9REOV	Q6una9 bluetongue	774	34	64.2	245	2	Q9SNW9_ARATH	Q9snw9 arabidopsis
702	34	64.2	78	2	Q6UNB0_9REOV	Q6unb0 bluetongue	775	34	64.2	246	2	Q391S3_ARATH	Q391s3 arabidopsis
703	34	64.2	83	2	Q81WP5_ANASP	Q81wp5 anabaena sp	776	34	64.2	246	2	Q9LNC9_ARATH	Q9lnc9 arabidopsis
704	34	64.2	87	2	Q8S424_MAIZE	Q8s424 zea mays (m	777	34	64.2	246	2	Q73KU2_TREDE	Q73ku2 treponema d
705	34	64.2	91	2	Q9S290_PIG	Q9s290 macaca fasc	778	34	64.2	247	2	Q9ATD9_GOSHI	Q9atd9 gossypium h
706	34	64.2	94	2	Q30559_MACFA	Q30559 macaca fasc	779	34	64.2	249	2	Q9SUX8_ARATH	Q9sux8 arabidopsis
707	34	64.2	99	2	Q99Q34_STRCO	Q99q34 streptomyce	780	34	64.2	255	2	Q5KQB8_ORYSA	Q5kqb8 oryza sativ
708	34	64.2	110	2	Q8AXW1_LOLPR	Q8axw1 lolium pere	781	34	64.2	255	2	Q9FZ13_SOLTU	Q9fz13 solanum tub
709	34	64.2	113	2	Q30562_MACFA	Q30562 macaca fasc	782	34	64.2	258	2	Q6K1S6_ORYSA	Q6k1s6 oryza sativ
710	34	64.2	113	2	Q7V714_PROHM	Q7v714 prochloroco	783	34	64.2	262	2	Q61S25_ORYSA	Q61s25 oryza sativ
711	34	64.2	115	2	Q58LA8_9CAUD	Q58la8 cyanophage	784	34	64.2	264	2	Q5SK43_THET8	Q5sk43 thermus the
712	34	64.2	122	2	Q39260_ARATH	Q39260 arabidopsis	785	34	64.2	264	2	Q72KR1_THET2	Q72kr1 thermus the
713	34	64.2	126	2	Q9L236_STRCO	Q9l236 streptomyce	786	34	64.2	266	2	Q94GA6_ARATH	Q94ga6 arabidopsis
714	34	64.2	129	2	Q7QCZ6_ANOGA	Q7qcz6 anopheles g	787	34	64.2	270	2	Q41Z31_AZOVI	Q41z31 azotobacter
715	34	64.2	130	2	Q6KIW2_ORYSA	Q6kiw2 oryza sativ	788	34	64.2	270	2	Q4KFP0_PSEF5	Q4kfp0 pseudomonas
716	34	64.2	131	2	Q9P1C1_HUMAN	Q9p1c1 homo sapien	789	34	64.2	273	2	Q49744_ARATH	Q49744 arabidopsis
717	34	64.2	140	2	Q6MYR7_BRARE	Q6myr7 brachydanio	790	34	64.2	275	2	Q4L214_MAIZE	Q4l214 zea mays (m
718	34	64.2	144	2	Q6MVX2_NEUCR	Q6mvx2 neurospora	791	34	64.2	275	2	Q23892_ORYSA	Q23892 oryza sativ
719	34	64.2	152	2	Q8VBQ2_9ORTO	Q8vbq2 thogoto vir	792	34	64.2	276	2	Q7F3D6_ORYSA	Q7f3d6 oryza sativ
720	34	64.2	152	2	Q8VBQ5_9ORTO	Q8vbq5 thogoto vir	793	34	64.2	276	2	Q74DG8_GEOSL	Q74dg8 geobacter s
721	34	64.2	152	2	Q8VBQ6_9ORTO	Q8vbq6 thogoto vir	794	34	64.2	277	2	Q61X77_WHEAT	Q61x77 triticum ae
722	34	64.2	152	2	Q8VBQ7_9ORTO	Q8vbq7 thogoto vir	795	34	64.2	279	2	Q72PE4_LEPIC	Q72pe4 leptospira
723	34	64.2	152	2	Q8VBQ8_9ORTO	Q8vbq8 thogoto vir	796	34	64.2	279	2	Q8F622_LEPIN	Q8f622 leptospira
724	34	64.2	152	2	Q8VBQ9_9ORTO	Q8vbq9 thogoto vir	797	34	64.2	281	2	Q9UFL2_HUMAN	Q9ufl2 homo sapien
725	34	64.2	153	2	Q49649_ARATH	Q49649 arabidopsis	798	34	64.2	281	2	Q7V7F0_PROHM	Q7v7f0 prochloroco
726	34	64.2	154	2	Q4T2Y0_TETNG	Q4t2y0 tetraodon n	799	34	64.2	282	2	Q8RVW3_ALLCE	Q8rvw3 allium cepa
727	34	64.2	155	2	Q5PR63_BRARE	Q5pr63 brachydanio	800	34	64.2	285	2	Q8R655_MELLI	Q8r655 melampora
728	34	64.2	157	2	Q6URR9_SORBI	Q6urr9 sorghum bic	801	34	64.2	285	2	Q8R660_MELLI	Q8r660 melampora
729	34	64.2	157	2	Q8S3Z1_SORBI	Q8s3z1 sorghum bic	802	34	64.2	285	2	Q8GRY3_ORYSA	Q8gry3 oryza sativ
730	34	64.2	160	2	Q9P1B9_HUMAN	Q9p1b9 homo sapien	803	34	64.2	285	2	Q9LTC4_ARATH	Q9ltc4 arabidopsis
731	34	64.2	161	2	Q6ZG29_ORYSA	Q6zgz29 oryza sativ	804	34	64.2	285	2	Q69SH8_ORYSA	Q69sh8 oryza sativ
732	34	64.2	166	2	Q8S3X8_ORYSA	Q8s3x8 oryza sativ	805	34	64.2	286	2	Q9WJ5_9VIRU	Q9wj5 faba bean n
733	34	64.2	166	2	Q8S3Z2_SORBI	Q8s3z2 sorghum bic	806	34	64.2	287	2	Q57MD8_SALCH	Q57md8 salmonella
734	34	64.2	169	2	Q9H5D8_HUMAN	Q9h5d8 homo sapien	807	34	64.2	287	2	Q5PE48_SALPA	Q5pe48 salmonella
735	34	64.2	170	2	Q9PQ09_HUMAN	Q9pq09 homo sapien	808	34	64.2	287	2	Q8Z595_SALTY	Q8z595 salmonella
736	34	64.2	173	2	Q9M4H7_VITVI	Q9m4h7 vitis vinif	809	34	64.2	287	2	Q8ZKN8_ORYSA	Q8zkn8 salmonella
737	34	64.2	173	2	Q7NHW9_GLOVI	Q7nhw9 gloeobacter	810	34	64.2	290	2	Q9S7K0_ORYSA	Q9s7k0 oryza sativ
738	34	64.2	184	2	Q9AVB7_9LILI	Q9avb7 lilium hybr	811	34	64.2	290	2	Q500L6_PSESY	Q500l6 pseudomonas
739	34	64.2	189	2	Q4WBQ8_ASFFU	Q4wbq8 aspergillus	812	34	64.2	290	2	Q8D3M0_ERWCT	Q8d3m0 erwinia car
740	34	64.2	190	2	Q7ORD2_GERHY	Q7ord2 gerbera hyb	813	34	64.2	290	2	Q88AS6_PSESM	Q88as6 pseudomonas
741	34	64.2	193	2	Q7XZ94_GRITJA	Q7xz94 griffithsia	814	34	64.2	290	2	Q88CL1_PSEPK	Q88cl1 pseudomonas
742	34	64.2	194	2	Q7QXQ2_GIALA	Q7qxq2 giardia lam	815	34	64.2	291	2	Q6EE24_9PERO	Q6ee24 siniperca c
743	34	64.2	198	2	P81396_ANTMA	P81396 antirrhinum	816	34	64.2	292	2	Q4KGB0_PSEF5	Q4kgb0 pseudomonas
744	34	64.2	203	2	Q54CW8_DICDI	P81396 antirrhinum	817	34	64.2	293	1	YBIE_ECOLI	P32484 escherichia
745	34	64.2	204	2	Q6LI77_PROPR	Q6li77 photobacter	818	34	64.2	293	2	Q55I34_CRYNE	Q55i34 cryptococcu
746	34	64.2	205	2	P81391_ANTMA	P81391 antirrhinum	819	34	64.2	293	2	Q5KCM5_CRYNE	Q5kcm5 cryptococcu
747	34	64.2	206	2	Q8L8W8_ARATH	Q8l8w8 arabidopsis	820	34	64.2	293	2	Q83QW7_SHIFL	Q83qw7 shigella fl
748	34	64.2	206	2	Q9SSA1_ARATH	Q9ssa1 arabidopsis	821	34	64.2	296	2	Q9T066_ARATH	Q9t066 arabidopsis
749	34	64.2	206	2	Q31145_MOUSE	Q31145 mus musculu	822	34	64.2	297	2	Q9M213_ARATH	Q9m213 arabidopsis
750	34	64.2	206	2	Q31151_MOUSE	Q31151 mus musculu	823	34	64.2	298	2	Q6PB00_XENLA	Q6pb00 xenopus lae
751	34	64.2	206	2	Q61641_MOUSE	Q61641 mus musculu	824	34	64.2	299	2	Q87P11_VIBPA	Q87p11 vibrio para
752	34	64.2	206	2	Q61643_MOUSE	Q61643 mus musculu	825	34	64.2	301	2	Q6Z998_ORYSA	Q6z998 oryza sativ
753	34	64.2	212	2	Q966H1_CAEEL	Q966h1 caenorhadi	826	34	64.2	301	2	Q6ZHS5_ORYSA	Q6zhs5 oryza sativ
754	34	64.2	212	2	Q8S3Z9_MAIZE	Q8s3z9 zea mays (m	827	34	64.2	302	1	MAK_ECOLI	P23917 escherichia
755	34	64.2	214	2	Q8LCG0_ARATH	Q8lcg0 arabidopsis	828	34	64.2	302	2	Q5R0A2_IDILO	Q5r0a2 idiomarina
756	34	64.2	214	2	Q9SPG9_ARATH	Q9spg9 arabidopsis	829	34	64.2	302	2	Q6DIY7_XENTR	Q6diy7 xenopus tro
757	34	64.2	216	2	Q7VTT5_BORPE	Q7vtt5 bordetella	830	34	64.2	303	2	Q9CL67_PASMU	Q9cl67 pasteurella
758	34	64.2	216	2	Q7WCC3_BORPA	Q7wcc3 bordetella	831	34	64.2	303	2	Q8D868_ERWCT	Q8d868 erwinia car
759	34	64.2	216	2	Q7WQC7_BORBP	Q7wqc7 bordetella	832	34	64.2	305	2	Q8LBC5_ARATH	Q8lbc5 arabidopsis
760	34	64.2	217	2	Q6ZDL4_ORYSA	Q6zdl4 oryza sativ	833	34	64.2	305	2	Q91514_ARATH	Q91514 arabidopsis
761	34	64.2	217	2	P93474_PEA	P93474 pisum sativ	834	34	64.2	305	2	Q941B3_ARATH	Q941b3 arabidopsis

835	34	64.2	305	2	Q9FDW1_ARATH	Q9fdw1 arabisopsie	908	34	64.2	364	2	Q5XBM5_STRP6	Q5xbm5 streptococc
836	34	64.2	305	2	Q8G706_BIFLO	Q8g706 bifidobacte	909	34	64.2	364	2	Q99298_STRPY	Q99298 streptococc
837	34	64.2	306	2	Q9FZ14_SOLTU	Q9fz14 solanum tub	910	34	64.2	364	2	Q63MM4_BURPS	Q63mm4 burkholderi
838	34	64.2	307	1	RNZ_PYRAB	Rnz_pyrab pyrococcus	911	34	64.2	364	2	Q9HX62_PSEAE	Q9hx62 pseudomonas
839	34	64.2	307	1	RNZ_PYRHO	Rnz_pyrho pyrococcus	912	34	64.2	364	2	Q8P019_STRPE	Q8p019 streptococc
840	34	64.2	307	1	RNZ_PYRHO	Rnz_pyrho pyrococcus	913	34	64.2	364	2	Q8K736_STRP3	Q8k736 streptococc
841	34	64.2	308	2	Q5NZ97_AZOSE	Q5nz97 azoarcus sp	914	34	64.2	366	2	Q8ZU49_PSESM	Q8zu49 pseudomonas
842	34	64.2	309	2	O8LA62_ARATH	O8la62 arabisopsie	915	34	64.2	366	2	Q882N6_PSESM	Q882n6 pseudomonas
843	34	64.2	309	2	O49746_ARATH	O49746 arabisopsie	916	34	64.2	367	2	Q4LUL1_9BURK	Q4lul1 burkholderi
844	34	64.2	309	2	O22179_ARATH	O22179 arabisopsie	917	34	64.2	368	2	Q4NUM8_9DELT	Q4num8 anaeromyxob
845	34	64.2	310	2	Q9M2Y9_ARATH	Q9m2y9 arabisopsie	918	34	64.2	369	2	Q96C28_HUMAN	Q96c28 homo sapien
846	34	64.2	311	2	Q58QD0_VITVI	Q58qd0 vitis vinif	919	34	64.2	371	2	Q82NPF_NOCPA	Q82nfp nocardia fa
847	34	64.2	311	2	Q4LRC4_9BURK	Q4lrc4 burkholderi	920	34	64.2	373	2	Q82NT3_STRAW	Q82nt3 streptomyc
848	34	64.2	316	2	Q8HDH3_TORAC	Q8hdh3 nicotiana t	921	34	64.2	374	2	Q49538_ARATH	Q49538 arabisopsie
849	34	64.2	316	2	Q6Z0A5_ORYSA	Q6z0a5 oryza sativ	922	34	64.2	376	2	Q9SBF7_ARATH	Q9sbf7 arabisopsie
850	34	64.2	316	2	Q9QMH4_5VIRU	Q9qmh4 parvo-like	923	34	64.2	377	2	Q9SYD0_ARATH	Q9syd0 arabisopsie
851	34	64.2	316	2	Q4U3C5_BMDNV	Q4u3c5 bombyx mori	924	34	64.2	383	2	Q7E2D5_ANOGA	Q7e2d5 escherichia
852	34	64.2	318	2	Q6U9P9_ORYSA	Q6u9p9 oryza sativ	925	34	64.2	388	1	SOPA_ECOLI	Sopa_ecoli escherichia
853	34	64.2	320	2	Q6Q789_VITVI	Q6q789 vitis vinif	926	34	64.2	388	1	SOPA_ECOLI	Sopa_ecoli escherichia
854	34	64.2	320	2	Q23160_ARATH	Q23160 arabisopsie	927	34	64.2	388	1	SOPA_ECOLI	Sopa_ecoli escherichia
855	34	64.2	321	2	Q6AU56_ORYSA	Q6au56 oryza sativ	928	34	64.2	390	2	Q5R6H4_PONPY	Q5r6h4 pongo pygma
856	34	64.2	321	2	Q5WVG4_LEGPL	Q5wvg4 legionella	929	34	64.2	390	2	Q7U6T3_SNPXP	Q7u6t3 synchococc
857	34	64.2	321	2	Q5X424_LEGPA	Q5x424 legionella	930	34	64.2	391	2	Q5QJ32_SALTY	Q5qj32 salmonella
858	34	64.2	321	2	Q5ZUB8_LEGPH	Q5zub8 legionella	931	34	64.2	391	2	Q8VNM4_ECOLI	Q8vnm4 escherichia
859	34	64.2	323	2	Q6R095_ARATH	Q6r095 arabisopsie	932	34	64.2	391	2	Q849W4_ECOLI	Q849w4 escherichia
860	34	64.2	323	2	Q9LDE1_ARATH	Q9lde1 arabisopsie	933	34	64.2	391	2	Q6U5J3_KLEPI	Q6u5j3 klebsiella
861	34	64.2	324	1	CBP21_HORVU	P55747 hordeum vul	934	34	64.2	392	2	Q49491_ARATH	Q49491 arabisopsie
862	34	64.2	324	1	Q5NBT2_ORYSA	Q5nbt2 oryza sativ	935	34	64.2	392	2	Q31280_RAT	Q31280 rattus norv
863	34	64.2	325	2	Q74AD3_GEOSL	Q74ad3 geobacter s	936	34	64.2	393	2	Q6MG01_RAT	Q6mg01 rattus norv
864	34	64.2	325	2	Q8HOH0_TOBAC	Q8hoh0 nicotiana t	937	34	64.2	393	2	Q6MG01_RAT	Q6mg01 rattus norv
865	34	64.2	332	2	Q8R3Y0_MOUSE	Q8r3y0 mus musculu	938	34	64.2	399	2	Q6R080_ARATH	Q6r080 arabisopsie
866	34	64.2	333	2	Q53SW4_HUMAN	Q53sw4 homo sapien	939	34	64.2	399	2	Q9LDW5_ARATH	Q9ldw5 arabisopsie
867	34	64.2	333	2	Q850X2_ORYSA	Q850x2 oryza sativ	940	34	64.2	400	2	Q4L6G1_STAHJ	Q4l6g1 staphylococ
868	34	64.2	333	2	Q8SAY7_ORYSA	Q8say7 oryza sativ	941	34	64.2	400	2	Q67QT1_SYMTH	Q67qt1 symbiobacte
869	34	64.2	333	2	Q9ZTE6_ARATH	Q9zte6 arabisopsie	942	34	64.2	413	2	Q745Y8_THRT2	Q745y8 thermus the
870	34	64.2	333	2	Q9FKL2_ARATH	Q9fkl2 arabisopsie	943	34	64.2	416	2	Q4HB53_9DEIU	Q4hb53 deinococcus
871	34	64.2	334	2	Q7S5A2_NEUCR	Q7s5a2 neurospora	944	34	64.2	419	2	Q8U0P7_PYRFO	Q8u0p7 pyrococcus
872	34	64.2	335	2	Q41352_GIBZE	Q41352 gibberella	945	34	64.2	429	2	Q8WXC9_HUMAN	Q8wxc9 homo sapien
873	34	64.2	336	1	VINT_BF186	P06723 bacterioph	946	34	64.2	432	1	AMIX_HAEIN	P44493 haemophilus
874	34	64.2	338	2	Q6MFEZ1_RAT	Q6mfz1 rattus norv	947	34	64.2	432	2	Q4QP88_HAEI8	Q4qp88 haemophilus
875	34	64.2	339	2	Q7UDK3_SHIFL	Q7udk3 shigella fl	948	34	64.2	432	2	Q7FB09_ORYSA	Q7fb09 oryza sativ
876	34	64.2	342	1	DHYS_PYRHO	O50105 pyrococcus	949	34	64.2	445	1	ASM3A_RAT	Q64127 rattus norv
877	34	64.2	344	2	Q6RK01_CAPAN	Q6rk01 capsicum an	950	34	64.2	448	2	Q4P235_USTMA	Q4p235 ustilago ma
878	34	64.2	344	2	Q6DRD7_XENLA	Q6ded7 xenopus lae	951	34	64.2	449	2	Q7NDY4_GLOVI	Q7ndy4 gloobacter
879	34	64.2	345	2	Q6G3R9_BARHE	Q6g3r9 bartonella	952	34	64.2	451	2	Q6G4G4_BARHE	Q6g4g4 bartonella
880	34	64.2	347	2	Q6G3J2_XENTR	Q6g3j2 xenopus tro	953	34	64.2	451	1	ASM3A_HUMAN	Q92484 homo sapien
881	34	64.2	347	2	Q5PQ39_XENLA	Q5pq39 xenopus lae	954	34	64.2	452	2	Q5LS29_MAGGR	Q51s29 magnaporthe
882	34	64.2	348	1	IRP2_CHICK	Q98925 gallus gall	955	34	64.2	460	2	Q7S2L3_NEUCR	Q7s2l3 neurospora
883	34	64.2	348	2	Q8FKD4_ECOL6	Q8fk4 escherichia	956	34	64.2	460	2	Q9C8H5_ARATH	Q9c8h5 arabisopsie
884	34	64.2	348	2	Q83SH3_SHIFL	Q83sh3 shigella fl	957	34	64.2	461	2	P94248_BIFBR	P94248 bifidobacte
885	34	64.2	348	2	Q8XEA0_ECO57	Q8xea0 escherichia	958	34	64.2	462	2	Q52920_MAGGR	Q52920 magnaporthe
886	34	64.2	349	1	IRF2_HUMAN	P14316 homo sapien	959	34	64.2	464	2	Q7NTP1_CHRVO	Q7ntp1 chromobacte
887	34	64.2	349	1	IRF2_MOUSE	P23906 mus musculu	960	34	64.2	468	2	Q50YK8_ENTHI	Q50yk8 entamoeba h
888	34	64.2	349	1	IRP2_SIGHI	Q8r460 sigmodon hi	961	34	64.2	477	2	Q7M6W2_MOUSE	Q7m6w2 mus musculu
889	34	64.2	349	2	O61A57_HUMAN	Q6ia57 homo sapien	962	34	64.2	478	2	Q6C8A7_YARLI	Q6c8a7 yarrowia li
890	34	64.2	349	2	Q9N137_SHEEP	Q9n137 ovis aries	963	34	64.2	485	2	Q9VDU9_DROME	Q9vdu9 drosophila
891	34	64.2	349	2	Q5R8L3_PONPY	Q5r8l3 pongo pygma	964	34	64.2	491	1	K6PF_METAC	P58847 methanosarc
892	34	64.2	349	2	Q923E9_MOUSE	Q923e9 mus musculu	965	34	64.2	495	2	Q6NU90_XENLA	Q6nu90 xenopus lae
893	34	64.2	351	2	Q5ZF11_MACMU	Q5zf11 macaca mula	966	34	64.2	497	2	Q9PJ03_CLAFU	Q9pj03 cladaporiu
894	34	64.2	351	2	Q9MV2_MOUSE	Q9mv2 mus musculu	967	34	64.2	498	2	Q9WXH4_ALCPA	Q9wxh4 alcaligenes
895	34	64.2	352	2	Q7TPP0_MOUSE	Q7tpf0 mus musculu	968	34	64.2	499	2	Q5FST7_GLUOX	Q5fst7 gluconobact
896	34	64.2	354	2	Q7Z518_HUMAN	Q7z518 homo sapien	969	34	64.2	503	2	Q21435_CABEL	Q21435 caenorhabdi
897	34	64.2	355	1	NUDM_HUMAN	Q95299 homo sapien	970	34	64.2	508	2	Q4SP90_TETNG	Q4sp90 tetraodon n
898	34	64.2	355	2	Q5R9E8_PONPY	Q5r9e8 pongo pygma	971	34	64.2	510	2	Q4MPQ0_BACCE	Q4mpq0 bacillus ce
899	34	64.2	358	2	Q5S0E5_DICDI	Q5se05 dictyosteli	972	34	64.2	519	2	Q5BCP9_EMENI	Q5bcp9 aspergillus
900	34	64.2	359	1	MODC_YERPE	Q8zgx6 yersinia pe	973	34	64.2	525	1	Y107_METJA	Q57571 methanococ
901	34	64.2	359	2	Q9XFN9_ANTMA	Q66d71 yersinia ps	974	34	64.2	526	2	Q7QCZ7_ANOGA	Q7qc7 anopheles g
902	34	64.2	359	2	Q9XFN9_ANTMA	Q9xfn9 antirrhinum	975	34	64.2	527	2	Q96T01_HUMAN	Q96t01 homo sapien
903	34	64.2	362	1	HAIL_MOUSE	P01897 mus musculu	976	34	64.2	530	2	Q9M1R2_ARATH	Q9m1r2 arabisopsie
904	34	64.2	362	2	Q5TM39_MACMU	Q5tm39 macaca mula	977	34	64.2	533	2	Q6T282_9ROSI	Q6t282 populus alb
905	34	64.2	363	2	Q65YW9_PSEPU	Q65yw9 pseudomonas	978	34	64.2	534	1	IMA1B_ORYSA	Q981x0 oryza sativ
906	34	64.2	364	2	Q9FZ15_SOLTU	Q9fz15 solanum tub	979	34	64.2	535	2	Q5Z7I6_ORYSA	Q5z7i6 oryza sativ
907	34	64.2	364	2	Q4IV58_AZOVI	Q4iv58 azotobacter	980	34	64.2	536	2	Q531Q1_ORYSA	Q531q1 oryza sativ

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981 34 64.2 543 2 Q7SCR5 NEUCR
982 34 64.2 543 2 Q8LDX9_ATH
983 34 64.2 544 2 Q7FM55_ATH
984 34 64.2 544 2 Q9SKH2_ATH
985 34 64.2 545 2 Q7M6W6_MOUSE
986 34 64.2 554 2 Q74ET8_GEOSL
987 34 64.2 563 2 Q6K9I8_ORYSA
988 34 64.2 570 2 Q8BL46_MOUSE
989 34 64.2 576 2 Q7M6U4_MOUSE
990 34 64.2 576 2 Q7M6W5_MOUSE
991 34 64.2 578 2 Q5FWE4_HUMAN
992 34 64.2 583 2 Q8S3D0_BROTE
993 34 64.2 583 2 Q8S3J0_BROTE
994 34 64.2 586 2 Q5FPJ6_GLOUX
995 34 64.2 586 2 Q9D5X3_MOUSE
996 34 64.2 598 2 Q8BM89_MOUSE
997 34 64.2 599 2 Q5FYB0_HUMAN
998 34 64.2 601 2 Q6N9S2_RHOPA
999 34 64.2 602 2 Q8SVK1_BRAJA
1000 34 64.2 604 2 Q4ZPB4_PSESY

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## ALIGNMENTS

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RESULT 1
GAST_DIDMA STANDARD; PRT; 33 AA.
AC P33713;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 33); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90298616; PubMed=2361360;
RA Shimomura Y., Eng J., Rattan S.C., Yalow R.S.;
RT "Opossum (Didelphis virginiana) 'little' and 'big' gastrins.";
RL Comp. Biochem. Physiol. 96B:239-242(1990).
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC PIR; A60506; A60506.
CC InterPro; IPR001651; Gastrin.
CC Pfam; PF00918; Gastrin; 1.
CC PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Pyrrolidone carboxylic acid;
KW Sulfation.
FT PEPTIDE 1 33 Big gastrin.
FT PEPTIDE 18 33 Gastrin.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 18 18 Pyrrolidone carboxylic acid.
FT MOD_RES 28 28 Sulfotyrosine.
FT MOD_RES 33 33 Phenylalanine amide.
FT SEQUENCE 33 AA; 3856 MW; 217D28C15027B661 CRC64;

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Query Match 94.3%; Score 50; DB 1; Length 33;
Best Local Similarity 88.9%; Pred No. 0.4; Mismatches 0; Gaps 0;
Matches 8; Conservative 1; Indels 0;
QY 1 EGPWLEEE 9
Db 18 QGPWLEEE 26
:|||||
:|||||

RESULT 2
GAST_HUMAN STANDARD; PRT; 101 AA.
ID P01350; P78463; P78464;
AC 21-JUL-1986 (Rel. 01, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Gastrin 71 (Component I); Gastrin 52; Big
DE Gastrin (Gastrin 34) (Component II); Gastrin (Gastrin 17) (Component
DE III); Gastrin 14; Gastrin 6].
GN Name=GAST; Synonyms=GAS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87219893; PubMed=3034736; DOI=10.1016/0378-1119(86)90338-0;
RA Kariya Y., Kato K., Hayashizaki Y., Himeno S., Tarui S., Matsubara K.;
RT "Expression of human gastrin gene in normal and gastrinoma tissues.";
RL Gene 50:345-352(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84273693; PubMed=6087340;
RA Ito R., Sato K., Helmer T., Jay G., Agarwal K.L.;
RT "Structural analysis of the gene encoding human gastrin: the large
RT intron contains an Alu sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4662-4666(1984).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84169471; PubMed=6324077;
RA Kato K., Hayashizaki Y., Takahashi Y., Himeno S., Matsubara K.;
RT "Molecular cloning of the human gastrin gene.";
RL Nucleic Acids Res. 11:8197-8203(1983).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83221503; PubMed=6574456;
RA Boel E., Vuust J., Norris F., Norris K., Wind A., Rehfeld J.F.,
RA Marcker K.A.;
RT "Molecular cloning of human gastrin cDNA: evidence for evolution of
RT gastrin by gene duplication.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2866-2869(1983).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84144842; PubMed=6322186;
RA Wiborg O., Berglund L., Boel E., Norris F., Norris K., Rehfeld J.F.,
RA Marcker K.A., Vuust J.;
RT "Structure of a human gastrin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:1067-1069(1984).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84159488; PubMed=6689486; DOI=10.1016/0378-1119(83)90035-5;
RA Kato K., Himeno S., Takahashi Y., Wakabayashi T., Tarui S.,
RA Matsubara K.;
RT "Molecular cloning of human gastrin precursor cDNA.";
RL Gene 26:53-57(1983).
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grumman J.J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [8]  
RN PROTEIN SEQUENCE OF 22-101, AND CHARACTERIZATION OF GASTRIN 71.  
RC TISSUE=Antral mucosa;  
RX MEDLINE=94333379; PubMed=8055952;  
RA Rehfeld J.F., Johnsen A.H.;  
RT "Identification of gastrin component I as gastrin-71. The largest  
RT possible bioactive progastrin product.";  
RL Eur. J. Biochem. 223:765-773 (1994).  
RN [9]  
RN PROTEIN SEQUENCE OF 76-92.  
RX MEDLINE=67021327; PubMed=5921183;  
RA Bentley P.H., Kenner G.W., Sheppard R.C.;  
RT "Structures of human gastrins I and II.";  
RL Nature 209:583-585 (1966).  
RN [10]  
RN PROTEIN SEQUENCE OF 59-68.  
RX MEDLINE=89273602; PubMed=2730647;  
RA Higashimoto Y., Himeno S., Shinomura Y., Nagao K., Tamura T.,  
RA Tarui S.;  
RT "Purification and structural determination of urinary NH2-terminal big  
RT gastrin fragments.";  
RL Biochem. Biophys. Res. Commun. 160:1364-1370 (1989).  
RN [11]  
RN PROTEIN SEQUENCE OF 76-92.  
RX MEDLINE=69298172; PubMed=5822140;  
RA Gregory R.A., Tracy H.J., Agarwal K.L., Grossman M.I.;  
RT "Amino acid constitution of two gastrins isolated from Zollinger-  
RT Ellison tumour tissue.";  
RL Gut 10:603-608 (1969).  
RN [12]  
RN CHARACTERIZATION OF GASTRIN 6, AND SULFATION OF TYR-87.  
RX MEDLINE=95137019; PubMed=7530658;  
RA Rehfeld J.F., Hansen C.P., Johnsen A.H.;  
RT "Post-poly(Glu) cleavage and degradation modified by O-sulfated  
RT tyrosine: a novel post-translational processing mechanism.";  
RL EMBO J. 14:389-396 (1995).  
RN [13]  
RN PROCESSING, AND SULFATION OF TYR-87.  
RX MEDLINE=20508341; PubMed=11052936;  
RA Paineas Hansen C., Stadil F., Rehfeld J.F.;  
RT "Metabolism and acid secretory effect of sulfated and nonsulfated  
RT gastrin-6 in humans.";  
RL Am. J. Physiol. 279:G903-G909 (2000).  
CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and  
CC secrete hydrochloric acid and the pancreas to secrete its  
CC digestive enzymes. It also stimulates smooth muscle contraction  
CC and increases blood circulation and water secretion in the stomach  
CC and intestine.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- PFM: Two different processing pathways probably exist in antral G-  
CC cells. In the dominant pathway progastrin is cleaved at three  
CC sites resulting in two major bioactive gastrins, gastrin-34 and  
CC gastrin-17. In the putative alternative pathway, progastrin may be  
CC processed only at the most C-terminal dibasic site resulting in  
CC the synthesis of gastrin-71.  
CC -1- PFM: Sulfation of Tyr-87 blocks peptide degradation and enhances  
CC activity.

CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC EMBL: X00183; CAA25005.1; -; Genomic DNA.  
DR EMBL: X00183; CAA25006.1; -; Genomic DNA.  
DR EMBL: X00183; CAA25007.1; -; Genomic DNA.  
DR EMBL: X00511; CAA23769.1; -; mRNA.  
DR EMBL: M15958; AAA52520.1; -; Genomic DNA.  
DR EMBL: K01254; AAB59533.1; -; Genomic DNA.  
DR EMBL: BC069724; AAH69724.1; -; mRNA.  
DR EMBL: BC069762; AAH69762.1; -; mRNA.  
DR FIR: A93997; GSWUB.  
DR Ensembl: ENSG00000184502; Homo sapiens.  
DR HGNC: HGNC:4164; GAST.  
DR MIM: 137250; -;  
DR GO: GO:0005179; P: hormone activity; TAS.  
DR GO: GO:0007165; P: signal transduction; NAS.  
DR InterPro: IPR001651; Gastrin.  
DR Pfam: PF00918; Gastrin; 1.  
DR SMART: SM00029; GASTRIN; 1.  
KW PROSITE: PS00259; GASTRIN; 1.  
KW Amidation; Cleavage on pair of basic residues;  
KW Direct protein sequencing; Hormone; Phosphorylation;  
KW Pyrrolidone carboxylic acid; Signal; Sulfation.  
FT SIGNAL 1 21  
FT PEPTIDE 22 92 Gastrin 71.  
FT PEPTIDE 41 92 Gastrin 52.  
FT PEPTIDE 59 92 Big gastrin.  
FT PEPTIDE 76 92 Gastrin.  
FT PEPTIDE 79 92 Gastrin 14.  
FT PEPTIDE 87 92 Gastrin 6.  
FT PROPEP 96 101 Removed in mature form.  
FT SITE 40 41 Cleavage.  
FT SITE 58 59 Cleavage.  
FT SITE 75 76 Cleavage.  
FT SITE 95 96 Cleavage.  
FT MOD\_RES 59 59 Pyrrolidone carboxylic acid.  
FT MOD\_RES 76 76 Pyrrolidone carboxylic acid.  
FT MOD\_RES 87 87 Sulfotyrosine (partial).  
FT MOD\_RES 92 92 Phenylalanine amide (G-93 provides amide group).  
FT MOD\_RES 96 96 Phosphoserine (By similarity).  
SQ SEQUENCE 101 AA; 11394 MW; A03C847FCFE7216C CRC64;  
Query Match 94.3%; Score 50; DB 1; Length 101;  
Best Local Similarity 88.9%; Pred. No. 1.3;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EGPWLEEEE 9  
Db 76 QGPWLEEEE 84  
RESULT 3  
GAST\_FELCA STANDARD; PRT; 104 AA.  
AC P01354;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].  
GN Names=GAST; Synonyms=GAS;  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;  
OC Felinae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]

RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92127058; PubMed=1773057;  
RA Kim S.J., Uhm K.N., Kang Y.K., Yoo O.J.;  
RT "Bovine and feline gastrin cDNA sequences and the amino acid and  
RT nucleotide sequence homologies among mammalian species.";  
RL DNA Seq. 1:181-187(1991).  
RN [2]  
RP PROTEIN SEQUENCE OF 76-92.  
RX MEDLINE=69206035; PubMed=5784957;  
RA Agarwal K.L., Kenner G.W., Sheppard R.C.;  
RT "Feline gastrin. An example of peptide sequence analysis by mass  
RT spectrometry.";  
RL J. Am. Chem. Soc. 91:3096-3097(1969).  
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and  
CC secrete hydrochloric acid and the pancreas to secrete its  
CC digestive enzymes. It also stimulates smooth muscle contraction  
CC and increases blood circulation and water secretion in the stomach  
CC and intestine.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
CC  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC removed.  
CC  
CC EMBL; X16582; CAA34599.1; -; mRNA.  
DR PIR; S14401; GMCT.  
DR InterPro; IPR001651; Gastrin.  
DR Pfam; PF00918; Gastrin; 1.  
DR SMART; SM00029; GASTRIN; 1.  
DR PROSITE; PS00259; GASTRIN; 1.  
KW Amidation; Cleavage on pair of basic residues;  
KW Direct protein sequencing; Hormone; Phosphorylation;  
KW Pyrrolidone carboxylic acid; Signal; Sulfation.  
FT SIGNAL 1 21  
FT PROPEP 22 58  
FT PEPTIDE 59 92  
FT PEPTIDE 76 92  
FT PROPEP 96 104  
FT MOD\_RES 59 59  
FT MOD\_RES 76 76  
FT MOD\_RES 87 87  
FT MOD\_RES 92 92  
FT MOD\_RES 96 96  
FT MOD\_RES 96 96  
FT SEQUENCE 104 AA; 11482 MW; 4DB92E4416A7AC9F CRC64;  
Query Match 94.3%; Score 50; DB 1; Length 104;  
Best Local Similarity 88.9%; Pred. No. 1.3;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EGPWLEEEE 9  
Db :|||||  
76 QGPWLEEEE 84  
RESULT 4  
GAST\_MACMU  
ID GAST\_MACMU STANDARD; PRT; 17 AA.  
AC P33714;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Gastrin  
GN Name=GAST; Synonyms=GAS;  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecoidea; Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]

RP PROTEIN SEQUENCE.  
RX MEDLINE=91164506; PubMed=2003150; DOI=10.1016/0167-0115(91)90005-2;  
RA Yu J.-H., Xin Y., Eng J., Yalow R.S.;  
RT "Rhesus monkey gastroenteropancreatic hormones: relationship to human  
RT sequences.";  
RL Regul. Pept. 32:39-45(1991).  
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and  
CC secrete hydrochloric acid and the pancreas to secrete its  
CC digestive enzymes. It also stimulates smooth muscle contraction  
CC and increases blood circulation and water secretion in the stomach  
CC and intestine.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
CC  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC PIR; A60071; A60071.  
DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; 1.  
KW Amidation; Direct protein sequencing; Hormone;  
KW Pyrrolidone carboxylic acid; Sulfation.  
FT MOD\_RES 1 1  
FT MOD\_RES 12 12  
FT MOD\_RES 17 17  
FT SEQUENCE 17 AA; 2076 MW; 6F6E92C73611D39A CRC64;  
Query Match 90.6%; Score 48; DB 1; Length 17;  
Best Local Similarity 77.8%; Pred. No. 0.44;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EGPWLEEEE 9  
Db :|||||  
1 QGPWLEEEE 9  
RESULT 5  
GAST\_CANFA  
ID GAST\_CANFA STANDARD; PRT; 104 AA.  
AC P01353;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].  
GN Name=GAST; Synonyms=GAS;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
OC Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Antral mucosa;  
RX MEDLINE=91085716; PubMed=2262079;  
RA Gantz I., Takeuchi T., Yamada T.;  
RT "Cloning of canine gastrin cDNA's encoding variant amino acid  
RT sequences.";  
RL Digestion 46:99-104(1990).  
RN [2]  
RP PROTEIN SEQUENCE OF 59-92.  
RC TISSUE=Antral mucosa;  
RX MEDLINE=87016557; PubMed=3763441; DOI=10.1016/0196-9781(86)90045-8;  
RA Bonato C., Eng J., Hulmes J.D., Miedel M., Pan Y.-C.E., Yalow R.S.;  
RT "Sequences of gastrins purified from a single antrum of dog and of  
RT goat.";  
RL Peptides 7:689-693(1986).  
RN [3]  
RP PROTEIN SEQUENCE OF 76-92, AND PHOSPHORYLATION.  
RX MEDLINE=69253357; PubMed=5799207;  
RA Agarwal K.L., Kenner G.W., Sheppard R.C.;

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RT "Structure and synthesis of canine gastrin.";
RL Experientia 25:346-348(1969).
RN [4]
RP PROTEIN SEQUENCE OF 96-104.
RX TISSUE=Antral mucosa;
RC MEDLINE=89331947; PubMed=2756156; DOI=10.1016/0167-0115(89)90264-4;
RA Desmond H., Varro A., Young J., Gregory H., Nemeth J., Dockray G.J.;
RT "The constitution and properties of phosphorylated and
unphosphorylated C-terminal fragments of progastrin from dog and
ferret antrum.";
RL Regul. Pept. 25:223-233(1989).
CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
secrete hydrochloric acid and the pancreas to secrete its
digestive enzymes. It also stimulates smooth muscle contraction
and increases blood circulation and water secretion in the stomach
and intestine.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC -----
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removed.
CC -----
DR PIR; B61053; GMDG.
DR Ensembl; ENSCAFG0000015924; Canis familiaris.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00918; Gastrin; 1.
DR SMART; SM00029; GASTRIN; 1.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Phosphorylation;
KW Pyrrolidone carboxylic acid; Signal; Sulfation.
FT SIGNAL 1 21
FT PROPEP 22 58
FT PEPTIDE 59 92
FT PROPEP 96 104
FT MOD_RES 59 59
FT MOD_RES 76 76
FT MOD_RES 87 87
FT MOD_RES 92 92
FT MOD_RES 96 96
FT VARIANT 85 85
FT CONFLICT 83 85
FT SEQUENCE 104 AA; 11519 MW; 73BF72A18DPE78CA CRC64;
SQ
Query Match 90.6%; Score 48; DB 1; Length 104;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EGPWLEEEE 9
Db 76 QGPWMEEEE 84
RESULT 6
GAST_PIG STANDARD; PRT; 104 AA.
AC P01351;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Name=GAST; Synonym=GAS;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82174533; PubMed=69511161;
RA Yoo O.J., Powell C.T., Agarwal K.L.;
RT "Molecular cloning and nucleotide sequence of full-length of cDNA
coding for porcine gastrin.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1049-1053(1982).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 56-82.
RX MEDLINE=80240380; PubMed=6930858;
RA Agarwal K.L., Noyes B.E.;
RT "Studies on gastrin mRNA structure using an oligonucleotide probe.";
RN Ann. N. Y. Acad. Sci. 343:433-442(1980).
RN [3]
RP PROTEIN SEQUENCE OF 76-92.
RX PubMed=14248711;
RA Gregory H., Hardy P.M., Jones D.S., Kenner G.W., Sheppard R.C.;
RT "The antral hormone gastrin.";
RL Nature 204:931-933(1964).
RN [4]
RP SYNTHESIS.
RX PubMed=14248712;
RA Anderson J.C., Barton M.A., Gregory R.A., Hardy P.M., Kenner G.W.,
RA McLeod J.K., Preston J., Sheppard R.C., Morley J.S.;
RT "Synthesis of gastrin.";
RL Nature 204:933-934(1964).
CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
secrete hydrochloric acid and the pancreas to secrete its
digestive enzymes. It also stimulates smooth muscle contraction
and increases blood circulation and water secretion in the stomach
and intestine.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC -----
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removed.
CC -----
DR EMBL; V01303; CAA24610.1; -; mRNA.
DR EMBL; M25036; AAA31111.1; -; mRNA.
DR PIR; A93903; GMPGB.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00918; Gastrin; 1.
DR SMART; SM00029; GASTRIN; 1.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Phosphorylation;
KW Pyrrolidone carboxylic acid; Signal; Sulfation.
FT SIGNAL 1 21
FT PROPEP 22 58
FT PEPTIDE 59 92
FT PROPEP 96 104
FT MOD_RES 59 59
FT MOD_RES 76 76
FT MOD_RES 87 87
FT MOD_RES 92 92
FT MOD_RES 96 96
FT SEQUENCE 104 AA; 11558 MW; B0BD1D7E05304B79 CRC64;
SQ
Query Match 90.6%; Score 48; DB 1; Length 104;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EGPWLEEEE 9
Db 76 QGPWMEEEE 84
RESULT 7
GAST_CAPHI

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ID  GAST_CAPHI  STANDARD;  PRT;  34 AA.
AC  P04564;
DT  13-AUG-1987 (Rel. 05, Created)
DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  13-SEP-2005 (Rel. 48, Last annotation update)
DE  Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN  Name=GAST; Synonyms=GAS;
OS  Capra hircus (Goat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC  Pecora; Bovidae; Caprinae; Capra.
OX  NCBI_TaxID=9925;
RN  [1]
RP  PROTEIN SEQUENCE.
RX  MEDLINE=87016557; PubMed=3763441; DOI=10.1016/0196-9781(86)90045-8;
RA  Bonato C., Eng J., Hulmes J.D., Medel M., Pan Y.-C.E., Yalow R.S.;
RT  "Sequences of gastrins purified from a single antrum of dog and of
RT  goat.";
RL  Peptides 7:689-693(1986).
CC  -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC  secrete hydrochloric acid and the pancreas to secrete its
CC  digestive enzymes. It also stimulates smooth muscle contraction
CC  and increases blood circulation and water secretion in the stomach
CC  and intestine.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  PIR; JS0426; JS0426.
DR  InterPro; IPR001651; Gastrin.
DR  Pfam; PF00318; Gastrin; 1.
DR  PROSITE; PS00259; GASTRIN; 1.
KW  Amidation; Cleavage on pair of basic residues;
KW  Direct protein sequencing; Hormone; Pyrrolidone carboxylic acid;
KW  Sulfation.
FT  PEPTIDE 1 34 Big gastrin.
FT  PEPTIDE 18 34 Gastrin.
FT  MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT  MOD_RES 18 18 Pyrrolidone carboxylic acid.
FT  MOD_RES 29 29 Sulfotyrosine.
FT  MOD_RES 34 34 Phenylalanine amide.
SQ  SEQUENCE 34 AA; 3903 MW; 67501111E76D0CF4 CRC64;

Query Match 88.7%; Score 47; DB 1; Length 34;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
DB 18 QGPWVEEEE 26

RESULT 8
GAST_BOVIN  STANDARD;  PRT;  104 AA.
AC  P01352; Q28114;
DT  21-JUL-1986 (Rel. 01, Created)
DT  01-NOV-1991 (Rel. 20, Last sequence update)
DT  13-SEP-2005 (Rel. 48, Last annotation update)
DE  Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN  Name=GAST; Synonyms=GAS;
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC  Pecora; Bovidae; Bovinae; Bos.
OX  NCBI_TaxID=9913;
RN  [1]

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RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Liver;
RX  MEDLINE=90114160; PubMed=2608050;
RA  Lund T., Olsen J., Rehfeld J.F.;
RT  "Cloning and sequencing of the bovine gastrin gene.";
RL  Mol. Endocrinol. 3:1585-1588(1989).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=92127058; PubMed=1773057;
RA  Kim S.J., Uhm K.N., Kang Y.K., Yoo O.J.;
RT  "Bovine and feline gastrin cDNA sequences and the amino acid and
RT  nucleotide sequence homologies among mammalian species.";
RL  DNA Seq. 1:181-187(1991).
RN  [3]
RP  PROTEIN SEQUENCE OF 76-92.
RX  MEDLINE=68357500; PubMed=5665711;
RA  Agarwal K.L., Beacham J., Bentley P.H., Gregory R.A., Kenner G.W.,
RA  Sheppard R.C., Tracy H.J.;
RT  "Isolation, structure and synthesis of ovine and bovine gastrins.";
RL  Nature 219:614-615(1968).
CC  -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC  secrete hydrochloric acid and the pancreas to secrete its
CC  digestive enzymes. It also stimulates smooth muscle contraction
CC  and increases blood circulation and water secretion in the stomach
CC  and intestine.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  EMBL; M31657; AAA30537.1; -; Genomic_DNA.
DR  EMBL; X16581; CAA34598.1; -; mRNA.
DR  PIR; S14400; GMEQ.
DR  InterPro; IPR001651; Gastrin.
DR  Pfam; PF00918; Gastrin; 1.
DR  SMART; SM00029; GASTRIN; 1.
DR  PROSITE; PS00259; GASTRIN; 1.
KW  Amidation; Cleavage on pair of basic residues;
KW  Direct protein sequencing; Hormone; Phosphorylation;
KW  Pyrrolidone carboxylic acid; Signal; Sulfation.
FT  SIGNAL 1 21
FT  PROPEP 22 58
FT  PEPTIDE 59 92
FT  PEPTIDE 76 92
FT  PROPEP 96 104
FT  MOD_RES 59 59
FT  MOD_RES 76 76
FT  MOD_RES 87 87
FT  MOD_RES 92 92
FT  MOD_RES 92 92
FT  MOD_RES 92 92
FT  MOD_RES 96 96
FT  CONFLICT 32 32 A -> L (in Ref. 1).
FT  CONFLICT 37 37 G -> R (in Ref. 1).
FT  CONFLICT 48 48 N -> T (in Ref. 1).
FT  CONFLICT 74 74 K -> N (in Ref. 1).
FT  CONFLICT 81 81 E -> G (in Ref. 1).
FT  CONFLICT 96 96 S -> M (in Ref. 1).
FT  CONFLICT 99 99 E -> G (in Ref. 1).
SQ  SEQUENCE 104 AA; 11573 MW; 54D03BF200F299F2 CRC64;

Query Match 88.7%; Score 47; DB 1; Length 104;
Best Local Similarity 77.8%; Pred. No. 4.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
DB 76 QGPWVEEEE 84

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RESULT 9
GAST_SHEEP
ID GAST_SHEEP STANDARD; PRT; 104 AA.
AC O02686;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
NUCLEOTIDE SEQUENCE.
RX MEDLINE=98182586; PubMed=9522119;
RA Moore C., Jie R., Shulkes A., Baldwin G.S.;
RT "Molecular cloning and sequence of the ovine gastrin gene.";
RL DNA Seq. 8:39-44(1997).
RN [2]
PROTEIN SEQUENCE OF 76-92.
RX MEDLINE=68357500; PubMed=5665711;
RA Agarwal K.L., Beacham J., Bentley P.H., Gregory R.A., Kenner G.W.,
RA Sheppard R.C., Tracy H.J.;
RT "Isolation, structure and synthesis of ovine and bovine gastrins.";
RL Nature 219:614-615(1968).
CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
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-----
EMBL: U92801; AAB51307.1; -; Genomic_DNA.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00918; Gastrin; 1.
DR SMART; SM00029; GASTRIN; 1.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Phosphorylation;
KW Pyrrolidone carboxylic acid; Signal; Sulfation.
FT SIGNAL 1 21
FT PROPEP 22 58
FT PEPTIDE 59 92
FT PEPTIDE 76 92
FT PROPEP 96 104
FT MOD_RES 59 59
FT MOD_RES 76 76
FT MOD_RES 87 87
FT MOD_RES 92 92
FT MOD_RES 96 96
FT SEQUENCE 104 AA; 11532 MW; 624063D4B5CE5AFD CRC64;
Query Match 88.7%; Score 47; DB 1; Length 104;
Best Local Similarity 77.8%; Pred. No. 4.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EGPWLEEEE 9
Db 76 QGPWVEEEE 84
RESULT 10
GAST_HORSE
ID GAST_HORSE STANDARD; PRT; 107 AA.
AC P55885;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OC NCBI_TaxID=9796;
RN [1]
NUCLEOTIDE SEQUENCE.
RX MEDLINE=98380242; PubMed=9716385;
RA Johnsen A.H., Sandin A., Rourke I.J., Bundgaard J.R., Nilsson G.,
RA Rehfeld J.F.;
RT "Unique progastrin processing in equine G-cells suggests marginal
RT tyrosyl sulfotransferase activity.";
RL Eur. J. Biochem. 255:432-438(1998).
CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
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-----
EMBL: Y09440; CAA70590.1; -; mRNA.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00918; Gastrin; 1.
DR SMART; SM00029; GASTRIN; 1.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues; Hormone;
KW Phosphorylation; Pyrrolidone carboxylic acid; Signal; Sulfation.
FT SIGNAL 1 21
FT PROPEP 22 61
FT PEPTIDE 62 95
FT PEPTIDE 79 95
FT PROPEP 99 107
FT MOD_RES 62 62
FT MOD_RES 79 79
FT MOD_RES 90 90
FT MOD_RES 95 95
FT MOD_RES 99 99
FT SEQUENCE 107 AA; 11884 MW; 104166CAAE5C234F CRC64;
Query Match 86.8%; Score 46; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 6.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EGPWLEEEE 9
Db 79 QGPWLEKEE 87
RESULT 11
Q9SCPI_ARATH
ID Q9SCPI_ARATH PRELIMINARY; PRT; 238 AA.
AC Q9SCPI;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative transcription factor MYB27 (At3G53200) (MYB transcription
DE factor).
DN Name=T4D2.130; Synonyms=At3G53200/T4D2_130; ORFNames=At3G53200;

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OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons;  
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 ON NCBI\_TaxID=3702;  
 RX NUCLEOTIDE SEQUENCE.  
 RP Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R., Quetier F.,  
 RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F.,  
 RA Salanoubat M.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,  
 RA Nakajima M., Enju A., Kamiya A., Naruseaka M., Carninci P., Kawai J.,  
 RA Hayashizaki Y., Shinozaki K.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,  
 RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,  
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,  
 RA Lee J.M., Lin J., Miranda M., Naruseaka M., Nguyen M., Onodera C.S.,  
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
 RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,  
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Qu L., Gu H.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL; AL132958; CAB64223.1; -; Genomic\_DNA.  
 DR EMBL; AK117256; BAC41933.1; -; mRNA.  
 DR EMBL; AY519599; AAS10069.1; -; mRNA.  
 DR EMBL; BT005257; AAO63321.1; -; mRNA.  
 DR PIR; T46166; T46166.  
 DR HSSP; P06876; 1MBK.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0045449; P:regulation of transcription; IEA.  
 DR InterPro; IPR012287; Homeodomain-rel.  
 DR InterPro; IPR001005; Myb DNA bd.  
 DR Pfam; PF00249; Myb DNA-binding; 2.  
 DR SMART; SM00717; SANT; 2.  
 DR PROSITE; PS50090; MYB\_3; 2.  
 KW Nuclear protein; Repeat.  
 SQ SEQUENCE 238 AA; 27996 MW; B6DDCF70E22DE62E CRC64;  
 Query Match 84.9%; Score 45; DB 2; Length 238;  
 Best Local Similarity 87.5%; Pred. No. 21;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GPWLEEEE 9  
 DB 12 GPWLEED 19  
 RESULT 12  
 DHYS PYRAB STANDARD; PRT; 335 AA.  
 ID Q9V0N5;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Probable deoxyhypusine synthase (EC 2.5.1.46) (DHS).  
 GN Name=dvs; OrderedLocusNames=PYRAB07540; ORFNames=PAB0511;  
 OS Pyrococcus abyssi.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;

OC Pyrococcus.  
 ON NCBI\_TaxID=29292;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=GES / Orsay;  
 RX MEDLINE=22511545; PubMed=12622808;  
 RX DOI=10.1046/j.1365-2958.2003.03381.x;  
 RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,  
 RA Poch O., Prier D., Querellou J., Ripp R., Thierry J.-C.,  
 RA van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;  
 RT "An integrated analysis of the genome of the hyperthermophilic  
 archaeon Pyrococcus abyssi.";  
 RL Mol. Microbiol. 47:1495-1512(2003).  
 CC -!- FUNCTION: Catalyzes the NAD-dependent oxidative cleavage of  
 spermidine and the subsequent transfer of the butylamine moiety of  
 spermidine to the epsilon-amino group of a specific lysine residue  
 of the eIF-5A precursor protein to form the intermediate  
 deoxyhypusine residue (By similarity).  
 CC -!- CATALYTIC ACTIVITY: [eIF5A-precursor]-lysine + spermidine =  
 [eIF5A-precursor]-deoxyhypusine + propane-1,3-diamine.  
 CC -!- COFACTOR: NAD (By similarity).  
 CC -!- PATHWAY: Hypusine biosynthesis; first step.  
 CC -!- SIMILARITY: Belongs to the deoxyhypusine synthase family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 DR EMBL; AJ248285; CAB49668.1; -; Genomic\_DNA.  
 DR PIR; C75119; C75119.  
 DR HSSP; P49366; 1DHS.  
 DR HAMAP; MF\_00153; -; 1.  
 DR InterPro; IPR002773; Deoxyhypus\_synth.  
 DR PANTHER; PTHR11703; Deoxyhypus\_synth; 1.  
 DR Pfam; PF01916; DS; 1.  
 DR ProDom; PD007730; Deoxyhypus\_synth; 1.  
 DR TIGRFAMs; TIGR00321; dvs; 1.  
 DR Complete proteome; Hypusine biosynthesis; NAD; Transferase.  
 KW SEQUENCE 335 AA; 37997 MW; 3DE853F38029EC55 CRC64;  
 Query Match 81.1%; Score 43; DB 1; Length 335;  
 Best Local Similarity 77.8%; Pred. No. 66;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEE 9  
 DB 20 EGPWLDEVE 28  
 RESULT 13  
 DHYS METJA STANDARD; PRT; 330 AA.  
 ID Q58224;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Probable deoxyhypusine synthase (EC 2.5.1.46) (DHS).  
 GN Name=dvs; OrderedLocusNames=MJ0814;  
 OS Methanococcus jannaschii.  
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
 OC Methanocaldococcaceae; Methanocaldococcus.  
 ON NCBI\_TaxID=2190;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
 RX MEDLINE=96337999; PubMed=868087;  
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,  
 RA Scott J.L., Geoghegan N.S.M., Weidman J.P., Fuhrmann J.L., Nguyen D.,



RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Tissue=Synthetic constructs;  
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC069071; AAH69071.1; -; mRNA.  
 DR HSP; P03001; IUN6.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0046872; F:metal ion binding; IEA.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR GO; GO:0006350; P:transcription; IEA.  
 DR InterPro; IPR001909; KRAB.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR Pfam; PF01352; KRAB; 1.  
 DR Pfam; PF00096; zf-C2H2; 11.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR ProDom; PD000003; Znf\_C2H2; 9.  
 DR SMART; SM00349; KRAB; 1.  
 DR SMART; SM00355; Znf\_C2H2; 11.  
 DR PROSITE; PS08065; KRAB; 1.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 11.  
 DR PROSITE; PS0157; ZINC\_FINGER\_C2H2\_2; 11.  
 SQ SEQUENCE 472 AA; 54598 MW; 1C857FF534B4F029 CRC64;  
  
 Query Match 79.2%; Score 42; DB 2; Length 472;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0;  
  
 QY 3 PWLEEE 9  
 DB 67 PWLEEE 73  
  
 RESULT 16  
 Q4SZ09 TETNG  
 ID Q4SZ09\_TETNG PRELIMINARY; PRT; 1103 AA.  
 AC Q4SZ09\_TETNG  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Chromosome undetermined SCAF11868, whole genome shotgun sequence.  
 DE (Fragment).  
 GN ORFNames=GSTENG00010070001;  
 OS Tetradon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OC NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,  
 RA Dasiva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anhouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,  
 RA Blemond C., Skalli Z., Cattolico L., Poutain J., De Berardinis V.,  
 RA Cruaud C., Duprat G., Brottier P., Coutanceau J.P., Guzy J.,  
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 RT the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAAE01011868; CAF94123.1; -; Genomic\_DNA.  
 DR InterPro; IPR001450; 4Fe4S\_Fe\_S\_b.  
 DR InterPro; IPR000759; Admnd\_reductase.  
 DR InterPro; IPR001295; DHO\_dh.  
 DR InterPro; IPR005720; DHO\_dhl.  
 DR InterPro; IPR001327; FAD\_pyr\_redox.  
 DR InterPro; IPR00103; Pyridine\_redox\_2.  
 DR InterPro; IPR003009; Related\_FMN\_bd.  
 DR Pfam; PF01180; DHO\_dh; 1.  
 DR Pfam; PF00037; Fer4; 2.  
 DR PRINTS; PR00419; ADXRDTASE.  
 DR PRINTS; PR00368; FADPNR.  
 DR PRINTS; PR00469; PNDRTASEII.  
 DR TIGRFAMs; TIGR01037; PYRD\_subl\_fam; 1.  
 DR PROSITE; PS00198; 4Fe4S\_FERREDOXIN; 1.  
 KW 4Fe-4S; Iron; Iron-sulfur; Metal-binding.  
 FT NON\_TER 1  
 SQ SEQUENCE 1103 AA; 120510 MW; 3303FE5045F9D559 CRC64;  
  
 Query Match 79.2%; Score 42; DB 2; Length 1103;  
 Best Local Similarity 77.8%; Pred. No. 3.3e+02; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 1;  
  
 QY 1 EGPWLEEE 9  
 DB 489 EGDWLEEE 497  
  
 RESULT 17  
 Q8LKG4 LOLPR  
 ID Q8LKG4\_LOLPR PRELIMINARY; PRT; 83 AA.  
 AC Q8LKG4\_LOLPR  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE R2R3 MYB protein MYB3 (Fragment).  
 DE Name=MYB3;  
 OS Lolium perenne (Perennial ryegrass).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Poaceae; Lolium.  
 OC NCBI\_TaxID=4522;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Frederiksen A., Larsen K.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF515725; AAM53962.1; -; Genomic\_DNA.  
 DR HSP; P06876; 1GVD.  
 DR Gramene; O8LKG4; -;  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0045449; F:regulation of transcription; IEA.  
 DR InterPro; IPR012287; Homeodomain-rel.  
 DR InterPro; IPR001005; Myb\_DNA\_bd.  
 DR Pfam; PF00249; Myb\_DNA-binding; 1.  
 DR SMART; SM00717; SANT; 1.  
 DR PROSITE; PS00037; MYB\_1; UNKNOWN\_1.  
 DR PROSITE; PS50090; MYB\_3; 1.  
 KW Nuclear protein.  
 FT NON\_TER 83  
 SQ SEQUENCE 83 AA; 9490 MW; BE7A9B43F62703AF CRC64;

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Query Match          77.4%; Score 41; DB 2; Length 83;
Best Local Similarity 66.7%; Pred. NO. 34;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
Db 15 KGPWTEED 23

RESULT 18
Q8S415 MAIZE
ID Q8S415_MAIZE PRELIMINARY; PRT; 160 AA.
AC Q8S415;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE P-type R2R3 Myb protein.
GN Name=Myb49;
OS Zea mays (Maize);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea;
OX NCBI_TaxID=4577;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14729259; DOI=10.1016/j.gene.2003.09.049;
RA Jiang C., Gu J., Chopra S., Gu X., Peterson T.;
RT "Ordered origin of the typical two- and three-repeat Myb genes.";
RL Gene 326;13-22(2004).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AF470090; AAL0658.1; -; Genomic_DNA.
DR HSSP; P06876; 1MBK.
DR Gramene; Q8S415; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; Myb DNA bd.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00037; MYB 1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PSS0090; MYB_3; 2.
KW Nuclear protein; Repeat.
SQ SEQUENCE 160 AA; 17920 MW; 1FCBA42C22AF1B89 CRC64;

Query Match          77.4%; Score 41; DB 2; Length 160;
Best Local Similarity 66.7%; Pred. NO. 68;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
Db 15 KGPWTEED 23

RESULT 19
Q8X4R9 ECO57
ID Q8X4R9_ECO57 PRELIMINARY; PRT; 248 AA.
AC Q8X4R9; Q7AB98;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein ECG3611.
GN OrderedLocName=ECG3611. z4066;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1];
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;

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RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.P., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=O157:H7 / Sakai / RMD 050952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AR005174; AAG57864.1; -; Genomic DNA.
DR EMBL; BA000007; BAB37034.1; -; Genomic_DNA.
DR PIR; C91080; C91080.
DR FIR; D85925; D85925.
DR InterPro; IPR010147; Cas_CTI976.
DR TIGRFAMs; TIGR01868; cas_CTI976; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 248 AA; 28619 MW; D0F452DA2299E3D8 CRC64;

Query Match          77.4%; Score 41; DB 2; Length 248;
Best Local Similarity 66.7%; Pred. NO. 11e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
Db 234 QGPWLSKEE 242

RESULT 20
O9A1F8 ARATH
ID O9A1F8_ARATH PRELIMINARY; PRT; 273 AA.
AC O9A1F8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MYB transcription factor Atmyb2.
GN Name=Atmyb2;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Dra-0;
RX MEDLINE=22422132; PubMed=12534212;
RA Kamiya T., Kawabe A., Miyashita N.T.;
RT "Nucleotide polymorphism at the Atmyb2 locus of the wild plant
RT Arabidopsis thaliana.";
RL Genet. Res. 80:89-98(2002).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AB052235; BAB62115.1; -; Genomic_DNA.
DR HSSP; P06876; LGVD.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR001395; Aldo/ket red.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; Myb DNA bd.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
DR PROSITE; PS00037; MYB 1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.

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DR PROSITE; PS50090; MYB\_3; 2.  
 KW Nuclear protein; Repeat.  
 SQ SEQUENCE 273 AA; 31429 MW; 52B5D2466790B9B6 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 273;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9  
 :||| |||:  
 Db 22 KGPWTEED 30

RESULT 21  
 ID Q94IF6 ARATH PRELIMINARY; PRT; 273 AA.  
 AC Q94IF6;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE MYB transcription factor Atmyb2.  
 GN Name=Atmyb2;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=In-0;  
 RX MEDLINE=22422132; PubMed=12534212;  
 RA Kamiya T., Kawabe A., Miyashita N.T.;  
 RT "Nucleotide polymorphism at the Atmyb2 locus of the wild plant  
 Arabidopsis thaliana."  
 RL Genet. Res. 80:89-98(2002).  
 CC -|- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL; AB052239; BAB62119.1; -; Genomic\_DNA.  
 DR HSSP; P06876; LGVD.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0045449; P:regulation of transcription; IEA.  
 DR InterPro; IPR001395; Aldo/ket red.  
 DR InterPro; IPR012287; Homeodomain-rel.  
 DR Pfam; PF00249; Myb\_DNA-binding; 2.  
 DR SMART; SM00717; SANT; 2.  
 DR PROSITE; PS00063; ALDO-KETO REDUCTASE\_3; UNKNOWN\_1.  
 DR PROSITE; PS00037; MYB\_1; UNKNOWN\_1.  
 DR PROSITE; PS00334; MYB\_2; 1.  
 DR PROSITE; PS50090; MYB\_3; 2.  
 KW Nuclear protein; Repeat.  
 SQ SEQUENCE 273 AA; 31433 MW; 726186432287049E CRC64;

Query Match 77.4%; Score 41; DB 2; Length 273;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9  
 :||| |||:  
 Db 22 KGPWTEED 30

RESULT 22  
 ID Q94IF9 ARATH PRELIMINARY; PRT; 273 AA.  
 AC Q94IF9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE MYB transcription factor Atmyb2.  
 GN Name=Atmyb2;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Ci-0;  
 RX MEDLINE=22422132; PubMed=12534212;  
 RA Kamiya T., Kawabe A., Miyashita N.T.;  
 RT "Nucleotide polymorphism at the Atmyb2 locus of the wild plant  
 Arabidopsis thaliana."  
 RL Genet. Res. 80:89-98(2002).  
 CC -|- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL; AB052234; BAB62114.1; -; Genomic\_DNA.  
 DR HSSP; P06876; LGVD.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0045449; P:regulation of transcription; IEA.  
 DR InterPro; IPR001395; Aldo/ket red.  
 DR InterPro; IPR012287; Homeodomain-rel.  
 DR Pfam; PF00249; Myb\_DNA-binding; 2.  
 DR SMART; SM00717; SANT; 2.  
 DR PROSITE; PS00063; ALDO-KETO REDUCTASE\_3; UNKNOWN\_1.  
 DR PROSITE; PS00037; MYB\_1; UNKNOWN\_1.  
 DR PROSITE; PS00334; MYB\_2; 1.  
 DR PROSITE; PS50090; MYB\_3; 2.  
 KW Nuclear protein; Repeat.  
 SQ SEQUENCE 273 AA; 31416 MW; 737F99A3C287049E CRC64;

Query Match 77.4%; Score 41; DB 2; Length 273;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9  
 :||| |||:  
 Db 22 KGPWTEED 30

RESULT 23  
 ID Q39028 ARATH PRELIMINARY; PRT; 273 AA.  
 AC Q39028;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE MYB transcription factor Atmyb2 (Atg47190).  
 GN Name=Atmyb2; ORFNames=At2g47190;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC MEDLINE=94146551; PubMed=8312738; DOI=10.1105/tpc.5.11.1529;  
 RA Urao T., Yamaguchi-Shinozaki K., Urao S., Shinozaki K.;  
 RT "An Arabidopsis myb homolog is induced by dehydration stress and its  
 gene product binds to the conserved MYB recognition sequence."  
 RL Plant Cell 5:1529-1539(1993).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=UK-2;  
 RX MEDLINE=22422132; PubMed=12534212;  
 RA Kamiya T., Kawabe A., Miyashita N.T.;  
 RT "Nucleotide polymorphism at the Atmyb2 locus of the wild plant  
 Arabidopsis thaliana."  
 RL Genet. Res. 80:89-98(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,  
 RA Spriggs T.A., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R.,  
 RA Venter J.C.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

CC	-1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR	EMBL; AB052250; BAB62130.1; -; Genomic_DNA.
DR	EMBL; AB052232; BAB62112.1; -; Genomic_DNA.
DR	EMBL; AB052233; BAB62113.1; -; Genomic_DNA.
DR	EMBL; AB052236; BAB62116.1; -; Genomic_DNA.
DR	EMBL; AB052240; BAB62120.1; -; Genomic_DNA.
DR	EMBL; AB052243; BAB62123.1; -; Genomic_DNA.
DR	EMBL; AB052246; BAB62126.1; -; Genomic_DNA.
DR	EMBL; AB052247; BAB62127.1; -; Genomic_DNA.
DR	EMBL; AB052245; BAB62125.1; -; Genomic_DNA.
DR	EMBL; AB052242; BAB62122.1; -; Genomic_DNA.
DR	EMBL; AB052237; BAB62117.1; -; Genomic_DNA.
DR	HSSP; P06876; 1GVD.
DR	GO; GO:0005634; C:nucleus; IEA.
DR	GO; GO:0003677; F:DNA binding; IEA.
DR	GO; GO:0045449; P:regulation of transcription; IEA.
DR	InterPro; IPR001395; Aldo/ket red.
DR	InterPro; IPR012287; Homeodomain-rel.
DR	InterPro; IPR001005; Myb DNA bd.
DR	Pfam; PF00249; Myb DNA-binding; 2.
DR	SMART; SM00717; SANT; 2.
DR	PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
DR	PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR	PROSITE; PS00334; MYB_2; 1.
DR	PROSITE; PS50090; MYB_3; 2.
KW	Nuclear protein; Repeat.
SQ	SEQUENCE 273 AA; 31434 MW; 726F88A3C287049E CRC64;
Query Match	77.4%; Score 41; DB 2; Length 273;
Best Local Similarity	66.7%; Pred. No. 1.2e+02;
Matches	6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY	1 EGPWLEEEE 9 :     :
DB	22 KGFWTEED 30
RESULT 25	
Q93V46 ARATH	
ID	Q93V46 ARATH PRELIMINARY; PRT; 273 AA.
AC	Q93V46;
DT	01-DEC-2001 (TREMBlrel. 19, Created)
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT	01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE	MYB transcription factor Atmyb2.
GN	Name=Atmyb2;
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC	Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi8.
OX	NCBI_TaxID=3702;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=ws-0, Kas-1, and Ost-0;
RC	MEDLINE=22422132; PubMed=12534212;
RA	Kamiya T., Kawabe A., Miyashita N.T.;
RT	"Nucleotide polymorphism at the Atmyb2 locus of the wild plant Arabidopsis thaliana.";
RL	Genet. Res. 80:89-98(2002).
CC	-1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR	EMBL; AB052249; BAB62129.1; -; Genomic_DNA.
DR	EMBL; AB052241; BAB62121.1; -; Genomic_DNA.
DR	EMBL; AB052244; BAB62124.1; -; Genomic_DNA.
DR	HSSP; P06876; 1GVD.
DR	GO; GO:0005634; C:nucleus; IEA.
DR	GO; GO:0003677; F:DNA binding; IEA.
DR	GO; GO:0045449; P:regulation of transcription; IEA.
DR	InterPro; IPR001395; Aldo/ket red.
DR	InterPro; IPR012287; Homeodomain-rel.
DR	InterPro; IPR001005; Myb DNA bd.
DR	Pfam; PF00249; Myb DNA-binding; 2.
DR	SMART; SM00717; SANT; 2.
DR	PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
DR	PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR	PROSITE; PS00334; MYB_2; 1.
DR	PROSITE; PS50090; MYB_3; 2.
KW	Nuclear protein; Repeat.
SQ	SEQUENCE 273 AA; 31448 MW; 94BAE5F38C3854DF CRC64;
Query Match	77.4%; Score 41; DB 2; Length 273;
Best Local Similarity	66.7%; Pred. No. 1.2e+02;
Matches	6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY	1 EGPWLEEEE 9 :     :
DB	22 KGFWTEED 30
RESULT 24	
Q93VZ0 ARATH	
ID	Q93VZ0 ARATH PRELIMINARY; PRT; 273 AA.
AC	Q93VZ0;
DT	01-DEC-2001 (TREMBlrel. 19, Created)
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT	01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE	MYB transcription factor Atmyb2.
GN	Name=Atmyb2;
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC	Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi8.
OX	NCBI_TaxID=3702;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=yo-0, As-0, Ag-0, Es-0, Gr-1, Ita-0, Mr-0, Mt-0, Shokei, Su-0,
RC	and Ts-1;
RC	MEDLINE=22422132; PubMed=12534212;
RX	Kamiya T., Kawabe A., Miyashita N.T.;
RT	"Nucleotide polymorphism at the Atmyb2 locus of the wild plant Arabidopsis thaliana.";
RL	Genet. Res. 80:89-98(2002).

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DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS00090; MYB_3; 2.
KW Nuclear protein; Repeat.
SQ SEQUENCE 273 AA; 31461 MW; F8472A327B97FA7E CRC64;

Query Match 77.4%; Score 41; DB 2; Length 273;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db :|||||:
22 KGPWTEED 30

RESULT 26
QBH257_9ROSI PRELIMINARY; PRT; 286 AA.
AC QBH257;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myb-like transcription factor 5 (Fragment).
GN Name=MYB5;
OS Gossypioideae kirkii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Gossypioideae.
OX NCBI_TaxID=47615;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22490468; PubMed=12602863; DOI=10.1023/A:1022051100610;
RA Cedroni M.L., Cronn R.C., Adams K.L., Wilkins T.A., Wendel J.F.;
RT "Evolution and expression of MYB genes in diploid and polyploid
cotton.";
RL Plant Mol. Biol. 51:313-325(2003).
DR EMBL; AY115512; AAN28284.1; -; Genomic_DNA.
DR HSSP; P06876; IGVD.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS001395; Aldo/ket-red
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; Myb DNA bd.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00063; ALDOKETO REDUCTASE_3; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS00090; MYB_3; 2.
KW Nuclear protein.
FT NON TER 286
SQ SEQUENCE 286 AA; 32565 MW; A03677BEE61EF2C7 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 286;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db :|||||:
23 KGPWTEED 31

RESULT 27
QBH261_GOSHI PRELIMINARY; PRT; 287 AA.
AC QBH261;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myb-like transcription factor 5 (Fragment).
GN Name=MYB5;
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Gossypium.
OX NCBI_TaxID=3635;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22490468; PubMed=12602863; DOI=10.1023/A:1022051100610;
RA Cedroni M.L., Cronn R.C., Adams K.L., Wilkins T.A., Wendel J.F.;
RT "Evolution and expression of MYB genes in diploid and polyploid
cotton.";
RL Plant Mol. Biol. 51:313-325(2003).
DR EMBL; AY115512; AAN28280.1; -; Genomic_DNA.
DR HSSP; P06876; IGVD.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS00090; MYB_3; 2.
KW Nuclear protein.
FT NON TER 287
SQ SEQUENCE 287 AA; 32724 MW; 701ADA7EB384F538 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 287;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db :|||||:
23 KGPWTEED 31

RESULT 28
QBH260_GOSHI PRELIMINARY; PRT; 287 AA.
AC QBH260;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myb-like transcription factor 5 (Fragment).
GN Name=MYB5;
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Gossypium.
OX NCBI_TaxID=3635;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22490468; PubMed=12602863; DOI=10.1023/A:1022051100610;
RA Cedroni M.L., Cronn R.C., Adams K.L., Wilkins T.A., Wendel J.F.;
RT "Evolution and expression of MYB genes in diploid and polyploid
cotton.";
RL Plant Mol. Biol. 51:313-325(2003).
DR EMBL; AY115513; AAN28281.1; -; Genomic_DNA.
DR HSSP; P06876; IGVD.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; Myb DNA bd.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS00090; MYB_3; 2.
KW Nuclear protein.
FT NON TER 287
SQ SEQUENCE 287 AA; 32893 MW; 753E33018004C699 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 287;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy Db

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RESULT 32
Q94JN4 GOSHI
ID Q94JN4_GOSHI PRELIMINARY; PRT; 293 AA.
AC Q94JN4_
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myb-like transcription factor Myb 5.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cronn R., Cedroni M., Haselkorn T., Osborne C., Wendel J.F.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AF377317; AAK57699.1; -; Genomic_DNA.
DR HSSP; P06876; 1GVD.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00249; Myb DNA bd.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
DR Nuclear protein; Repeat.
KW NUCLEAR PROTEIN; REPEAT.
SQ SEQUENCE 293 AA; 33407 MW; C1FIADBA5966401A CRC64;

Query Match 77.4%; Score 41; DB 2; Length 293;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 23 KGPWTEED 31

RESULT 33
Q94JN5 GOSHI
ID Q94JN5_GOSHI PRELIMINARY; PRT; 293 AA.
AC Q94JN5_
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myb-like transcription factor Myb 5.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cronn R., Cedroni M., Haselkorn T., Osborne C., Wendel J.F.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AF377316; AAK57698.1; -; Genomic_DNA.
DR HSSP; P06876; 1GVD.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00249; Myb DNA bd.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
DR Nuclear protein; Repeat.
KW NUCLEAR PROTEIN; REPEAT.
SQ SEQUENCE 293 AA; 33407 MW; C1FIADBA5966401A CRC64;

Query Match 77.4%; Score 41; DB 2; Length 293;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 23 KGPWTEED 31

RESULT 34
Q7F9M1 ORYSA
ID Q7F9M1_ORYSA PRELIMINARY; PRT; 340 AA.
AC Q7F9M1; Q5VSV3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE OSUNBA0008A01.3 protein (OSUNBA0009P12.23 protein).
GN Name=OSUNBA0006A01.3; Synonyms=OSUNBA0009P12.23;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22337377; PubMed=12447439; DOI=10.1038/nature01183;
RA Peng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu J., Zhang L.S., Yu Z., Fan Y.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AL731579; CAE05467.3; -; Genomic DNA.
DR EMBL; AL662952; CAE04136.3; -; Genomic_DNA.
DR Gramene; Q5VSV3; -.
DR Gramene; Q7F9M1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00334; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
DR Nuclear protein; Repeat.
KW NUCLEAR PROTEIN; REPEAT.
SQ SEQUENCE 340 AA; 36877 MW; BEFD3DCF88168C85 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 340;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 15 KGPWTEED 23

RESULT 35
Q72IA2 THET2
ID Q72IA2_THET2 PRELIMINARY; PRT; 652 AA.
AC Q72IA2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
KW NUCLEAR PROTEIN; REPEAT.

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DE	Serine/threonine protein kinase (EC 2.7.1.37).	DR	InterPro; IPR000719; Prot_kinase.
GN	OrderedLocusNames=TTCL230;	DR	InterPro; IPR008271; Ser_thr_pkin_AS.
OS	Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).	DR	InterPro; IPR002290; Ser_thr_pkinase.
OC	Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;	DR	InterPro; IPR001245; Tyr_pkinase.
OC	Thermus.	DR	Pfam; PF01436; NHL; 3.
OX	NCBI_TaxID=262724;	DR	Pfam; PF00069; Pkinase; 1.
RN	[1]_TaxID=262724;	DR	ProDom; PD000001; Prot_kinase; 1.
RP	NUCLEOTIDE SEQUENCE.	DR	SMART; SM00220; S_TKC; 1.
RX	PubMed=15064768; DOI=10.1038/nbt956;	DR	SMART; SM00219; TYRKC; 1.
RA	Henne A., Brueggemann H., Raasch C., Wieser A., Hartsch T.,	DR	PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
RA	Liesegang H., Johann A., Lienhard T., Gohl O., Martinez-Arias R.,	DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
RA	Jacobi C., Starkuviene V., Schlenczek S., Dencker S., Huber R.,	DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
RA	Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;	KW	Complete proteome; Kinase; Serine/threonine-protein kinase.
RT	"The genome sequence of the extreme thermophile Thermus	SQ	SEQUENCE 652 AA; 71217 MW; 5CDD4C2D08AEFCBA CRC64;
RT	thermophilus."		
RL	Nat. Biotechnol. 22:547-553(2004).		
DR	EMBL; AB017305; AAS81572.1; -; Genomic_DNA.	Query Match	77.4%; Score 41; DB 2; Length 652;
DR	GO; GO:0005524; F:ATP binding; IEA.	Best Local Similarity	77.8%; Pred. No. 2.9e+02;
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.	Matches	7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.		
DR	GO; GO:0016740; F:transferase activity; IEA.	QY	1 EGPWLEEE 9
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.	Db	361 EGPWEERE 369
DR	InterPro; IPR001258; NHL.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR008271; Ser_thr_pkin_AS.		
DR	InterPro; IPR002290; Ser_thr_pkinase.		
DR	InterPro; IPR001245; Tyr_pkinase.		
DR	Pfam; PF01436; NHL; 3.		
DR	Pfam; PF00069; Pkinase; 1.		
DR	ProDom; PD000001; Prot_kinase; 1.		
DR	SMART; SM00220; S_TKC; 1.		
DR	SMART; SM00219; TYRKC; 1.		
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.		
DR	PROSITE; PS00111; PROTEIN KINASE_DOM; 1.		
DR	PROSITE; PS00108; PROTEIN KINASE_ST; 1.		
KW	Complete proteome; Kinase; Serine/threonine-protein kinase;		
SW	Transferase.		
SQ	SEQUENCE 652 AA; 71203 MW; B396886E8B546A1 CRC64;		
		Query Match	77.4%; Score 41; DB 2; Length 652;
		Best Local Similarity	77.8%; Pred. No. 2.9e+02;
		Matches	7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 EGPWLEEE 9		
Db	361 EGPWEERE 369		
		Query Match	77.4%; Score 41; DB 2; Length 1424;
		Best Local Similarity	77.8%; Pred. No. 6.4e+02;
		Matches	7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
RESULT 36			
Q5SHY6_THET8		QY	1 EGPWLEEE 9
ID	Q5SHY6_THET8 PRELIMINARY; PRT; 652 AA.	Db	720 EDPWLEERE 728
AC	Q5SHY6;		
DT	01-FEB-2005 (TrEMBLrel. 29, Created)		
DT	01-FEB-2005 (TrEMBLrel. 29, Last sequence update)		
DT	01-FEB-2005 (TrEMBLrel. 29, Last annotation update)		
DE	Serine/threonine protein kinase.		
GN	OrderedLocusNames=TTA1594;		
OS	Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579).		
OC	Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;		
OC	Thermus.		
OX	NCBI_TaxID=300852;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Maui R., Kurokawa K., Nakagawa N., Tokunaga F., Koyama Y.,		
RA	Shibata T., Oshima T., Yokoyama S., Yagunaga T., Kuramitsu S.;		
RT	"Complete genome sequence of Thermus thermophilus HB8."		
RL	Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AP008226; BAD71417.1; -; Genomic_DNA.		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.		
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.		
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.		
DR	InterPro; IPR001258; NHL.		
		Query Match	77.4%; Score 41; DB 2; Length 1424;
		Best Local Similarity	77.8%; Pred. No. 6.4e+02;
		Matches	7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 EGPWLEEE 9		
Db	361 EGPWEERE 369		
		Query Match	77.4%; Score 41; DB 2; Length 1424;
		Best Local Similarity	77.8%; Pred. No. 6.4e+02;
		Matches	7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
RESULT 37			
Q5RG88_BRARE		QY	1 EGPWLEEE 9
ID	Q5RG88_BRARE PRELIMINARY; PRT; 1424 AA.	Db	361 EGPWEERE 369
AC	Q5RG88;		
DT	01-FEB-2005 (TrEMBLrel. 29, Created)		
DT	01-FEB-2005 (TrEMBLrel. 29, Last sequence update)		
DT	01-FEB-2005 (TrEMBLrel. 29, Last annotation update)		
DE	Novel protein similar to vertebrate YLP motif containing 1		
DE	(YLPW1).		
GN	Name=OTDARP0000008511; ORFNames=CH211-59D15.5-001;		
OS	Brachydanio rerio (Zebrafish) (Danio rerio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;		
OC	Cyprinidae; Danio.		
OX	NCBI_TaxID=7955;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Donaldson S.;		
RL	Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BX942841; CA112027.1; -; Genomic DNA.		
SQ	SEQUENCE 1424 AA; 163360 MW; 3C44FEFF711DFB08 CRC64;		
		Query Match	77.4%; Score 41; DB 2; Length 1424;
		Best Local Similarity	77.8%; Pred. No. 6.4e+02;
		Matches	7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 EGPWLEEE 9		
Db	720 EDPWLEERE 728		
		Query Match	77.4%; Score 41; DB 2; Length 1424;
		Best Local Similarity	77.8%; Pred. No. 6.4e+02;
		Matches	7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
RESULT 38			
GAST_CAVPO		QY	1 EGPWLEEE 9
ID	GAST_CAVPO STANDARD; PRT; 33 AA.	Db	720 EDPWLEERE 728
AC	P06885;		
DT	01-JAN-1988 (Rel. 06, Created)		
DT	01-JUL-1993 (Rel. 26, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		
DE	Gastrin precursor [Contains: Big gastrin (Gastrin 33); Gastrin].		
GN	Name=GAST; Synonyms=GAS;		
OS	Cavia porcellus (Guinea pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;		
OC	Hystricognathi; Caviidae; Cavia.		
OX	NCBI_TaxID=10141;		
RN	[1]		
RP	PROTEIN SEQUENCE.		
RA	PubMed=3747718; DOI=10.1016/0024-3205(86)90283-3;		
RX	MEDLINE=86309993; PubMed=3747718; DOI=10.1016/0024-3205(86)90283-3;		
RA	Bonato C., Eng J., Pan Y.-C.E., Miedel M., Hulmes J.D., Yalow R.S.;		

RT "Guinea pig 33-amino acid gastrin."; Life Sci. 39:959-964(1986).  
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stomach and intestine.  
CC  
CC  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
CC  
CC PIR; A26089; GMPGB.  
DR InterPro; IPR001651; Gastrin.  
DR Pfam; PF00318; GASTRIN; 1.  
DR PROSITE; PS00259; GASTRIN; 1.  
KW Amidation; Cleavage on pair of basic residues; Direct protein sequencing; Hormone; Pyrrolidone carboxylic acid.  
FT PEPTIDE 1 33 Big gastrin.  
FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
FT MOD\_RES 18 18 Pyrrolidone carboxylic acid.  
FT MOD\_RES 33 33 Phenylalanine amide.  
SQ SEQUENCE 33 AA; 3757 MW; B37C251CD40EB30C CRC64;  
  
Query Match 75.5%; Score 40; DB 1; Length 33;  
Best Local Similarity 75.0%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 EGPWLEEE 8  
DB :||| |||  
18 QGPWABEE 25  
  
RESULT 39  
GAST\_CHIBR STANDARD; PRT; 33 AA.  
AC P10034;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Gastrin precursor [Ontario: Big gastrin (Gastrin 33); Gastrin].  
GN Name=GAST; Synonyms=GAS;  
OS Chinchilla brevicaudata (Chinchilla).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Hystriognathi; Chinchillidae; Chinchilla.  
OX NCBI\_TaxID=10152;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=87156784; PubMed=3827930;  
RA Shinomura Y., Eng J., Yalow R.S.;  
RT "Chinchilla 'big' and 'little' gastrins."; Biochem. Biophys. Res. Commun. 143:7-14(1987).  
RL -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stomach and intestine.  
CC  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
CC  
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CC  
CC PIR; A29541; A29541.

DR PIR; B29541; B29541.  
DR InterPro; IPR001651; Gastrin.  
DR Pfam; PF00318; GASTRIN; 1.  
DR PROSITE; PS00259; GASTRIN; 1.  
KW Amidation; Cleavage on pair of basic residues; Direct protein sequencing; Hormone; Pyrrolidone carboxylic acid; Sulfation.  
FT PEPTIDE 1 33 Big gastrin.  
FT MOD\_RES 18 18 Pyrrolidone carboxylic acid.  
FT MOD\_RES 28 28 Sulfotyrosine.  
FT MOD\_RES 33 33 Phenylalanine amide.  
SQ SEQUENCE 33 AA; 3715 MW; 6F11P5CD50FAA2D CRC64;  
  
Query Match 75.5%; Score 40; DB 1; Length 33;  
Best Local Similarity 75.0%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 EGPWLEEE 8  
DB :||| |||  
18 QGPWABEE 25  
  
RESULT 40  
2SSI\_BRANA STANDARD; PRT; 110 AA.  
ID 2SSI\_BRANA  
AC P24565;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Napin IA and IB small chain and large chains.  
OS Brassica napus (Rape).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
OX NCBI\_TaxID=3708;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX TISSUE=Seed;  
RC MEDLINE=92111741; PubMed=1765156; DOI=10.1016/0014-5793(91)81419-9;  
RA Monsalve R.I., Lopez-Otin C., Villalba M., Rodriguez R.;  
RT "A new distinct group of 2 S albumins from rapeseed. Amino acid sequence of two low molecular weight napins."; FEBS Lett. 295:207-210(1991).  
RL -!- FUNCTION: The small, basic, water-soluble napins are one of the two major kinds of storage proteins synthesized in the seed during its maturation.  
CC  
CC -!- SUBUNIT: The mature protein consists of a small and a large chain linked by disulfide bonds.  
CC  
CC -!- MISCELLANEOUS: Napin IA and IB are minor component of seed 2S albumin.  
CC  
CC -!- MISCELLANEOUS: The sequence shown is that of napin IA.  
CC  
CC -!- SIMILARITY: Belongs to the 2S seed storage albumins family.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
CC  
CC PIR; S20350; S20350.  
DR PIR; S26636; S26636.  
DR PDB; 1PNB; NMR; A=1-31, B=32-106.  
DR SMR; P24565; 1-106.  
DR InterPro; IPR003612; AAI.  
DR InterPro; IPR000617; Napin.  
DR Pfam; PF00234; TYP\_alpha\_amyl; 1.  
DR PRINTS; PR00496; NAFIN.  
DR ProDom; PD002498; NAFIN.  
DR SMART; SM00499; AAI; 1.  
KW 3D-structure; Direct protein sequencing; Seed storage protein; Storage protein.  
FT CHAIN 1 31 Napin IA small chain.

FT	CHAIN	32	110	Napin IA large chain.
FT	VARIANT	31	31	Missing (in minor form "SM", less than 7%).
FT				E -> Q (in napin IB).
FT	VARIANT	37	37	Missing (in napin IB).
FT	VARIANT	107	110	
FT	NON CONS	31	32	
FT	HELIX	3	12	
FT	TURN	13	13	
FT	TURN	17	18	
FT	TURN	19	24	
FT	TURN	25	26	
FT	TURN	42	42	
FT	HELIX	43	50	
FT	TURN	51	51	
FT	HELIX	54	56	
FT	HELIX	58	69	
FT	HELIX	71	73	
FT	HELIX	79	85	
FT	TURN	96	98	
SQ	SEQUENCE	110 AA;	12691 MW;	3A2938ADA2C1E995 CRC64;
Query Match 75.5%; Score 40; DB 1; Length 110;				
Best Local Similarity 75.0%; Pred. No. 68;				
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;				
QY		1	EGPWLEEE 8	
DB		37	EGPWLEEQ 44	
RESULT 41				
Q7XKD8	ORYSA			PRT; 129 AA.
ID	Q7XKD8_ORYSA	PRELIMINARY;		
AC	Q7XKD8;			
DT	01-OCT-2003	(TREMBlrel. 25, Created)		
DT	01-OCT-2003	(TREMBlrel. 25, Last sequence update)		
DT	01-MAR-2004	(TREMBlrel. 26, Last annotation update)		
DE	OSJNB0017101.16	protein.		
GN	Names=OSJNB0017101.16;			
OS	Oryza sativa (japonica cultivar-group).			
OC	Eukaryota; Viridiplantae; Streptophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Ehrhartoideae; Oryzeae; Oryza.			
OX	NCBI_TaxID=39947;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	PubMed=12447439; DOI=10.1038/nature01183;			
RA	Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,			
RA	Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,			
RA	Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,			
RA	Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,			
RA	Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,			
RA	Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,			
RA	Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang W.,			
RA	Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,			
RA	Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,			
RA	Han B.;			
RL	"Sequence and analysis of rice chromosome 4.";			
RL	Nature 420:316-320(2002).			
DR	EMBL; AL606456; CA905736.1; -; Genomic_DNA.			
DR	Gramene; Q7XKD8; -;			
DR	InterPro; IPR008162; Pyrophosphatase.			
DR	PROSITE; PS00387; PPASE; UNKNOWN 1.			
SQ	SEQUENCE	129 AA;	13322 MW;	EB85F75BB8454F21 CRC64;
Query Match 75.5%; Score 40; DB 2; Length 129;				
Best Local Similarity 87.5%; Pred. No. 80;				
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY		2	GPWLEEEE 9	
DB		94	GPWDEEE 101	

RESULT 42				
P81394	ANTMA			PRT; 268 AA.
ID	P81394_ANTMA	PRELIMINARY;		
AC	P81394;			
DT	01-JUN-1998	(TREMBlrel. 06, Created)		
DT	01-JUN-1998	(TREMBlrel. 06, Last sequence update)		
DT	01-MAR-2004	(TREMBlrel. 26, Last annotation update)		
DE	MYB-related protein 315.			
GN	Name=MYB 315;			
OS	Antirrhinum majus (Garden snapdragon).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	Lamiids; Lamiales; Plantaginaceae; Antirrhineae; Antirrhinum.			
OX	NCBI_TaxID=4151;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=J1.522; TISSUE=FLOWER BUDS;			
RX	MEDLINE=93005689; PubMed=1840903; DOI=10.1105/tpc.3.2.115;			
RA	Jackeon D., Cullane-Macia F., Prescott A.G., Roberts K., Martin C.;			
RT	"Expression patterns of myb genes from Antirrhinum flowers.";			
RL	Plant Cell 3:115-125(1991).			
CC	-1- FUNCTION: MAY BE A TRANSCRIPTIONAL ACTIVATOR.			
CC	-1- TISSUE SPECIFICITY: ROOT, STEM, LEAF, SEED FOD, IMMATURE FLOWER			
CC	AND MATURE FLOWER.			
CC	-1- SIMILARITY: BELONGS TO THE MYB FAMILY OF PROTEINS.			
DR	PIR; JQ0961; JQ0961.			
DR	HSSP; Q03237; LA5U.			
DR	TRANSFAC; T02927; -.			
DR	GO; GO:0005634; C:nucleus; IEA.			
DR	GO; GO:0003677; F:DNA binding; IEA.			
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.			
DR	InterPro; IPR012287; Homeodomain-rel.			
DR	InterPro; IPR001005; Myb_DNA-binding.			
DR	Pfam; PF00249; Myb_DNA-binding; 2.			
DR	SMART; SM00717; SANT; 2.			
DR	PROSITE; PS00037; MYB_1; UNKNOWN 1.			
DR	PROSITE; PS00334; MYB_2; UNKNOWN 1.			
DR	PROSITE; PS50090; MYB_3; 2.			
KW	DNA-binding; Nuclear protein; Repeat; Transcription regulation.			
FT	DNA BIND	9	61	MYB.
FT	DNA BIND	62	102	MYB.
SQ	SEQUENCE	268 AA;	31110 MW;	886C04A4F45D26D1 CRC64;
Query Match 75.5%; Score 40; DB 2; Length 268;				
Best Local Similarity 75.0%; Pred. No. 1.7e+02;				
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;				
QY		2	GPWLEEEE 9	
DB		15	GPWTEED 22	
RESULT 43				
Q8C5S5	MOUSE			PRT; 269 AA.
ID	Q8C5S5_MOUSE	PRELIMINARY;		
AC	Q8C5S5;			
DT	01-MAR-2003	(TREMBlrel. 23, Created)		
DT	01-MAR-2003	(TREMBlrel. 23, Last sequence update)		
DT	01-JUN-2003	(TREMBlrel. 24, Last annotation update)		
DE	Mus musculus adult male testis cDNA, RIKEN full-length enriched			
DE	library, clone:4933417H09 product:hypothetical protein, full insert			
DE	sequence.			
GN	Name=493041302Rik;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muroidea; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=C57BL/6J; TISSUE=Testis;			
RX	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;			

RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44 (1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuoka H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Resole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Tovo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630 (2000).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771 (2000).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akai H., Tanaka T., Tanaka T.,  
 RA Tomaru A., Tova T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AK077173; BAC36660.1; -; mRNA.  
 DR Ensembl: ENSMUSG0000025918; Mus musculus.  
 DR MGI: MGI:1915236; 4930413O2Rik.  
 KW Hypothetical protein.  
 SQ SEQUENCE 269 AA; 30837 MW; AB7A5F99D64613C1 CRC64;  
 Query Match 75.5%; Score 40; DB 2; Length 269;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEE 9  
 Db 191 EGPWLSRQE 199  
 RESULT 44  
 Q9FJP2 ARATH PRELIMINARY;  
 ID Q9FJP2 ARATH PRELIMINARY; PRT; 310 AA.  
 AC Q9FJP2  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)  
 DE MYB transcription factor.  
 GN ORFNames=At5G652230;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 ON NCBI TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=98403884; PubMed=9734815;  
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.  
 RT Sequence features of the regions of 1,367,185 bp covered by 19  
 RT physically assigned P1 and TAC clones.";  
 RL DNA Res. 5:203-216 (1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Qu L., Gu H.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL: AB013395; BAB11659.1; -; Genomic\_DNA.  
 DR EMBL: AY519646; AAS10116.1; -; mRNA.  
 DR HSP; P06876; IGVD.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003677; F:DNA binding; IEA.  
 DR GO: GO:0045449; P:regulation of transcription; IEA.  
 DR InterPro: IPR012287; Homeodomain-rel.  
 DR InterPro: IPR001005; MYB\_DNA\_bd.  
 DR Pfam: PF00249; MYB\_DNA-binding; 2.  
 DR SMART: SM00717; SANT; 2.  
 DR PROSITE: PS00334; MYB 2; 1.  
 DR PROSITE: PS00090; MYB\_3; 2.  
 KW Nuclear protein; Repeat.  
 SQ SEQUENCE 310 AA; 35136 MW; 9070DD86A4C2AF9D CRC64;  
 Query Match 75.5%; Score 40; DB 2; Length 310;  
 Best Local Similarity 66.7%; Pred. No. 2e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEE 9  
 Db 14 KGPWLPEED 22  
 RESULT 45  
 Q4IRA3 GIBZE PRELIMINARY;  
 ID Q4IRA3 GIBZE PRELIMINARY; PRT; 311 AA.  
 AC Q4IRA3;  
 DT 13-SEP-2005 (TRENBLrel. 31, Created)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)

DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)  
DE Predicted protein.  
GN ORFNames=FG00255.1;  
OS Gibberella zeae PH-1.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.  
OX NCBI\_TaxID=229533;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=PH-1;  
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,  
RA Arachi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,  
RA Boukhaltier B., Butler J., Calvo S.E., Camarata J., Chang J.,  
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,  
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,  
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,  
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,  
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,  
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,  
RA Kelle C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,  
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,  
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,  
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,  
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,  
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,  
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,  
RA Roman J., Schauer S., Schupack R., Seaman S., Severi P., Smirnov S.,  
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,  
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,  
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,  
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,  
RA Lander E.;  
RT "Fusarium graminearum genome sequence.";  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR ENBL; AACM0100010; EAA69665.1; -; Genomic DNA.  
SQ SEQUENCE 311 AA; 35193 MW; 0A60FDBE1045238D CRC64;  
Query Match 75.5%; Score 40; DB 2; Length 311;  
Best Local Similarity 75.0%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EGPWLEEE 8  
DB 95 EGPWLEENQ 102  
RESULT 46  
Q8VE83 MOUSE  
ID Q8VE83\_MOUSE PRELIMINARY; PRT; 311 AA.  
AC Q8VE83;  
DT 01-MAR-2002 (T-EMBLrel. 20, Created)  
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)  
DE Tissue=Testis, and whole body;  
DE MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
DE 4930413022Rik protein.  
DE NCBI\_TaxID=10090;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CZECH II;  
RX TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CZECH II;  
RX TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR ENBL; BC019581; AAH19581.1; -; mRNA.  
DR Ensembl; ENSMUSG00000025918; Mus musculus.  
DR MGI; MGI:1915236; 4930413022Rik.  
SQ SEQUENCE 311 AA; 35902 MW; 98371209D95C91C7 CRC64;  
Query Match 75.5%; Score 40; DB 2; Length 311;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 EGPWLEEE 9  
DB 191 EGPWLSRQE 199  
RESULT 47  
Q9CQD5 MOUSE  
ID Q9CQD5\_MOUSE PRELIMINARY; PRT; 311 AA.  
AC Q9CQD5;  
DT 01-JUN-2001 (T-EMBLrel. 17, Created)  
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)  
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched  
DE library, clone:4930413022 product:hypothetical protein, full insert  
DE sequence (Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-  
DE length enriched library, clone:2810410C16 product:hypothetical  
DE protein, full insert sequence).  
DE NCBI\_TaxID=10090;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis, and whole body;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RX Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis, and whole body;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischnmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pebole G., Quackenbush J.,  
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyoko-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RL "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis, and Whole body;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis, and Whole body;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis, and Whole body;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwaagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis, and Whole body;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori P.,

RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK015133; BAB29721.1; -; mRNA.  
DR EMBL; AK013065; BAB28630.1; -; mRNA.  
DR Ensembl; ENSMUSG0000025918; Mus musculus.  
DR MGI; MGI:1915236; 4930413022Rik.  
KW Hypothetical protein.  
SQ SEQUENCE 311 AA; 35830 MW; 9B571209DB5E91C5 CRC64;  
Query Match 75.5%; Score 40; DB 2; Length 311;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 EGPWLEEE 9  
DB 191 EGPWLSRQE 199  
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AC Q4LGN3;  
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DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Carbohydrate kinase, PfkB.  
GN ORFNames=Bcen2424DRAFT\_0124;  
OS Burkholderia cenocepacia HI2424.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.  
OX NCBI\_TaxID=331272;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=HI2424;  
RG US DOE Joint Genome Institute (JGI-PGF);  
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,  
RA Hammon N., Istrani S., Pitluck S., Richardson P.;  
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia  
RT HI2424.";  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=HI2424;  
RG US DOE Joint Genome Institute (JGI-ORNL);  
RA Larimer F., Land M.;  
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia  
RT HI2424.";  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAHL01000158; EAM15222.1; -; Genomic\_DNA.  
KW Kinase.  
SQ SEQUENCE 316 AA; 34026 MW; 156788812C6FB5FA CRC64;  
Query Match 75.5%; Score 40; DB 2; Length 316;  
Best Local Similarity 75.0%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GPWLEEE 9  
DB 211 GPWLDSE 218  
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RESULT 49  
Q8CCQ4\_MOUSE



DR PROSITE; PSS0090; MYB\_3; 2.  
KW Nuclear protein; Repeat.  
SQ SEQUENCE 349 AA; 38884 MW; A37C22AAB96D891 CRC64;  
Query Match 75.5%; Score 40; DB 2; Length 349;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EGFWLEEE 9  
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Db 15 KGFWLPEED 23

Search completed: January 3, 2006, 09:49:51  
Job time : 118.143 secs

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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:20:09 ; Search time 12.1429 Seconds  
(without alignments)  
10.484 Million cell updates/sec

Title: US-10-759-832-1  
Perfect score: 103  
Sequence: 1 EGPWLEEEERAYGWDF 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published Applications AA New.\*  
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3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	93.2	17	6	US-10-997-066-31
2	96	93.2	19	7	US-11-145-566-38
3	46.5	45.1	3803	6	US-10-995-561-773
4	46.5	45.1	3960	6	US-10-995-561-771
5	46.5	45.1	5335	6	US-10-995-561-777
6	46.5	45.1	5406	6	US-10-995-561-774
7	46.5	45.1	5415	6	US-10-995-561-779
8	46.5	45.1	5464	6	US-10-995-561-775
9	45	43.7	21	6	US-10-939-890-559
10	43	41.7	264	6	US-10-821-234-1660
11	43	41.7	264	7	US-11-053-185-10
12	41	39.8	1119	7	US-11-115-639-1
13	40	38.8	734	6	US-10-652-893-2
14	40	38.8	734	6	US-11-137-465-65
15	39.5	38.3	389	7	US-11-060-008-11
16	39	37.9	700	7	US-11-186-284-141
17	38.5	37.4	397	7	US-11-060-008-8
18	38.5	37.4	413	7	US-11-060-008-9
19	38	36.9	170	7	US-11-069-642-12
20	38	36.9	241	6	US-10-467-657-1330
21	38	36.9	369	7	US-11-000-463-398
22	38	36.9	615	6	US-10-982-545-14
23	38	36.9	616	6	US-10-982-545-5
24	38	36.9	941	6	US-10-131-826A-464
25	37.5	36.4	338	6	US-10-793-626-1756
26	37	35	37	5	US-11-113-424-53
27	37	35.9	64	6	US-10-467-657-6478
28	37	35.9	82	6	US-10-821-234-1694
29	37	35.9	121	7	US-11-105-268-23
30	37	35.9	242	7	US-11-102-240-136
31	37	35.9	242	7	US-11-080-991-30
32	37	35.9	253	6	US-10-821-234-865
33	37	35.9	310	6	US-10-454-437-328
34	37	35.9	330	7	US-11-184-380-12
35	37	35.9	390	7	US-11-184-380-2
36	37	35.9	550	7	US-11-184-380-14
37	37	35.9	610	7	US-11-184-380-3
38	37	35.9	826	7	US-11-055-822-214
39	37	35.9	826	7	US-11-055-822-712
40	37	35.9	833	7	US-11-055-822-212
41	37	35.9	833	7	US-11-055-822-710
42	37	35.9	1176	6	US-10-821-234-897
43	37	35.9	1221	6	US-10-858-730-222
44	36.5	35.4	358	6	US-10-821-234-1563
45	36.5	35.4	575	7	US-11-131-212-24
46	36	35.0	22	6	US-10-939-890-453
47	36	35.0	22	6	US-10-939-890-684
48	36	35.0	22	6	US-10-939-890-685
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51	36	35.0	87	6	US-10-467-657-6302
52	36	35.0	159	7	US-11-055-822-700
53	36	35.0	159	7	US-11-055-822-786
54	36	35.0	306	6	US-10-467-657-2476
55	36	35.0	361	7	US-11-129-143-108
56	36	35.0	618	7	US-11-078-735-18
57	36	35.0	627	6	US-10-873-528-191
58	36	35.0	638	6	US-10-995-561-1025
59	36	35.0	1160	6	US-10-995-561-1019
60	36	35.0	1302	6	US-10-995-561-1024
61	36	35.0	1306	6	US-10-995-561-1027
62	36	35.0	5935	6	US-10-995-561-776
63	35.5	34.5	271	6	US-10-667-295-98
64	35.5	34.5	277	6	US-10-667-295-97
65	35.5	34.5	281	7	US-11-082-389-58
66	35.5	34.5	296	6	US-10-667-295-96
67	35.5	34.5	365	6	US-10-821-234-1575
68	35.5	34.5	535	7	US-11-106-672A-44
69	35.5	34.5	543	7	US-11-106-672A-10
70	35.5	34.5	543	7	US-11-057-732-6
71	35.5	34.5	592	7	US-11-106-672A-14
72	35	34.0	115	6	US-10-821-234-1433
73	35	34.0	195	7	US-11-038-284-26
74	35	34.0	257	6	US-10-821-234-1455
75	35	34.0	335	6	US-10-995-561-970
76	35	34.0	337	6	US-10-875-716-2
77	35	34.0	341	6	US-10-467-657-864
78	35	34.0	345	6	US-10-995-561-971
79	35	34.0	403	6	US-10-793-626-1522
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82	35	34.0	513	6	US-10-650-326B-16
83	35	34.0	521	7	US-11-105-268-58
84	35	34.0	521	7	US-11-078-189-18
85	35	34.0	820	7	US-11-147-047-31
86	35	34.0	919	6	US-10-821-234-951
87	35	34.0	3144	7	US-11-055-035-1
88	35	34.0	3433	6	US-10-714-781A-67
89	34.5	33.5	338	6	US-10-821-234-1565
90	34.5	33.5	398	6	US-10-509-773-10
91	34.5	33.5	400	6	US-10-467-657-7664
92	34.5	33.5	470	6	US-10-467-657-8420
93	34.5	33.5	482	6	US-10-467-657-7660
94	34	33.0	8	7	US-11-022-341-67
95	34	33.0	8	7	US-11-146-377-5
96	34	33.0	8	7	US-11-075-792-5
97	34	33.0	22	6	US-10-939-890-456
98	34	33.0	80	6	US-10-467-657-1988

99	34	33.0	119	6	US-10-793-626-2406	Sequence 2406, Ap	172	33	32.0	623	6	US-10-719-311-11	Sequence 11, Appl
100	34	33.0	146	7	US-11-083-800-8	Sequence 8, Appli	173	33	33.0	639	7	US-11-074-176-222	Sequence 222, App
101	34	33.0	158	6	US-10-793-626-3316	Sequence 3316, Ap	174	33	32.0	648	6	US-10-793-626-568	Sequence 568, App
102	34	33.0	190	6	US-10-466-794A-6	Sequence 6, Appli	175	33	32.0	687	6	US-10-485-517-274	Sequence 274, App
103	34	33.0	244	7	US-11-195-459-21	Sequence 21, Appl	176	33	32.0	720	7	US-11-103-957-88	Sequence 88, Appl
104	34	33.0	303	6	US-10-467-657-7918	Sequence 7918, Ap	177	33	32.0	723	6	US-10-467-657-1316	Sequence 1316, Ap
105	34	33.0	338	6	US-10-467-657-136	Sequence 136, App	178	33	32.0	1177	7	US-11-115-639-22	Sequence 22, Appl
106	34	33.0	338	6	US-10-467-657-6798	Sequence 6798, Ap	179	33	32.0	1177	7	US-11-115-639-23	Sequence 23, Appl
107	34	33.0	351	7	US-11-194-246-327	Sequence 327, App	180	33	32.0	1177	7	US-11-115-639-24	Sequence 24, Appl
108	34	33.0	362	7	US-11-012-762-62	Sequence 62, Appl	181	33	32.0	1177	7	US-11-115-639-25	Sequence 25, Appl
109	34	33.0	366	7	US-11-000-463-897	Sequence 897, App	182	33	32.0	1177	7	US-11-115-639-26	Sequence 26, Appl
110	34	33.0	400	7	US-11-000-463-425	Sequence 425, App	183	33	32.0	1177	7	US-11-115-639-27	Sequence 27, Appl
111	34	33.0	419	7	US-11-174-150-40	Sequence 40, Appl	184	33	32.0	1177	7	US-11-115-639-28	Sequence 28, Appl
112	34	33.0	436	7	US-11-174-150-39	Sequence 39, Appl	185	33	32.0	1177	7	US-11-115-639-29	Sequence 29, Appl
113	34	33.0	485	6	US-10-204-029-7	Sequence 7, Appli	186	33	32.0	1177	7	US-11-115-639-30	Sequence 30, Appl
114	34	33.0	534	7	US-11-055-822-268	Sequence 268, App	187	33	32.0	1183	7	US-11-115-639-13	Sequence 13, Appl
115	34	33.0	547	7	US-11-156-003-16	Sequence 16, Appl	188	33	32.0	1183	7	US-11-115-639-14	Sequence 14, Appl
116	34	33.0	550	7	US-11-156-003-2	Sequence 2, Appli	189	33	32.0	1183	7	US-11-115-639-15	Sequence 15, Appl
117	34	33.0	550	7	US-11-156-003-3	Sequence 3, Appli	190	33	32.0	1183	7	US-11-115-639-16	Sequence 16, Appl
118	34	33.0	553	7	US-11-055-822-266	Sequence 266, App	191	33	32.0	1183	7	US-11-115-639-17	Sequence 17, Appl
119	34	33.0	572	6	US-10-793-626-2974	Sequence 2974, Ap	192	33	32.0	1183	7	US-11-115-639-18	Sequence 18, Appl
120	34	33.0	575	6	US-11-131-212-23	Sequence 23, Appl	193	33	32.0	1184	7	US-11-115-639-49	Sequence 49, Appl
121	34	33.0	643	6	US-10-873-427A-4	Sequence 4, Appli	194	33	32.0	1184	7	US-11-115-639-50	Sequence 50, Appl
122	34	33.0	644	6	US-10-821-234-1107	Sequence 1107, Ap	195	33	32.0	1184	7	US-11-115-639-51	Sequence 51, Appl
123	34	33.0	664	6	US-10-485-517-308	Sequence 308, App	196	33	32.0	1193	7	US-11-115-639-19	Sequence 19, Appl
124	34	33.0	692	7	US-11-103-957-29	Sequence 29, Appl	197	33	32.0	1193	7	US-11-115-639-20	Sequence 20, Appl
125	34	33.0	782	6	US-10-995-561-861	Sequence 861, App	198	33	32.0	1193	7	US-11-115-639-21	Sequence 21, Appl
126	34	33.0	847	6	US-10-995-561-863	Sequence 863, App	199	33	32.0	1213	7	US-11-074-176-256	Sequence 256, App
127	34	33.0	847	6	US-10-995-561-865	Sequence 865, App	200	33	32.0	1881	7	US-11-040-472-8	Sequence 8, Appli
128	34	33.0	1023	6	US-10-821-234-1377	Sequence 1377, Ap	201	33	32.0	1960	7	US-11-063-834-48	Sequence 48, Appl
129	34	33.0	1031	6	US-10-857-780-22	Sequence 22, Appl	202	33	32.0	1960	7	US-11-063-834-50	Sequence 50, Appl
130	34	33.0	1114	6	US-10-857-780-27	Sequence 27, Appl	203	33	32.0	2644	6	US-10-770-726-45	Sequence 45, Appl
131	34	33.0	3507	7	US-11-075-185-7	Sequence 7, Appli	204	33	32.0	3674	7	US-11-000-463-454	Sequence 454, App
132	33.5	32.5	130	6	US-10-507-275-1	Sequence 1, Appli	205	32.5	31.6	175	6	US-10-995-561-708	Sequence 708, App
133	33.5	32.5	222	6	US-10-793-626-2474	Sequence 2474, Ap	206	32.5	31.6	194	6	US-10-981-873-44	Sequence 44, Appl
134	33.5	32.5	222	6	US-10-793-626-2732	Sequence 2732, Ap	207	32.5	31.6	377	6	US-10-467-657-8228	Sequence 8228, Ap
135	33.5	32.5	574	6	US-10-770-726-50	Sequence 50, Appl	208	32.5	31.6	3655	7	US-11-080-981-100	Sequence 100, App
136	33.5	32.5	574	6	US-10-770-726-50	Sequence 50, Appl	209	32.5	31.6	3655	7	US-11-075-185-5	Sequence 5, Appli
137	33.5	32.5	617	7	US-11-143-980-35	Sequence 35, Appl	210	32	31.1	20	6	US-10-939-890-171	Sequence 171, App
138	33.5	32.5	892	6	US-10-507-275-3	Sequence 3, Appli	211	32	31.1	20	6	US-10-939-890-394	Sequence 394, App
139	33.5	32.5	904	7	US-11-087-227-12	Sequence 12, Appl	212	32	31.1	22	6	US-10-939-890-409	Sequence 409, App
140	33	32.0	20	6	US-10-939-890-160	Sequence 160, App	213	32	31.1	22	6	US-10-939-890-428	Sequence 428, App
141	33	32.0	22	6	US-10-939-890-457	Sequence 457, App	214	32	31.1	22	6	US-10-939-890-454	Sequence 454, App
142	33	32.0	27	6	US-10-939-890-352	Sequence 352, App	215	32	31.1	22	6	US-10-939-890-353	Sequence 353, App
143	33	32.0	27	6	US-10-939-890-828	Sequence 828, App	216	32	31.1	28	6	US-10-939-890-829	Sequence 829, App
144	33	32.0	116	6	US-10-467-657-2422	Sequence 2422, Ap	217	32	31.1	30	7	US-11-106-932-1	Sequence 1, Appli
145	33	32.0	142	6	US-10-821-234-1235	Sequence 1235, Ap	218	32	31.1	45	7	US-11-123-896-300	Sequence 300, App
146	33	32.0	145	6	US-10-467-657-264	Sequence 264, App	219	32	31.1	56	7	US-11-123-896-111	Sequence 111, App
147	33	32.0	145	6	US-10-467-657-3600	Sequence 3600, Ap	220	32	31.1	56	7	US-11-123-896-114	Sequence 114, App
148	33	32.0	152	6	US-10-467-657-2466	Sequence 2466, Ap	221	32	31.1	64	7	US-11-123-896-239	Sequence 239, App
149	33	32.0	192	6	US-10-467-657-6808	Sequence 6808, Ap	222	32	31.1	90	7	US-11-123-896-110	Sequence 110, App
150	33	32.0	206	6	US-10-467-657-3730	Sequence 3730, Ap	223	32	31.1	91	7	US-11-123-896-113	Sequence 113, App
151	33	32.0	264	7	US-11-082-389-282	Sequence 282, App	224	32	31.1	154	6	US-10-467-657-158	Sequence 158, App
152	33	32.0	279	6	US-10-878-556A-157	Sequence 157, App	225	32	31.1	154	6	US-10-467-657-6520	Sequence 6520, Ap
153	33	32.0	313	6	US-10-719-311-8	Sequence 8, Appli	226	32	31.1	154	6	US-10-467-657-7634	Sequence 7634, Ap
154	33	32.0	376	7	US-11-060-008-32	Sequence 32, Appl	227	32	31.1	157	6	US-10-467-657-4392	Sequence 4392, App
155	33	32.0	376	7	US-11-055-822-152	Sequence 152, App	228	32	31.1	160	7	US-11-010-874-13	Sequence 13, Appl
156	33	32.0	379	6	US-10-131-826A-308	Sequence 308, App	229	32	31.1	160	7	US-11-010-874-14	Sequence 14, Appl
157	33	32.0	399	6	US-10-719-311-9	Sequence 9, Appli	230	32	31.1	175	6	US-10-467-657-1524	Sequence 1524, Ap
158	33	32.0	400	6	US-10-467-657-2702	Sequence 2702, Ap	231	32	31.1	240	6	US-10-878-556A-37	Sequence 37, Appl
159	33	32.0	400	7	US-11-117-169-2	Sequence 2, Appli	232	32	31.1	247	6	US-10-995-561-790	Sequence 790, App
160	33	32.0	400	7	US-11-117-169-4	Sequence 4, Appli	233	32	31.1	251	7	US-11-135-855-38	Sequence 38, Appl
161	33	32.0	406	7	US-11-107-028-7	Sequence 7, Appli	234	32	31.1	254	7	US-11-067-323-578	Sequence 578, App
162	33	32.0	413	7	US-11-032-951-12	Sequence 12, Appl	235	32	31.1	254	6	US-10-485-517-354	Sequence 354, App
163	33	32.0	414	6	US-10-631-558-2	Sequence 2, Appli	236	32	31.1	261	6	US-10-485-517-150	Sequence 150, App
164	33	32.0	435	6	US-10-454-437-254	Sequence 254, App	237	32	31.1	288	6	US-10-467-657-1248	Sequence 1248, Ap
165	33	32.0	440	7	US-11-108-172-1059	Sequence 1059, Ap	238	32	31.1	327	6	US-10-821-234-884	Sequence 884, App
166	33	32.0	492	6	US-10-467-962B-51	Sequence 51, Appl	239	32	31.1	332	6	US-10-793-626-550	Sequence 550, App
167	33	32.0	513	6	US-10-485-517-160	Sequence 160, App	240	32	31.1	332	6	US-10-467-657-3668	Sequence 3668, Ap
168	33	32.0	537	6	US-10-719-311-10	Sequence 10, Appl	241	32	31.1	332	6	US-10-467-657-7154	Sequence 7154, Ap
169	33	32.0	585	6	US-10-878-556A-42	Sequence 42, Appl	242	32	31.1	336	7	US-11-152-892-4	Sequence 4, Appli
170	33	32.0	621	7	US-11-184-380-26	Sequence 26, Appl	243	32	31.1	339	7	US-11-010-874-3	Sequence 3, Appli
171	33	32.0	623	6	US-10-719-311-2	Sequence 2, Appli	244	32	31.1	339	7	US-11-010-874-4	Sequence 4, Appli

245	32	31.1	345	6	US-10-821-234-1104	Sequence 1104, Ap	318	31	30.1	26	6	US-10-939-890-239	Sequence 299, App
246	32	31.1	395	7	US-11-084-220-2	Sequence 2, Appl	319	31	30.1	26	6	US-10-939-890-445	Sequence 445, App
247	32	31.1	398	6	US-10-996-628-4	Sequence 4, Appl	320	31	30.1	26	6	US-10-939-890-712	Sequence 712, App
248	32	31.1	408	7	US-11-103-957-23	Sequence 23, Appl	321	31	30.1	26	6	US-10-939-890-796	Sequence 796, App
249	32	31.1	414	7	US-11-089-551A-28	Sequence 28, Appl	322	31	30.1	26	6	US-10-939-890-835	Sequence 835, App
250	32	31.1	417	6	US-10-995-561-791	Sequence 791, App	323	31	30.1	28	6	US-10-997-201A-13	Sequence 13, Appl
251	32	31.1	417	7	US-11-110-851-61	Sequence 61, Appl	324	31	30.1	55	6	US-10-467-657-3322	Sequence 3322, Ap
252	32	31.1	425	6	US-10-793-626-110	Sequence 110, App	325	31	30.1	55	6	US-10-467-657-6878	Sequence 6878, Ap
253	32	31.1	434	6	US-10-793-626-1456	Sequence 1456, Ap	326	31	30.1	104	6	US-10-793-626-1880	Sequence 1880, Ap
254	32	31.1	437	7	US-11-073-626-3	Sequence 3, Appl	327	31	30.1	104	6	US-10-793-626-2200	Sequence 2200, Ap
255	32	31.1	437	6	US-10-632-150-8	Sequence 8, Appl	328	31	30.1	113	6	US-10-995-561-690	Sequence 690, App
256	32	31.1	472	7	US-11-073-457-8	Sequence 8, Appl	329	31	30.1	134	7	US-11-088-686-35	Sequence 1136, Ap
257	32	31.1	472	7	US-11-073-460-8	Sequence 8, Appl	330	31	30.1	144	7	US-11-055-822-1136	Sequence 1136, Ap
258	32	31.1	489	6	US-10-793-626-2632	Sequence 2632, Ap	331	31	30.1	152	6	US-10-467-657-6526	Sequence 6526, Ap
259	32	31.1	490	7	US-11-074-176-316	Sequence 316, App	332	31	30.1	169	6	US-10-467-657-2258	Sequence 2258, Ap
260	32	31.1	495	7	US-11-074-176-60	Sequence 60, Appl	333	31	30.1	192	6	US-10-793-626-1224	Sequence 1224, Ap
261	32	31.1	529	6	US-10-632-150-44	Sequence 44, Appl	334	31	30.1	192	6	US-10-793-626-1524	Sequence 1524, Ap
262	32	31.1	529	7	US-11-073-457-44	Sequence 44, Appl	335	31	30.1	207	7	US-11-022-562-222	Sequence 222, App
263	32	31.1	529	7	US-11-073-460-44	Sequence 44, Appl	336	31	30.1	208	7	US-11-088-686-39	Sequence 39, Appl
264	32	31.1	530	7	US-11-055-822-256	Sequence 256, App	337	31	30.1	231	6	US-10-454-437-414	Sequence 414, App
265	32	31.1	556	6	US-10-613-744-8	Sequence 8, Appl	338	31	30.1	243	6	US-10-131-826A-164	Sequence 164, App
266	32	31.1	557	6	US-10-793-626-1486	Sequence 1486, Ap	339	31	30.1	254	6	US-10-995-561-1021	Sequence 1021, Ap
267	32	31.1	559	6	US-10-793-626-1376	Sequence 1376, Ap	340	31	30.1	257	6	US-10-632-150-40	Sequence 40, Appl
268	32	31.1	567	6	US-10-995-561-764	Sequence 764, App	341	31	30.1	257	7	US-11-073-457-40	Sequence 40, Appl
269	32	31.1	578	7	US-11-083-800-2	Sequence 2, Appl	342	31	30.1	257	7	US-11-073-460-40	Sequence 40, Appl
270	32	31.1	605	6	US-10-131-826A-160	Sequence 160, App	343	31	30.1	271	7	US-11-058-817A-4	Sequence 4, Appl
271	32	31.1	608	6	US-10-873-528-8	Sequence 8, Appl	344	31	30.1	272	7	US-11-058-817A-6	Sequence 6, Appl
272	32	31.1	654	6	US-10-770-726-82	Sequence 82, Appl	345	31	30.1	273	6	US-10-995-561-689	Sequence 689, App
273	32	31.1	690	6	US-10-613-744-19	Sequence 19, Appl	346	31	30.1	285	6	US-10-467-657-222	Sequence 222, App
274	32	31.1	697	6	US-10-821-234-905	Sequence 905, App	347	31	30.1	285	6	US-10-467-657-8230	Sequence 8230, Ap
275	32	31.1	729	7	US-11-057-047-2	Sequence 2, Appl	348	31	30.1	289	7	US-11-000-463-764	Sequence 764, App
276	32	31.1	764	7	US-11-057-047-1	Sequence 1, Appl	349	31	30.1	291	7	US-11-065-943-50	Sequence 50, Appl
277	32	31.1	791	7	US-11-056-621-4	Sequence 4, Appl	350	31	30.1	312	7	US-11-058-817A-8	Sequence 8, Appl
278	32	31.1	798	6	US-10-821-234-1034	Sequence 1034, Ap	351	31	30.1	314	7	US-11-058-817A-2	Sequence 2, Appl
279	32	31.1	810	6	US-10-995-561-761	Sequence 761, App	352	31	30.1	319	7	US-11-109-156-38	Sequence 38, Appl
280	32	31.1	810	6	US-10-220-824-2	Sequence 2, Appl	353	31	30.1	322	6	US-10-821-234-1354	Sequence 1354, Ap
281	32	31.1	904	6	US-10-507-275-5	Sequence 5, Appl	354	31	30.1	322	6	US-10-878-556A-59	Sequence 59, Appl
282	32	31.1	1086	7	US-11-055-822-370	Sequence 370, App	355	31	30.1	323	6	US-10-878-556A-184	Sequence 184, App
283	32	31.1	1066	7	US-11-055-822-1002	Sequence 1002, Ap	356	31	30.1	323	7	US-11-109-156-37	Sequence 37, Appl
284	32	31.1	1113	7	US-11-055-822-368	Sequence 368, App	357	31	30.1	329	6	US-10-981-873-29	Sequence 29, Appl
285	32	31.1	1113	7	US-11-055-822-1000	Sequence 1000, Ap	358	31	30.1	336	7	US-11-129-143-105	Sequence 105, App
286	32	31.1	1158	6	US-10-958-730-70	Sequence 70, Appl	359	31	30.1	338	6	US-10-878-556A-19	Sequence 19, Appl
287	32	31.1	1496	7	US-11-186-284-35	Sequence 35, Appl	360	31	30.1	338	6	US-10-454-437-136	Sequence 136, App
288	32	31.1	1897	6	US-10-821-234-1635	Sequence 1635, App	361	31	30.1	352	7	US-11-108-528-20	Sequence 20, Appl
289	32	31.1	1907	7	US-11-000-463-250	Sequence 250, App	362	31	30.1	352	7	US-11-108-528-22	Sequence 22, Appl
290	32	31.1	2630	7	US-11-186-731-2	Sequence 2, Appl	363	31	30.1	355	7	US-11-108-528-16	Sequence 16, Appl
291	32	31.1	3690	6	US-10-995-561-1016	Sequence 1016, Ap	364	31	30.1	355	7	US-11-108-528-18	Sequence 18, Appl
292	32	31.1	3714	6	US-10-995-561-1015	Sequence 1015, Ap	365	31	30.1	366	7	US-11-000-463-292	Sequence 292, App
293	32	31.1	4868	7	US-11-044-111-24	Sequence 24, Appl	366	31	30.1	368	6	US-10-689-743-100	Sequence 100, App
294	32	31.1	7968	7	US-11-186-731-5	Sequence 5, Appl	367	31	30.1	389	7	US-11-088-686-1	Sequence 1, Appl
295	31.5	30.6	86	6	US-10-467-657-3580	Sequence 3580, Ap	368	31	30.1	389	7	US-11-088-686-3	Sequence 3, Appl
296	31.5	30.6	86	6	US-10-467-657-6444	Sequence 6444, Ap	369	31	30.1	389	7	US-11-088-686-5	Sequence 5, Appl
297	31.5	30.6	211	6	US-10-467-657-5620	Sequence 5620, Ap	370	31	30.1	389	7	US-11-088-686-7	Sequence 7, Appl
298	31.5	30.6	215	7	US-11-119-212-9	Sequence 9, Appl	371	31	30.1	389	7	US-11-088-686-9	Sequence 9, Appl
299	31.5	30.6	302	7	US-11-119-212-13	Sequence 13, Appl	372	31	30.1	389	7	US-11-088-686-11	Sequence 11, Appl
300	31.5	30.6	302	7	US-11-119-212-25	Sequence 25, Appl	373	31	30.1	389	7	US-11-088-686-13	Sequence 13, Appl
301	31.5	30.6	324	7	US-11-119-212-15	Sequence 15, Appl	374	31	30.1	394	6	US-10-878-556A-50	Sequence 50, Appl
302	31.5	30.6	326	7	US-11-119-212-19	Sequence 19, Appl	375	31	30.1	400	6	US-10-821-234-1534	Sequence 1534, Ap
303	31.5	30.6	384	6	US-10-467-657-508	Sequence 508, App	376	31	30.1	410	6	US-10-995-561-969	Sequence 969, App
304	31.5	30.6	411	7	US-11-119-212-17	Sequence 17, Appl	377	31	30.1	411	7	US-11-092-140-114	Sequence 114, App
305	31.5	30.6	413	7	US-11-119-212-21	Sequence 21, Appl	378	31	30.1	423	7	US-11-110-851-62	Sequence 62, Appl
306	31.5	30.6	417	6	US-10-858-730-60	Sequence 60, Appl	379	31	30.1	424	6	US-10-995-561-1017	Sequence 1017, Ap
307	31.5	30.6	534	7	US-11-075-185-17	Sequence 17, Appl	380	31	30.1	427	7	US-11-186-284-91	Sequence 91, Appl
308	31.5	30.6	705	7	US-11-102-240-162	Sequence 162, App	381	31	30.1	432	6	US-10-836-953-1	Sequence 1, Appl
309	31.5	30.6	1126	7	US-11-075-185-3	Sequence 3, Appl	382	31	30.1	432	6	US-10-793-626-2942	Sequence 2942, Ap
310	31.5	30.6	1234	6	US-10-995-561-870	Sequence 870, App	383	31	30.1	448	6	US-10-467-657-4416	Sequence 4416, Ap
311	31.5	30.6	1365	6	US-10-995-561-867	Sequence 867, App	384	31	30.1	475	7	US-11-174-150-45	Sequence 45, Appl
312	31.5	30.6	1366	6	US-10-995-561-868	Sequence 868, App	385	31	30.1	488	7	US-11-092-140-110	Sequence 110, App
313	31.5	30.6	1388	6	US-10-821-234-1143	Sequence 1143, Ap	386	31	30.1	499	6	US-10-508-263-94	Sequence 94, Appl
314	31.5	30.6	1411	6	US-10-995-561-869	Sequence 869, App	387	31	30.1	509	6	US-10-770-726-74	Sequence 74, Appl
315	31	30.1	10	7	US-11-045-024-1530	Sequence 1530, Ap	388	31	30.1	502	6	US-10-454-437-134	Sequence 134, App
316	31	30.1	10	7	US-11-045-024-7445	Sequence 7445, Ap	389	31	30.1	513	7	US-11-000-463-816	Sequence 816, App
317	31	30.1	21	6	US-10-939-890-578	Sequence 578, App	390	31	30.1	516	6	US-10-508-263-26	Sequence 26, Appl

391	31	30.1	529	7	US-11-174-150-46	Sequence 46, Appl	464	30	29.1	26	6	US-10-939-890-833	Sequence 833, App
392	31	30.1	534	7	US-11-057-732-2	Sequence 2, Appl	465	30	29.1	48	6	US-10-957-887B-267	Sequence 267, App
393	31	30.1	554	7	US-11-074-176-320	Sequence 320, App	466	30	29.1	91	6	US-10-454-437-332	Sequence 332, App
394	31	30.1	560	6	US-10-995-561-1026	Sequence 1026, Ap	467	30	29.1	99	6	US-10-467-657-2852	Sequence 2852, Ap
395	31	30.1	564	6	US-10-821-234-1340	Sequence 1340, Ap	468	30	29.1	118	6	US-10-467-657-390	Sequence 390, App
396	31	30.1	570	6	US-11-074-176-68	Sequence 68, Appl	469	30	29.1	149	6	US-10-793-626-1682	Sequence 1682, Ap
397	31	30.1	600	6	US-10-606-302-3	Sequence 3, Appl	470	30	29.1	157	6	US-10-793-626-2870	Sequence 2870, Ap
398	31	30.1	610	6	US-10-606-302-1	Sequence 1, Appl	471	30	29.1	172	7	US-11-137-465-49	Sequence 49, Appl
399	31	30.1	616	6	US-10-995-561-1018	Sequence 1018, Ap	472	30	29.1	184	7	US-11-084-591-5	Sequence 5, Appl
400	31	30.1	617	6	US-10-995-561-1022	Sequence 1022, Ap	473	30	29.1	188	6	US-10-793-626-3272	Sequence 3272, Ap
401	31	30.1	696	7	US-11-074-176-214	Sequence 214, App	474	30	29.1	188	6	US-10-467-657-332	Sequence 332, Ap
402	31	30.1	732	6	US-10-518-593-23	Sequence 23, Appl	475	30	29.1	206	6	US-10-467-657-524	Sequence 524, App
403	31	30.1	732	6	US-10-995-561-1020	Sequence 1020, Ap	476	30	29.1	213	7	US-11-038-284-22	Sequence 22, Appl
404	31	30.1	751	6	US-11-012-762-26	Sequence 26, Appl	477	30	29.1	223	6	US-10-793-626-2824	Sequence 2824, Ap
405	31	30.1	752	6	US-10-131-826A-120	Sequence 120, App	478	30	29.1	224	7	US-11-055-822-858	Sequence 858, App
406	31	30.1	834	6	US-10-131-826A-148	Sequence 148, App	479	30	29.1	240	6	US-10-866-530-1	Sequence 1, Appl
407	31	30.1	841	6	US-10-624-932-6	Sequence 6, Appl	480	30	29.1	243	6	US-10-467-657-3362	Sequence 3362, Ap
408	31	30.1	841	6	US-10-624-932-8	Sequence 8, Appl	481	30	29.1	252	7	US-11-102-240-92	Sequence 92, Appl
409	31	30.1	879	6	US-10-770-726-78	Sequence 78, Appl	482	30	29.1	269	7	US-11-055-822-856	Sequence 856, App
410	31	30.1	882	7	US-11-012-762-34	Sequence 34, Appl	483	30	29.1	291	6	US-10-454-437-36	Sequence 36, Appl
411	31	30.1	922	7	US-11-115-086-9	Sequence 9, Appl	484	30	29.1	291	6	US-10-793-626-1324	Sequence 1324, Ap
412	31	30.1	968	7	US-11-000-463-281	Sequence 281, App	485	30	29.1	308	6	US-10-131-826A-100	Sequence 100, App
413	31	30.1	974	7	US-11-115-086-7	Sequence 7, Appl	486	30	29.1	310	7	US-11-053-185-14	Sequence 14, Appl
414	31	30.1	980	7	US-11-064-246-10	Sequence 10, Appl	487	30	29.1	317	7	US-11-051-568-11	Sequence 11, Appl
415	31	30.1	1023	6	US-10-995-561-968	Sequence 968, App	488	30	29.1	318	7	US-11-000-463-331	Sequence 331, App
416	31	30.1	1042	7	US-11-067-811-1	Sequence 1, Appl	489	30	29.1	318	7	US-11-000-463-803	Sequence 803, App
417	31	30.1	1122	6	US-10-821-234-1657	Sequence 1657, Ap	490	30	29.1	327	6	US-11-129-143-89	Sequence 89, Appl
418	31	30.1	1192	6	US-10-858-730-72	Sequence 72, Appl	491	30	29.1	329	7	US-10-995-561-694	Sequence 694, App
419	31	30.1	1208	7	US-11-115-639-46	Sequence 46, Appl	492	30	29.1	329	7	US-11-082-389-226	Sequence 226, App
420	31	30.1	1208	7	US-11-115-639-47	Sequence 47, Appl	493	30	29.1	331	7	US-11-195-459-25	Sequence 25, Appl
421	31	30.1	1208	7	US-11-115-639-48	Sequence 48, Appl	494	30	29.1	332	7	US-11-083-389-224	Sequence 224, App
422	31	30.1	1342	6	US-10-770-726-63	Sequence 63, Appl	495	30	29.1	349	6	US-10-515-419-2	Sequence 2, Appl
423	31	30.1	1342	7	US-11-113-202-12	Sequence 12, Appl	496	30	29.1	349	7	US-11-074-176-226	Sequence 226, App
424	31	30.1	1342	7	US-11-113-202-14	Sequence 14, Appl	497	30	29.1	352	6	US-10-515-419-3	Sequence 3, Appl
425	31	30.1	1377	6	US-10-821-234-1070	Sequence 1070, Ap	498	30	29.1	354	6	US-10-821-234-974	Sequence 974, App
426	31	30.1	1442	6	US-10-793-626-2052	Sequence 2052, Ap	499	30	29.1	356	6	US-10-980-388-70	Sequence 70, Appl
427	31	30.1	1468	6	US-10-467-657-1088	Sequence 1088, Ap	500	30	29.1	358	6	US-10-793-626-18	Sequence 18, Appl
428	31	30.1	1804	6	US-10-513-786-2	Sequence 2, Appl	501	30	29.1	364	6	US-10-467-657-2822	Sequence 2822, Ap
429	31	30.1	3704	6	US-10-513-786-1	Sequence 1, Appl	502	30	29.1	372	6	US-10-467-657-752	Sequence 752, App
430	30.5	29.6	132	6	US-10-821-234-1249	Sequence 1249, Ap	503	30	29.1	373	7	US-11-044-051-71	Sequence 71, Appl
431	30.5	29.6	161	6	US-10-995-561-653	Sequence 653, App	504	30	29.1	373	7	US-11-044-051-105	Sequence 105, App
432	30.5	29.6	175	6	US-10-995-561-650	Sequence 650, App	505	30	29.1	398	6	US-10-467-657-5642	Sequence 5642, Ap
433	30.5	29.6	203	7	US-11-165-141-4	Sequence 4, Appl	506	30	29.1	401	6	US-10-131-826A-486	Sequence 486, App
434	30.5	29.6	211	7	US-11-098-662-16	Sequence 16, Appl	507	30	29.1	404	7	US-11-000-463-384	Sequence 384, App
435	30.5	29.6	211	7	US-11-165-141-21	Sequence 21, Appl	508	30	29.1	408	7	US-11-051-568-15	Sequence 15, Appl
436	30.5	29.6	242	6	US-10-995-561-648	Sequence 648, App	509	30	29.1	410	6	US-10-467-657-4094	Sequence 4094, Ap
437	30.5	29.6	244	7	US-11-184-399-10	Sequence 10, Appl	510	30	29.1	410	6	US-10-467-657-7680	Sequence 7680, Ap
438	30.5	29.6	246	7	US-11-055-822-888	Sequence 888, App	511	30	29.1	415	7	US-11-110-851-64	Sequence 110, App
439	30.5	29.6	256	6	US-10-995-561-654	Sequence 654, App	512	30	29.1	420	6	US-10-454-437-110	Sequence 110, App
440	30.5	29.6	268	6	US-10-821-234-866	Sequence 866, App	513	30	29.1	430	6	US-10-650-326B-19	Sequence 19, Appl
441	30.5	29.6	280	6	US-10-995-561-655	Sequence 655, App	514	30	29.1	430	7	US-11-051-568-25	Sequence 25, Appl
442	30.5	29.6	325	6	US-10-995-561-652	Sequence 652, App	515	30	29.1	431	6	US-10-816-768-39	Sequence 39, Appl
443	30.5	29.6	334	6	US-10-995-561-658	Sequence 658, App	516	30	29.1	431	6	US-10-650-326B-3	Sequence 3, Appl
444	30.5	29.6	348	6	US-10-995-561-649	Sequence 649, App	517	30	29.1	431	7	US-11-051-568-2	Sequence 2, Appl
445	30.5	29.6	383	6	US-10-989-313-2	Sequence 2, Appl	518	30	29.1	431	7	US-11-186-284-10	Sequence 10, Appl
446	30.5	29.6	429	6	US-10-525-710-12	Sequence 12, Appl	519	30	29.1	432	7	US-11-000-463-365	Sequence 365, App
447	30.5	29.6	452	7	US-11-074-176-274	Sequence 274, App	520	30	29.1	433	6	US-10-131-826A-6	Sequence 6, Appl
448	30.5	29.6	473	7	US-11-165-141-23	Sequence 23, Appl	521	30	29.1	433	7	US-11-110-851-65	Sequence 65, Appl
449	30.5	29.6	491	7	US-11-098-662-14	Sequence 14, Appl	522	30	29.1	475	6	US-10-878-556A-115	Sequence 115, App
450	30.5	29.6	491	7	US-11-165-141-2	Sequence 2, Appl	523	30	29.1	484	7	US-11-051-568-13	Sequence 13, Appl
451	30.5	29.6	512	6	US-10-821-234-1032	Sequence 1032, Ap	524	30	29.1	508	6	US-10-980-388-112	Sequence 112, App
452	30.5	29.6	520	7	US-11-098-662-12	Sequence 12, Appl	525	30	29.1	516	6	US-10-467-657-7038	Sequence 7038, Ap
453	30.5	29.6	520	7	US-11-165-141-19	Sequence 19, Appl	526	30	29.1	519	6	US-10-821-234-1373	Sequence 1373, Ap
454	30.5	29.6	522	7	US-11-184-399-8	Sequence 8, Appl	527	30	29.1	548	7	US-11-133-142-5	Sequence 5, Appl
455	30.5	29.6	527	7	US-11-090-878-22	Sequence 22, Appl	528	30	29.1	551	6	US-10-793-626-1668	Sequence 1668, Ap
456	30.5	29.6	599	7	US-11-165-141-33	Sequence 33, Appl	529	30	29.1	568	7	US-11-043-348-5	Sequence 5, Appl
457	30.5	29.6	617	7	US-11-090-878-18	Sequence 18, Appl	530	30	29.1	579	7	US-11-045-802-32	Sequence 32, Appl
458	30.5	29.6	739	10	US-11-078-189-12	Sequence 12, Appl	531	30	29.1	579	6	US-11-045-802-33	Sequence 33, Appl
459	30	29.1	10	6	US-10-929-988-14	Sequence 14, Appl	532	30	29.1	589	6	US-10-821-234-1687	Sequence 1687, Ap
460	30	29.1	12	6	US-10-929-988-164	Sequence 164, App	533	30	29.1	593	7	US-11-040-488-2	Sequence 2, Appl
461	30	29.1	18	6	US-10-929-988-190	Sequence 190, App	534	30	29.1	611	7	US-11-082-389-436	Sequence 436, App
462	30	29.1	26	6	US-10-939-890-366	Sequence 366, App	535	30	29.1	611	7	US-11-043-348-4	Sequence 4, Appl
463	30	29.1	26	6	US-10-939-890-486	Sequence 486, App	536	30	29.1	614	7	US-11-126-841A-2	Sequence 2, Appl

537	30	29.1	614	7	US-11-126-841A-13	Sequence 13, Appl	610	29	28.2	98	6	US-10-467-657-4206	Sequence 4206, Ap
538	30	29.1	616	6	US-10-131-825A-206	Sequence 206, App	611	29	28.2	103	7	US-11-090-916-7	Sequence 7, Appli
539	30	29.1	633	7	US-11-063-343-26	Sequence 26, Appl	612	29	28.2	106	6	US-10-467-657-1488	Sequence 148, App
540	30	29.1	646	6	US-10-995-561-695	Sequence 695, Appl	613	29	28.2	106	6	US-10-467-657-4188	Sequence 4188, Ap
541	30	29.1	659	6	US-10-467-657-6006	Sequence 6006, Ap	614	29	28.2	106	6	US-10-467-657-7080	Sequence 7080, Ap
542	30	29.1	673	7	US-11-102-240-16	Sequence 16, Appl	615	29	28.2	119	6	US-10-477-950-2	Sequence 2, Appli
543	30	29.1	687	7	US-11-117-169-6	Sequence 6, Appli	616	29	28.2	119	6	US-11-105-268-21	Sequence 21, Appl
544	30	29.1	708	6	US-10-636-320-2	Sequence 2, Appli	617	29	28.2	120	6	US-10-932-334-78	Sequence 78, Appl
545	30	29.1	718	6	US-10-467-962B-29	Sequence 29, Appl	618	29	28.2	120	7	US-11-103-268-15	Sequence 15, Appl
546	30	29.1	718	6	US-10-467-962B-65	Sequence 65, Appl	619	29	28.2	120	7	US-11-105-268-17	Sequence 17, Appl
547	30	29.1	727	7	US-11-117-169-8	Sequence 8, Appli	620	29	28.2	122	7	US-11-105-268-29	Sequence 29, Appl
548	30	29.1	729	6	US-11-099-691-3	Sequence 3, Appli	621	29	28.2	124	7	US-11-105-268-9	Sequence 9, Appli
549	30	29.1	748	6	US-10-821-234-1479	Sequence 1479, Ap	622	29	28.2	133	6	US-10-821-234-1224	Sequence 1224, Ap
550	30	29.1	763	6	US-10-821-234-1619	Sequence 1619, Ap	623	29	28.2	133	7	US-11-088-008-1	Sequence 1, Appli
551	30	29.1	812	7	US-11-010-874-1	Sequence 1, Appli	624	29	28.2	137	6	US-10-485-517-159	Sequence 159, App
552	30	29.1	840	6	US-10-645-441-1	Sequence 1, Appli	625	29	28.2	141	6	US-10-793-626-2886	Sequence 2886, Ap
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997      28 27.2 482 6 US-10-793-626-1314
998      28 27.2 486 6 US-10-467-962B-59
999      28 27.2 491 7 US-11-037-829A-9
1000     28 27.2 494 7 US-11-165-697-48
```

ALIGNMENTS

```
RESULT 1
US-10-997-066-31
; Sequence 31, Application US/10997066
; Publication No. US20050244891A1
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, RONALD J.
; APPLICANT: LEE, LINDA G.
; APPLICANT: SUN, HONGYE
; TITLE OF INVENTION: LIGAND-CONTAINING MICELLES AND USES THEREOF
; FILE REFERENCE: 375461-011US
; CURRENT APPLICATION NUMBER: US/10/997,066
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/525,492
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/628,509
; PRIOR FILING DATE: 2004-11-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-997-066-31

Query Match          93.2%; Score 96; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 4e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1  EGPWLEEEEEAYGWMD 17
       :|||||:|||||:|
Db      1  KGPWLEEEEEAYGWLD 17
       :|||||:|||||:|

RESULT 2
US-11-145-566-38
; Sequence 38, Application US/11145566
; Publication No. US20050272083A1
; GENERAL INFORMATION:
; APPLICANT: SOMASEKAR SESHAGIRI
; APPLICANT: SOMASEKAR SESHAGIRI

Query Match          93.2%; Score 96; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 4e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1  EGPWLEEEEEAYGWMD 17
       :|||||:|||||:|
Db      1  KGPWLEEEEEAYGWLD 17
       :|||||:|||||:|

RESULT 3
US-10-995-561-773
; Sequence 773, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 773
; LENGTH: 3803
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-995-561-773

Query Match          45.1%; Score 46.5; DB 6; Length 3803;
Best Local Similarity 62.5%; Pred. No. 57;
Matches 10; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY      4  WL---EEEEAYGWMD 16
       |||:|||||:|
Db      695  WLNEKEEEELAYDMSD 710
       |||:|||||:|

RESULT 4
US-10-995-561-771
; Sequence 771, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 771
; LENGTH: 3960
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
```

```

US-10-995-561-771
Query Match 45.1%; Score 46.5; DB 6; Length 3960;
Best Local Similarity 62.5%; Pred. No. 60;
Matches 10; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

Qy 4 WL---EEEEEAYGWM 16
Db 695 WLNEKEEELAYDWS 710

RESULT 5
US-10-995-561-777
; Sequence 777, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 777
; LENGTH: 5335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-777

Query Match 45.1%; Score 46.5; DB 6; Length 5335;
Best Local Similarity 62.5%; Pred. No. 79;
Matches 10; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

Qy 4 WL---EEEEEAYGWM 16
Db 603 WLNEKEEELAYDWS 618

RESULT 6
US-10-995-561-774
; Sequence 774, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 774
; LENGTH: 5406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-774

Query Match 45.1%; Score 46.5; DB 6; Length 5406;
Best Local Similarity 62.5%; Pred. No. 80;
Matches 10; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

Qy 4 WL---EEEEEAYGWM 16
Db 695 WLNEKEEELAYDWS 710

RESULT 7
US-10-995-561-779
; Sequence 779, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 779
; LENGTH: 5415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-779

Query Match 45.1%; Score 46.5; DB 6; Length 5415;
Best Local Similarity 62.5%; Pred. No. 80;
Matches 10; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

Qy 4 WL---EEEEEAYGWM 16
Db 695 WLNEKEEELAYDWS 710

RESULT 8
US-10-995-561-775
; Sequence 775, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 775
; LENGTH: 5464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-775

Query Match 45.1%; Score 46.5; DB 6; Length 5464;
Best Local Similarity 62.5%; Pred. No. 81;
Matches 10; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

Qy 4 WL---EEEEEAYGWM 16
Db 695 WLNEKEEELAYDWS 710

RESULT 9
US-10-939-890-559
; Sequence 559, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
US-10-939-890-559

```

```
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 559
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-559
```

```
Query Match 43.7%; Score 45; DB 6; Length 21;
Best Local Similarity 37.5%; Pred. No. 0.65;
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 EGPWLEEEAYGMD 16
|||:|:|:|:|:|
Db 4 EGCWVEDQTSPPCWD 19
```

```
RESULT 10
US-10-821-234-1660
; Sequence 1660, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1660
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1660
```

```
Query Match 41.7%; Score 43; DB 6; Length 264;
Best Local Similarity 54.5%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 4 WLEEEAYGMD 14
|||:|:|:|:|
Db 97 WLKKEPEAFDW 107
```

```
RESULT 11
US-11-053-185-10
; Sequence 10, Application US/11053185
```

```
; Publication No. US20050267023A1
; GENERAL INFORMATION:
; APPLICANT: SINCLAIR, DAVID A.
; APPLICANT: BITTERMAN, KEVIN J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXTENDING THE LIFE SPAN
; TITLE OF INVENTION: AND INCREASING THE STRESS RESISTANCE OF CELLS AND
; TITLE OF INVENTION: ORGANISMS
; FILE REFERENCE: HMV-085.01
; CURRENT APPLICATION NUMBER: US/11/053,185
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: PCT/US03/025016
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 60/402,254
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/428,614
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 10
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-053-185-10
```

```
Query Match 41.7%; Score 43; DB 7; Length 264;
Best Local Similarity 54.5%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 4 WLEEEAYGMD 14
|||:|:|:|:|
Db 97 WLKKEPEAFDW 107
```

```
RESULT 12
US-11-115-639-1
; Sequence 1, Application US/11115639
; Publication No. US2005028242A1
; GENERAL INFORMATION:
; APPLICANT: Rothstein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1119
; TYPE: PRT
; ORGANISM: T. aquaticus
US-11-115-639-1
```

```
Query Match 39.8%; Score 41; DB 7; Length 1119;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 GPWLEEEAYG 13
|||:|:|:|:|
Db 169 GPWLEVEASG 180
```

```
RESULT 13
US-10-652-893-2
; Sequence 2, Application US/10652893
; Publication No. US20050249733A1
; GENERAL INFORMATION:
; APPLICANT: Balasubramanian, Sriram
```

RESULT 15  
US-11-060-008-11  
; Sequence 11. Application US/11060008

Query Match 37.9%; Score 39; DB 7; Length 700;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 4; Mismatches 1; Indels

Query Match      36.9%;      Score 38;      DB 6;      Length 241;

Best Local Similarity 60.0%; Pred. No. 63;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 10  
Db 194 EGGWTEEEQ 203

## RESULT 21

US-11-000-463-398  
; Sequence 398, Application US/11000463  
; Publication No. US20050266423A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Qian, Xiaohong B.  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhou, Ping  
; APPLICANT: Cao, Yi-Cheng  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
; FILE REFERENCE: 785CIP4CN  
; CURRENT APPLICATION NUMBER: US/11/000,463  
; CURRENT FILING DATE: 2004-11-29  
; PRIOR APPLICATION NUMBER: 10/291,365  
; PRIOR FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: PCT/US01/02623  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 09/922,279  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/617,746  
; PRIOR FILING DATE: 2000-07-17  
; PRIOR APPLICATION NUMBER: 09/631,451  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 09/633,870  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 944  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 398  
; LENGTH: 369  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-000-463-398

Query Match 36.9%; Score 38; DB 7; Length 369;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEE 7  
Db 47 GPWLEE 52

## RESULT 22

US-10-982-545-14  
; Sequence 14, Application US/10982545  
; Publication No. US20050244890A1  
; GENERAL INFORMATION:  
; APPLICANT: Davies, Huw Alun  
; APPLICANT: McGuire, James  
; APPLICANT: Simonsen, Anja Hviid  
; APPLICANT: Blennow, Kaj  
; APPLICANT: Podust, Vladimir  
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease  
; FILE REFERENCE: 016866-011550US  
; CURRENT APPLICATION NUMBER: US/10/982,545

; CURRENT FILING DATE: 2004-11-06  
; PRIOR APPLICATION NUMBER: US 60/518,360  
; PRIOR FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: US 60/526,753  
; PRIOR FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: US 60/546,423  
; PRIOR FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/547,250  
; PRIOR FILING DATE: 2004-02-23  
; PRIOR APPLICATION NUMBER: US 60/558,896  
; PRIOR FILING DATE: 2004-04-02  
; PRIOR APPLICATION NUMBER: US 60/572,617  
; PRIOR FILING DATE: 2004-05-18  
; PRIOR APPLICATION NUMBER: US 60/586,503  
; PRIOR FILING DATE: 2004-07-08  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 615  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: nerve growth factor inducible Neurosecretory  
; OTHER INFORMATION: protein vaccinia virus growth factor (VGF)  
; OTHER INFORMATION: precursor  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)..(22)  
; OTHER INFORMATION: signal peptide  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (23)..(615)  
; OTHER INFORMATION: nerve growth factor inducible Neurosecretory  
; OTHER INFORMATION: protein vaccinia virus growth factor (VGF)  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (373)..(417)  
; OTHER INFORMATION: biomarker peptide 4808 Da, 4812 Da (Q10),  
; OTHER INFORMATION: processed fragment of nerve growth factor  
; OTHER INFORMATION: inducible Neurosecretory protein vaccinia virus  
; OTHER INFORMATION: growth factor (VGF)  
US-10-982-545-14

Query Match 36.9%; Score 38; DB 6; Length 615;  
Best Local Similarity 60.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PWLEEEAY 12  
Db 529 PWDREDEVY 538

## RESULT 23

US-10-982-545-5  
; Sequence 5, Application US/10982545  
; Publication No. US20050244890A1  
; GENERAL INFORMATION:  
; APPLICANT: Davies, Huw Alun  
; APPLICANT: McGuire, James  
; APPLICANT: Simonsen, Anja Hviid  
; APPLICANT: Blennow, Kaj  
; APPLICANT: Podust, Vladimir  
; APPLICANT: CIPHERGEN Biosystems, Inc.  
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease  
; FILE REFERENCE: 016866-011550US  
; CURRENT APPLICATION NUMBER: US/10/982,545  
; CURRENT FILING DATE: 2004-11-06  
; PRIOR APPLICATION NUMBER: US 60/518,360  
; PRIOR FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: US 60/526,753  
; PRIOR FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: US 60/546,423  
; PRIOR FILING DATE: 2004-02-19

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; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: nerve growth factor inducible Neurosecretory
; OTHER INFORMATION: protein vaccinia virus growth factor (VGF)
; FEATURE: precursor
; NAME/KEY: SIGNAL
; LOCATION: (1)..(22)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (23)..(616)
; OTHER INFORMATION: biomarker peptide M3951.6, nerve growth factor
; OTHER INFORMATION: inducible Neurosecretory protein vaccinia virus
; OTHER INFORMATION: growth factor (VGF) mature peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (26)..(62)
; OTHER INFORMATION: biomarker peptide M3687.7, N-terminal fragment of
; OTHER INFORMATION: nerve growth factor inducible Neurosecretory
; OTHER INFORMATION: protein vaccinia virus growth factor (VGF)
US-10-982-545-5

Query Match 36.9%; Score 38; DB 6; Length 616;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PWLEEEERY 12
DB 529 PWDREDEYV 538

RESULT 24
US-10-131-826A-464
; Sequence 464, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
```

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; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 464
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-464

Query Match 36.9%; Score 38; DB 6; Length 941;
Best Local Similarity 58.3%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 LEEEEEYGVMD 16
DB 912 IETIEENIGVMD 923

RESULT 25
US-10-793-626-1756
; Sequence 1756, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1756
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1756

Query Match 36.4%; Score 37.5; DB 6; Length 338;
Best Local Similarity 25.0%; Pred. No. 1e+02;
Matches 8; Conservative 4; Mismatches 3; Indels 17; Gaps 1;

QY 2 GPWLEE-----EEAYGVMD 16
DB 302 GPWLKDTLRREIEIAVISNQIVNTKBEILEWVD 333

RESULT 26
US-11-113-424-53
; Sequence 53, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
```

```
/ APPLICANT: Gargolli et al.
/ TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-225
/ CURRENT APPLICATION NUMBER: US/11/113,424
/ CURRENT FILING DATE: 2005-04-21
/ PRIOR APPLICATION NUMBER: 60/256,704
/ PRIOR FILING DATE: 2000-12-19
/ PRIOR APPLICATION NUMBER: 60/311,590
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: 60/257,314
/ PRIOR FILING DATE: 2000-12-20
/ PRIOR APPLICATION NUMBER: 60/311,613
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: 60/315,617
/ PRIOR FILING DATE: 2001-08-29
/ PRIOR APPLICATION NUMBER: 60/307,506
/ PRIOR FILING DATE: 2001-07-24
/ PRIOR APPLICATION NUMBER: 60/322,358
/ PRIOR FILING DATE: 2001-09-14
/ PRIOR APPLICATION NUMBER: 60/294,075
/ PRIOR FILING DATE: 2001-05-29
/ PRIOR APPLICATION NUMBER: 60/288,153
/ PRIOR FILING DATE: 2001-05-02
/ NUMBER OF SEQ ID NOS: 190
/ SOFTWARE: PatentIn ver. 2.1
/ SEQ ID NO 53
/ LENGTH: 2515
/ TYPE: PRT
/ ORGANISM: Drosophila melanogaster
US-11-113-424-53
```

```
Query Match 36.4%; Score 37.5; DB 7; Length 2515;
Best Local Similarity 40.0%; Pred. No. 6.9e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 7; Gaps 1;
```

```
QY 2 GPWLEEEERAY-----GW 14
DB 2442 GDWTEEBKEELVQHGDVDGW 2461
```

```
RESULT 27
US-10-467-657-6478
/ Sequence 6478, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SpA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 6478
/ LENGTH: 64
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6478
```

```
Query Match 35.9%; Score 37; DB 6; Length 64;
Best Local Similarity 53.8%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;
```

```
QY 4 WLEEEERAYGMD 16
DB 45 WKKEVE--GWL 55
```

```
RESULT 28
US-10-821-234-1694
/ Sequence 1694, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pt_seq_genes Version 1.0
/ SEQ ID NO 1694
/ LENGTH: 82
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-1694
```

```
Query Match 35.9%; Score 37; DB 6; Length 82;
Best Local Similarity 35.3%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
```

```
QY 1 EGPWLEEEERAYGMDP 17
DB 64 KGPWTRLPRGLRWHP 80
```

```
RESULT 29
US-11-105-268-23
/ Sequence 23, Application US/11105268
/ Publication No. US20050260204A1
/ GENERAL INFORMATION:
/ APPLICANT: Allan, Christian
/ TITLE OF INVENTION: ANTI-IL-9 ANTIBODY FORMULATIONS AND USES THEREOF
/ FILE REFERENCE: 10271-126-999
/ CURRENT APPLICATION NUMBER: US/11/105,268
/ CURRENT FILING DATE: 2005-04-12
/ PRIOR APPLICATION NUMBER: 60/561,845
/ PRIOR FILING DATE: 2004-04-12
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 23
/ LENGTH: 121
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-105-268-23
```

```
Query Match 35.9%; Score 37; DB 7; Length 121;
Best Local Similarity 44.4%; Pred. No. 45;
Matches 8; Conservative 2; Mismatches 4; Indels 4; Gaps 1;
```

```
QY 2 GPWLEEEERAYG----WM 15
DB 31 GYWIEEVQAPGQGLEWM 48
```

```
RESULT 30
US-11-102-240-136
/ Sequence 136, Application US/11102240
/ Publication No. US20050260647A1
/ GENERAL INFORMATION:
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRES
```

```
; FILE REFERENCE: P3230R1C106C
; CURRENT APPLICATION NUMBER: US/11/102,240
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 10/063662
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 199-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 136
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-102-240-136
```

```
Query Match 35.9%; Score 37; DB 7; Length 242;
Best Local Similarity 50.0%; Pred. No. 87;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 8 EEEAYGWMDP 17
: |::|||
Db 151 KRESGWGTFD 160
```

```
RESULT 31
US-11-080-991-30
; Sequence 30, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petteer Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-30
```

```
Query Match 35.9%; Score 37; DB 7; Length 242;
Best Local Similarity 50.0%; Pred. No. 87;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 8 EEEAYGWMDP 17
: |::|||
Db 151 KRESGWGTFD 160
```

```
RESULT 32
US-10-821-234-865
; Sequence 865, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Suan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
```

```
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 865
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-865
```

```
Query Match 35.9%; Score 37; DB 6; Length 253;
Best Local Similarity 50.0%; Pred. No. 91;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 8 EEEAYGWMDP 17
: |::|||
Db 162 KRESGWGTFD 171
```

```
RESULT 33
US-10-454-437-328
; Sequence 328, Application US/10454437
; Publication No. US20050277115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128PCPN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 328
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-328
```

```
Query Match 35.9%; Score 37; DB 6; Length 310;
Best Local Similarity 54.5%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 PWLEEEEAAYG 13
: |::|||
Db 173 PWSIDIEHAHG 183
```

```
RESULT 34
US-11-184-380-12
; Sequence 12, Application US/11184380
; Publication No. US20050255089A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Chlorini, John
; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS
; FILE REFERENCE: 14014.032303
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: US/11/184,380
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
; OTHER INFORMATION: synthetic construct
US-11-184-380-12

Query Match          35.9%; Score 37; DB 7; Length 330;
Best Local Similarity 41.7%; Pred. No. 1.2e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAY 12
| : : : : :
DB 15 EKQWIQENQESY 26
```

```
RESULT 35
US-11-184-380-2
; Sequence 2, Application US/11184380
; Publication No. US20050255089A1
; GENERAL INFORMATION:
; APPLICANT: Chlorini, John
; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS
; FILE REFERENCE: 14014.032303
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: US/11/184,380
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence, Note =
; OTHER INFORMATION: synthetic construct
US-11-184-380-2
```

```
Query Match          35.9%; Score 37; DB 7; Length 390;
Best Local Similarity 41.7%; Pred. No. 1.4e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAY 12
| : : : : :
DB 15 EKQWIQENQESY 26
```

```
RESULT 36
US-11-184-380-14
; Sequence 14, Application US/11184380
; Publication No. US20050255089A1
; GENERAL INFORMATION:
; APPLICANT: Chlorini, John
; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS
; FILE REFERENCE: 14014.032303
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: US/11/184,380
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence, Note =
; OTHER INFORMATION: synthetic construct
US-11-184-380-2
```

```
Query Match          35.9%; Score 37; DB 7; Length 390;
Best Local Similarity 41.7%; Pred. No. 1.4e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAY 12
| : : : : :
DB 15 EKQWIQENQESY 26
```

```
RESULT 37
US-11-184-380-3
; Sequence 3, Application US/11184380
; Publication No. US20050255089A1
; GENERAL INFORMATION:
; APPLICANT: Kotin, Robert M.
; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS
; FILE REFERENCE: 14014.032303
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: US/11/184,380
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence, Note =
; OTHER INFORMATION: synthetic construct
US-11-184-380-3
```

```
Query Match          35.9%; Score 37; DB 7; Length 610;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAY 12
| : : : : :
DB 235 EKQWIQENQESY 246
```

```
; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS
; FILE REFERENCE: 14014.032303
; CURRENT APPLICATION NUMBER: US/11/184,380
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence, Note =
; OTHER INFORMATION: synthetic construct
US-11-184-380-14
```

```
Query Match          35.9%; Score 37; DB 7; Length 550;
Best Local Similarity 41.7%; Pred. No. 1.9e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAY 12
| : : : : :
DB 235 EKQWIQENQESY 246
```

```
RESULT 37
US-11-184-380-3
; Sequence 3, Application US/11184380
; Publication No. US20050255089A1
; GENERAL INFORMATION:
; APPLICANT: Chlorini, John
; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS
; FILE REFERENCE: 14014.032303
; CURRENT APPLICATION NUMBER: US/11/184,380
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence, Note =
; OTHER INFORMATION: synthetic construct
US-11-184-380-3
```

```
Query Match          35.9%; Score 37; DB 7; Length 610;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAY 12
| : : : : :
DB 235 EKQWIQENQESY 246
```

```
RESULT 38
US-11-055-822-214
; Sequence 214, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habernauer, Gregor
```

```
/ TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
/ TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
/ FILE REFERENCE: BGI-121PCPN
/ CURRENT APPLICATION NUMBER: US/11/055,822
/ CURRENT FILING DATE: 2005-02-11
/ PRIOR APPLICATION NUMBER: 09/606,740
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: 60/141,031
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 60/142,101
/ PRIOR FILING DATE: 1999-07-02
/ PRIOR APPLICATION NUMBER: 60/148,613
/ PRIOR FILING DATE: 1999-08-12
/ PRIOR APPLICATION NUMBER: 60/187,970
/ PRIOR FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: DE 19930476.9
/ PRIOR FILING DATE: 1999-07-01
/ PRIOR APPLICATION NUMBER: DE 19931415.2
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931418.7
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931419.5
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931420.9
/ PRIOR FILING DATE: 1999-07-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1158
/ SEQ ID NO 214
/ LENGTH: 826
/ TYPE: PRT
/ ORGANISM: Corynebacterium glutamicum
/ US-11-055-822-214

Query Match 35.9%; Score 37; DB 7; Length 826;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PWLEEEEAAYG 13
Db 742 PFMEEEAATG 752

RESULT 39
US-11-055-822-712
/ Sequence 712, Application US/11055822
/ Publication No. US20050260707A1
/ GENERAL INFORMATION:
/ APPLICANT: Pompejus, Markus
/ APPLICANT: Kroger, Burkhard
/ APPLICANT: Schroder, Hartwig
/ APPLICANT: Zelder, Oskar
/ APPLICANT: Haberhauer, Gregor
/ TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
/ TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
/ FILE REFERENCE: BGI-121PCPN
/ CURRENT APPLICATION NUMBER: US/11/055,822
/ CURRENT FILING DATE: 2005-02-11
/ PRIOR APPLICATION NUMBER: 09/606,740
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/141,031
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 60/142,101
/ PRIOR FILING DATE: 1999-07-02
/ PRIOR APPLICATION NUMBER: 60/148,613
/ PRIOR FILING DATE: 1999-08-12
/ PRIOR APPLICATION NUMBER: 60/187,970
/ PRIOR FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: DE 19930476.9
/ PRIOR FILING DATE: 1999-07-01
/ PRIOR APPLICATION NUMBER: DE 19931415.2
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931418.7
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931419.5
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931420.9
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1158
/ SEQ ID NO 212
/ LENGTH: 833
/ TYPE: PRT
/ ORGANISM: Corynebacterium glutamicum
/ US-11-055-822-212

Query Match 35.9%; Score 37; DB 7; Length 833;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PWLEEEEAAYG 13
Db 742 PFMEEEAATG 752
```

```
/ TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
/ TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
/ FILE REFERENCE: BGI-121PCPN
/ CURRENT APPLICATION NUMBER: US/11/055,822
/ CURRENT FILING DATE: 2005-02-11
/ PRIOR APPLICATION NUMBER: 09/606,740
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: 60/141,031
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 60/142,101
/ PRIOR FILING DATE: 1999-07-02
/ PRIOR APPLICATION NUMBER: 60/148,613
/ PRIOR FILING DATE: 1999-08-12
/ PRIOR APPLICATION NUMBER: 60/187,970
/ PRIOR FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: DE 19930476.9
/ PRIOR FILING DATE: 1999-07-01
/ PRIOR APPLICATION NUMBER: DE 19931415.2
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931418.7
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931419.5
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931420.9
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1158
/ SEQ ID NO 712
/ LENGTH: 826
/ TYPE: PRT
/ ORGANISM: Corynebacterium glutamicum
/ US-11-055-822-712

Query Match 35.9%; Score 37; DB 7; Length 826;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PWLEEEEAAYG 13
Db 742 PFMEEEAATG 752

RESULT 40
US-11-055-822-212
/ Sequence 212, Application US/11055822
/ Publication No. US20050260707A1
/ GENERAL INFORMATION:
/ APPLICANT: Pompejus, Markus
/ APPLICANT: Kroger, Burkhard
/ APPLICANT: Schroder, Hartwig
/ APPLICANT: Zelder, Oskar
/ APPLICANT: Haberhauer, Gregor
/ TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
/ TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
/ FILE REFERENCE: BGI-121PCPN
/ CURRENT APPLICATION NUMBER: US/11/055,822
/ CURRENT FILING DATE: 2005-02-11
/ PRIOR APPLICATION NUMBER: 09/606,740
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: 60/141,031
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 60/142,101
/ PRIOR FILING DATE: 1999-07-02
/ PRIOR APPLICATION NUMBER: 60/148,613
/ PRIOR FILING DATE: 1999-08-12
/ PRIOR APPLICATION NUMBER: 60/187,970
/ PRIOR FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: DE 19930476.9
/ PRIOR FILING DATE: 1999-07-01
/ PRIOR APPLICATION NUMBER: DE 19931415.2
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931418.7
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931419.5
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931420.9
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1158
/ SEQ ID NO 212
/ LENGTH: 833
/ TYPE: PRT
/ ORGANISM: Corynebacterium glutamicum
/ US-11-055-822-212

Query Match 35.9%; Score 37; DB 7; Length 833;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PWLEEEEAAYG 13
Db 742 PFMEEEAATG 752
```

## RESULT 41

US-11-055-822-710  
; Sequence 710, Application US/11055822  
; Publication No. US20050260707A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
; FILE REFERENCE: BGI-121CPCN  
; CURRENT APPLICATION NUMBER: US/11/055,822  
; CURRENT FILING DATE: 2005-02-11  
; PRIOR APPLICATION NUMBER: 09/606,740  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: 60/141,031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: 60/142,101  
; PRIOR FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: 60/148,613  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 60/187,970  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: DE 19930476.9  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931415.2  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931418.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931419.5  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931420.9  
; PRIOR FILING DATE: 1999-07-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1158  
; SEQ ID NO 710  
; LENGTH: 833  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-11-055-822-710

Query Match 35.9%; Score 37; DB 7; Length 833;  
Best Local Similarity 63.6%; Pred. No. 2.8e+02;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PWTLEEEERAYG 13  
|:|||||  
DB 742 PFMEERAEATG 752

## RESULT 42

US-10-821-234-897  
; Sequence 897, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_SEQ\_genes Version 1.0  
; SEQ ID NO 897  
; LENGTH: 1176  
; TYPE: PRT  
; ORGANISM: Homo sapiens

Query Match 35.9%; Score 37; DB 6; Length 1221;  
Best Local Similarity 63.6%; Pred. No. 4.1e+02;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PWTLEEEERAYG 13  
|:|||||  
DB 742 PFMEERAEATG 752

## RESULT 44

US-10-821-234-1563  
; Sequence 1563, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_SEQ\_genes Version 1.0  
; SEQ ID NO 1563  
; LENGTH: 358  
; TYPE: PRT  
; ORGANISM: Homo sapiens

## US-10-821-234-897

Query Match 35.9%; Score 37; DB 6; Length 1176;  
Best Local Similarity 54.5%; Pred. No. 4e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGPWLEEEEREA 11  
|:|||||  
DB 240 KGPWKQENVEA 250

## RESULT 43

US-10-858-730-222  
; Sequence 222, Application US/10858730  
; Publication No. US20050255568A1  
; GENERAL INFORMATION:  
; APPLICANT: Bailey, Richard B.  
; APPLICANT: Blomquist, Paul  
; APPLICANT: Doten, Reed  
; APPLICANT: Driggers, Edward M.  
; APPLICANT: Madden, Kevin T.  
; APPLICANT: O'Leary, Jessica  
; APPLICANT: O'Toole, George  
; APPLICANT: Trueheart, Joshua  
; APPLICANT: Walbridge, Michael J.  
; APPLICANT: Yorgey, Peter S.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID  
; FILE REFERENCE: 14184-030001  
; CURRENT APPLICATION NUMBER: US/10/858,730  
; CURRENT FILING DATE: 2004-06-01  
; PRIOR APPLICATION NUMBER: US 60/475,000  
; PRIOR FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: US 60/551,860  
; PRIOR FILING DATE: 2004-03-10  
; NUMBER OF SEQ ID NOS: 364  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 222  
; LENGTH: 1221  
; TYPE: PRT  
; ORGANISM: Coryne-bacterium glutamicum  
US-10-858-730-222

Query Match 35.9%; Score 37; DB 6; Length 1221;  
Best Local Similarity 63.6%; Pred. No. 4.1e+02;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PWTLEEEERAYG 13  
|:|||||  
DB 742 PFMEERAEATG 752

US-10-821-234-1563

Query Match 35.4%; Score 36.5; DB 6; Length 358;  
Best Local Similarity 50.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 3 PWLEEEAYGW 14  
||:|:|  
DB 71 PWMEGGSSEY-W 81

## RESULT 45

US-11-131-212-24  
; Sequence 24, Application US/11131212  
; Publication No. US20050262593A1  
; GENERAL INFORMATION:  
; APPLICANT: Yutaka KANDA  
; APPLICANT: Mitsuo SATOH  
; APPLICANT: Kazuyasu NAKAMURA  
; APPLICANT: Kazuhisa UCHIDA  
; APPLICANT: Toyohide SHINKAWA  
; APPLICANT: Naoko YAMANE  
; APPLICANT: Motoo HANAKI  
; APPLICANT: Nobuo HANAI  
; TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL  
; FILE REFERENCE: 249-202  
; CURRENT APPLICATION NUMBER: US/11/131,212  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US/09/971,773  
; PRIOR FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: JP 2000-308526  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: US 60/268,926  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 575  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-131-212-24

Query Match 35.4%; Score 36.5; DB 7; Length 575;  
Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 3 PWLEEE-EEA 11  
||:|:|  
DB 340 PWLEKEIEEA 349

## RESULT 46

US-10-939-890-453  
; Sequence 453, Application US/10939890  
; Publication No. US20050250700A1  
; GENERAL INFORMATION:  
; APPLICANT: Sato, Aaron K.  
; APPLICANT: Sexton, Daniel J.  
; APPLICANT: Dransfield, Daniel T.  
; APPLICANT: Ladner, Robert C.  
; APPLICANT: Arbogast, Christophe  
; APPLICANT: Bussat, Philippe  
; APPLICANT: Fan, Hong  
; APPLICANT: Khurana, Sudha  
; APPLICANT: Linder, Karen E.  
; APPLICANT: Marinelli, Edmund R.  
; APPLICANT: Nanjappan, Palaniappa  
; APPLICANT: Nunn, Adrian D.  
; APPLICANT: Pillai, Radhakrishna  
; APPLICANT: Pochon, Sibylle  
; APPLICANT: Ramalingam, Kondareddiar  
; APPLICANT: Shrivastava, Ajay  
; APPLICANT: Song, Bo

; APPLICANT: Swenson, Rolf E.  
; APPLICANT: Von Wronski, Mathew A.  
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES  
; FILE REFERENCE: D0617.70014US00  
; CURRENT APPLICATION NUMBER: US/10/939,890  
; CURRENT FILING DATE: 2004-09-13  
; PRIOR APPLICATION NUMBER: US 10/661,156  
; PRIOR FILING DATE: 2003-09-11  
; PRIOR APPLICATION NUMBER: US 10/382,082  
; PRIOR FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: PCT/US03/06731  
; PRIOR FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/440,411  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US 60/360,851  
; PRIOR FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 883  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 453  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Library Isolate  
US-10-939-890-453

Query Match 35.0%; Score 36; DB 6; Length 22;  
Best Local Similarity 42.9%; Pred. No. 12;  
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 GPWLEEEAYGWM 15  
||:|:|  
DB 2 GPTWEEDWYKWL 15

## RESULT 47

US-10-939-890-684  
; Sequence 684, Application US/10939890  
; Publication No. US20050250700A1  
; GENERAL INFORMATION:  
; APPLICANT: Sato, Aaron K.  
; APPLICANT: Sexton, Daniel J.  
; APPLICANT: Dransfield, Daniel T.  
; APPLICANT: Ladner, Robert C.  
; APPLICANT: Arbogast, Christophe  
; APPLICANT: Bussat, Philippe  
; APPLICANT: Fan, Hong  
; APPLICANT: Khurana, Sudha  
; APPLICANT: Linder, Karen E.  
; APPLICANT: Marinelli, Edmund R.  
; APPLICANT: Nanjappan, Palaniappa  
; APPLICANT: Nunn, Adrian D.  
; APPLICANT: Pillai, Radhakrishna  
; APPLICANT: Pochon, Sibylle  
; APPLICANT: Ramalingam, Kondareddiar  
; APPLICANT: Shrivastava, Ajay  
; APPLICANT: Song, Bo  
; APPLICANT: Swenson, Rolf E.  
; APPLICANT: Von Wronski, Mathew A.  
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES  
; FILE REFERENCE: D0617.70014US00  
; CURRENT APPLICATION NUMBER: US/10/939,890  
; CURRENT FILING DATE: 2004-09-13  
; PRIOR APPLICATION NUMBER: US 10/661,156  
; PRIOR FILING DATE: 2003-09-11  
; PRIOR APPLICATION NUMBER: US 10/382,082  
; PRIOR FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: PCT/US03/06731  
; PRIOR FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/440,411  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US 60/360,851  
; PRIOR FILING DATE: 2002-03-01

```

; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 684.
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: Thr residue modified with tBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Trp residue modified with Boc
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)..(6)
; OTHER INFORMATION: Glu residue modified with OAlI
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: Glu residue modified with OtBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: Asp residue modified with OtBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: Trp residue modified with Boc
; NAME/KEY: MOD_RES
; LOCATION: (11)..(12)
; OTHER INFORMATION: Tyr residue modified with tBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (13)..(13)
; OTHER INFORMATION: Lys residue modified with Aloc
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: Trp residue modified with Boc
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (18)..(18)
; OTHER INFORMATION: Thr residue modified with tBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (22)..(22)
; OTHER INFORMATION: Lys residue modified with Boc
US-10-939-890-684

Query Match          35.08; Score 36; DB 6; Length 22;
Best Local Similarity 42.9%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      2  GPWLEEEAYGWM 15
      |||::|||:
Db      2  GPTWEEDWYKWL 15

RESULT 48
US-10-939-890-685
; Sequence 685, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Buseat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 685
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: Thr residue modified with tBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Trp residue modified with Boc
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: Glu residue modified with OtBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(9)
; OTHER INFORMATION: Asp residue modified with OtBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: Trp residue modified with Boc
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11)..(12)
; OTHER INFORMATION: Tyr residue modified with tBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: Trp residue modified with Boc
; FEATURE:

```

```
/ NAME/KEY: MOD_RES
/ LOCATION: (18)..(18)
/ OTHER INFORMATION: Thr residue modified with tBu
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (22)..(22)
/ OTHER INFORMATION: Lys residue modified with Boc
US-10-939-890-685
```

```
Query Match 35.0%; Score 36; DB 6; Length 22;
Best Local Similarity 42.9%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 2 GPWLEEEERAYGWM 15
Db 2 GPTWEEDDWYKWL 15
```

## RESULT 49

```
US-10-939-890-686
; Sequence 686, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 686
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: Thr residue modified with tBu
; FEATURE:
```

```
/ NAME/KEY: MOD_RES
/ LOCATION: (5)..(5)
/ OTHER INFORMATION: Trp residue modified with Boc
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (6)..(6)
/ OTHER INFORMATION: Glu residue modified with cyclic modification to Lys residue at
/ OTHER INFORMATION: position 13
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (7)..(7)
/ OTHER INFORMATION: Glu residue modified with OtBu
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (8)..(9)
/ OTHER INFORMATION: Asp residue modified with OtBu
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (10)..(10)
/ OTHER INFORMATION: Trp residue modified with Boc
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (11)..(12)
/ OTHER INFORMATION: Tyr residue modified with tBu
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (13)..(13)
/ OTHER INFORMATION: Lys residue modified with cyclic modification to Glu residue at
/ OTHER INFORMATION: position 6
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (14)..(14)
/ OTHER INFORMATION: Trp residue modified with Boc
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (18)..(18)
/ OTHER INFORMATION: Thr residue modified with tBu
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (22)..(22)
/ OTHER INFORMATION: Lys residue modified with Boc
US-10-939-890-686
```

```
Query Match 35.0%; Score 36; DB 6; Length 22;
Best Local Similarity 42.9%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 2 GPWLEEEERAYGWM 15
Db 2 GPTWEEDDWYKWL 15
```

## RESULT 50

```
US-10-939-890-687
; Sequence 687, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
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; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
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; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (16)..(16)
; OTHER INFORMATION: Phe modified with cyclic modification to Glu residue at position
; OTHER INFORMATION: 7
; US-10-939-890-687

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OM protein - protein search, using sw model

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	103	100.0	17	4 US-10-372-317-13	Sequence 13, Appl
4	103	100.0	17	5 US-10-759-832-1	Sequence 1, Appl
5	103	100.0	17	5 US-10-760-085-60	Sequence 60, Appl
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171	43	41.7	152	4	US-10-767-701-42087	Sequence 42087, A	244	43	41.7	785	3	US-09-989-890-244	Sequence 244, App
172	43	41.7	154	4	US-10-282-122A-44926	Sequence 44926, A	245	43	41.7	792	4	US-10-369-493-9698	Sequence 9698, Ap
173	43	41.7	161	4	US-10-238-075-1051	Sequence 1051, Ap	246	43	41.7	792	5	US-10-737-318-10	Sequence 10, Appl

247	43	41.7	805	4	US-10-042-865-4	Sequence 4, Appl	320	42	40.8	463	5	US-10-893-315-72	Sequence 72, Appl
248	43	41.7	829	5	US-10-737-318-12	Sequence 12, Appl	321	42	40.8	477	3	US-09-972-715-9	Sequence 9, Appl
249	43	41.7	833	4	US-10-149-819-4	Sequence 4, Appl	322	42	40.8	485	5	US-10-893-315-107	Sequence 107, Appl
250	43	41.7	833	4	US-10-190-115-14	Sequence 14, Appl	323	42	40.8	502	6	US-11-097-143-15231	Sequence 15231, A
251	43	41.7	833	4	US-10-190-115-16	Sequence 16, Appl	324	42	40.8	530	4	US-10-437-963-182342	Sequence 182342, A
252	43	41.7	833	4	US-10-190-115-18	Sequence 18, Appl	325	42	40.8	583	3	US-09-911-077A-2	Sequence 2, Appl
253	43	41.7	833	4	US-10-369-072-14	Sequence 14, Appl	326	42	40.8	580	3	US-09-911-077A-10	Sequence 10, Appl
254	43	41.7	833	4	US-10-369-072-16	Sequence 16, Appl	327	42	40.8	580	3	US-09-911-077A-11	Sequence 11, Appl
255	43	41.7	833	4	US-10-369-072-18	Sequence 18, Appl	328	42	40.8	580	3	US-09-911-077A-12	Sequence 12, Appl
256	43	41.7	833	4	US-10-403-676-6	Sequence 6, Appl	329	42	40.8	580	4	US-10-408-765A-1145	Sequence 1145, Ap
257	43	41.7	833	4	US-10-403-676-12	Sequence 12, Appl	330	42	40.8	580	5	US-10-724-806-2	Sequence 2, Appl
258	43	41.7	833	4	US-10-312-352-31	Sequence 31, Appl	331	42	40.8	580	5	US-10-724-806-10	Sequence 10, Appl
259	43	41.7	882	5	US-10-737-318-6	Sequence 6, Appl	332	42	40.8	580	5	US-10-724-806-11	Sequence 11, Appl
260	43	41.7	963	4	US-10-190-115-46	Sequence 46, Appl	333	42	40.8	580	5	US-10-724-806-12	Sequence 12, Appl
261	43	41.7	963	4	US-10-369-072-46	Sequence 46, Appl	334	42	40.8	600	4	US-10-437-963-170981	Sequence 170981, A
262	43	41.7	963	4	US-10-042-865-57	Sequence 57, Appl	335	42	40.8	606	4	US-10-425-115-321514	Sequence 321514, A
263	43	41.7	1159	4	US-10-282-122A-70505	Sequence 70505, A	336	42	40.8	627	4	US-10-437-963-119856	Sequence 119856, A
264	43	41.7	1162	4	US-10-724-972A-5815	Sequence 5815, Ap	337	42	40.8	664	4	US-10-425-115-320445	Sequence 320445, A
265	43	41.7	2203	4	US-10-437-963-112320	Sequence 112320, A	338	42	40.8	740	4	US-10-017-161-2418	Sequence 2418, Ap
266	43	41.7	2291	5	US-10-952-315-29	Sequence 29, Appl	339	42	40.8	740	4	US-10-292-798-2058	Sequence 2058, Ap
267	42.5	41.3	274	5	US-10-450-763-52713	Sequence 52713, A	340	42	40.8	758	4	US-10-087-192-219	Sequence 219, App
268	42.5	41.3	275	4	US-10-425-115-206178	Sequence 206178, A	341	42	40.8	842	4	US-10-087-192-897	Sequence 897, App
269	42.5	41.3	297	4	US-10-094-749-1748	Sequence 1748, Ap	342	42	40.8	909	4	US-10-437-963-105153	Sequence 105153, A
270	42.5	41.3	302	4	US-10-425-114-68448	Sequence 68448, A	343	42	40.8	1223	4	US-10-425-115-321581	Sequence 321581, A
271	42.5	41.3	329	4	US-10-225-066A-634	Sequence 634, App	344	42	40.8	1282	4	US-10-259-194A-184	Sequence 184, App
272	42.5	41.3	329	4	US-10-302-267-144	Sequence 144, App	345	42	40.8	1421	4	US-10-437-963-149400	Sequence 149400, A
273	42.5	41.3	329	4	US-10-374-780A-2570	Sequence 2570, Ap	346	42	40.8	1431	5	US-10-840-512-218	Sequence 512, App
274	42.5	41.3	329	4	US-10-412-699B-832	Sequence 832, App	347	42	40.8	4868	4	US-10-668-767-57	Sequence 57, Appl
275	42.5	41.3	329	5	US-10-225-066A-634	Sequence 634, App	348	41.5	40.3	45	5	US-10-450-763-39974	Sequence 39974, A
276	42.5	41.3	357	5	US-10-739-930-10239	Sequence 10239, A	349	41.5	40.3	66	5	US-10-472-533-412	Sequence 412, App
277	42.5	41.3	393	4	US-10-425-114-57890	Sequence 57890, A	350	41.5	40.3	67	4	US-10-097-065-187	Sequence 187, App
278	42.5	41.3	463	5	US-10-739-930-9747	Sequence 9747, Ap	351	41.5	40.3	67	4	US-10-372-876-187	Sequence 187, App
279	42.5	41.3	509	4	US-10-425-115-361848	Sequence 361848, A	352	41.5	40.3	90	4	US-10-425-115-290496	Sequence 290496, A
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281	42	40.8	78	4	US-10-029-386-28627	Sequence 28627, A	354	41.5	40.3	91	4	US-10-372-876-543	Sequence 543, App
282	42	40.8	122	4	US-10-425-115-207718	Sequence 207718, A	355	41.5	40.3	101	3	US-09-864-408A-3432	Sequence 3432, Ap
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285	42	40.8	157	4	US-10-425-115-303691	Sequence 303691, A	358	41.5	40.3	278	4	US-10-437-963-203340	Sequence 203340, A
286	42	40.8	158	4	US-10-767-701-57258	Sequence 57258, A	359	41.5	40.3	288	4	US-10-128-714-3054	Sequence 3054, Ap
287	42	40.8	173	4	US-10-424-599-206487	Sequence 206487, A	360	41.5	40.3	288	4	US-10-128-714-8054	Sequence 8054, Ap
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289	42	40.8	221	4	US-10-021-811-14	Sequence 14, Appl	362	41.5	40.3	375	4	US-10-282-122A-4958	Sequence 4958, A
290	42	40.8	221	4	US-10-659-869-14	Sequence 14, Appl	363	41.5	40.3	492	6	US-10-050-200-9	Sequence 9, Appl
291	42	40.8	235	3	US-09-833-245-1991	Sequence 1991, Ap	364	41.5	40.3	451	4	US-11-012-797A-9	Sequence 9, Appl
292	42	40.8	242	4	US-10-424-599-240202	Sequence 240202, A	365	41.5	40.3	521	4	US-10-425-115-324849	Sequence 324849, A
293	42	40.8	268	3	US-09-738-626-4092	Sequence 4092, Ap	366	41.5	40.3	567	4	US-10-358-283-10	Sequence 10, Appl
294	42	40.8	268	4	US-10-781-014-696	Sequence 696, App	367	41.5	40.3	628	4	US-10-358-283-8	Sequence 8, Appl
295	42	40.8	278	4	US-10-437-963-142633	Sequence 142633, A	368	41.5	40.3	644	4	US-10-156-761-13556	Sequence 13556, A
296	42	40.8	292	4	US-10-424-599-205655	Sequence 205655, A	369	41.5	40.3	691	4	US-10-437-963-104654	Sequence 104654, A
297	42	40.8	304	3	US-09-934-455-64	Sequence 64, Appl	370	41.5	40.3	722	4	US-10-289-762-513	Sequence 513, App
298	42	40.8	304	4	US-10-225-068-188	Sequence 188, App	371	41.5	40.3	752	4	US-10-358-283-6	Sequence 6, Appl
299	42	40.8	304	4	US-10-225-066A-772	Sequence 772, App	372	41.5	40.3	753	4	US-10-358-283-4	Sequence 4, Appl
300	42	40.8	304	4	US-10-374-780A-2256	Sequence 2256, Ap	373	41.5	40.3	763	4	US-10-358-283-15	Sequence 15, Appl
301	42	40.8	304	4	US-10-412-699B-118	Sequence 118, App	374	41.5	40.3	816	5	US-10-450-763-34394	Sequence 34394, A
302	42	40.8	304	5	US-10-225-068-188	Sequence 188, App	375	41.5	40.3	816	5	US-10-450-763-56142	Sequence 56142, A
303	42	40.8	304	5	US-10-225-068-188	Sequence 188, App	376	41.5	40.3	872	6	US-11-097-143-13395	Sequence 13395, A
304	42	40.8	307	4	US-10-425-115-235876	Sequence 235876, A	377	41.5	40.3	930	4	US-10-247-685-15	Sequence 15, Appl
305	42	40.8	310	4	US-10-389-566-1005	Sequence 1005, Ap	378	41.5	40.3	930	4	US-10-358-283-2	Sequence 2, Appl
306	42	40.8	311	4	US-10-437-963-185993	Sequence 185993, A	379	41.5	40.3	930	4	US-10-358-283-30	Sequence 30, Appl
307	42	40.8	318	4	US-10-032-201B-284	Sequence 2804, App	380	41.5	40.3	930	4	US-10-788-792-246	Sequence 246, App
308	42	40.8	330	5	US-10-732-923-3807	Sequence 3807, Ap	381	41.5	40.3	930	5	US-10-728-082-6	Sequence 6, Appl
309	42	40.8	349	4	US-10-278-173-138	Sequence 138, App	382	41	39.8	6	5	US-10-719-450-6	Sequence 417, App
310	42	40.8	349	4	US-10-278-536-114	Sequence 114, App	383	41	39.8	6	5	US-10-813-336-8	Sequence 8, Appl
311	42	40.8	349	4	US-10-412-699B-134	Sequence 134, App	384	41	39.8	7	5	US-10-424-599-284220	Sequence 284220, A
312	42	40.8	352	4	US-10-437-963-192043	Sequence 192043, A	385	41	39.8	46	4	US-10-437-963-134280	Sequence 134280, A
313	42	40.8	370	5	US-10-732-923-3808	Sequence 3808, Ap	386	41	39.8	49	4	US-10-437-963-178411	Sequence 178411, A
314	42	40.8	379	4	US-10-425-114-65015	Sequence 65015, A	387	41	39.8	55	3	US-09-984-276-147	Sequence 147, App
315	42	40.8	381	4	US-10-437-963-105149	Sequence 105149, A	388	41	39.8	66	3	US-09-984-271-147	Sequence 271-147
316	42	40.8	463	3	US-09-963-875-4	Sequence 4, Appl	389	41	39.8	66	3	US-10-767-701-56510	Sequence 56510, A
317	42	40.8	463	4	US-10-120-687-4	Sequence 4, Appl	390	41	39.8	68	4	US-10-424-599-159478	Sequence 159478, A
318	42	40.8	463	4	US-10-225-567A-400	Sequence 400, App	391	41	39.8	91	4	US-10-424-599-159478	Sequence 234, App
319	42	40.8	463	4	US-10-292-798-882	Sequence 882, App	392	41	39.8	95	3		

393	41	39.8	95	3	US-09-984-271-234	Sequence 234, App	466	41	39.8	1088	5	US-10-741-600-936	Sequence 936, App
394	41	39.8	103	3	US-09-974-879-178	Sequence 178, App	467	41	39.8	1094	4	US-10-437-963-164644	Sequence 164644, App
395	41	39.8	103	4	US-10-621-401-178	Sequence 178, App	468	41	39.8	1099	5	US-10-741-600-934	Sequence 934, App
396	41	39.8	103	5	US-10-644-765-174	Sequence 174, App	469	41	39.8	1119	3	US-09-782-714-2	Sequence 2, Appli
397	41	39.8	103	5	US-10-644-765-250	Sequence 250, App	470	41	39.8	1119	3	US-09-802-755A-2	Sequence 2, Appli
398	41	39.8	104	3	US-09-305-736-178	Sequence 178, App	471	41	39.8	1119	5	US-10-783-206-2	Sequence 2, Appli
399	41	39.8	104	3	US-09-818-683-178	Sequence 178, App	472	41	39.8	1125	4	US-10-437-963-156833	Sequence 156833, App
400	41	39.8	104	3	US-09-818-683-178	Sequence 178, App	473	41	39.8	1125	4	US-10-282-122A-63717	Sequence 63717, A
401	41	39.8	111	4	US-10-437-963-186770	Sequence 186770, App	474	41	39.8	1223	4	US-10-282-122A-62131	Sequence 62131, A
402	41	39.8	123	3	US-09-738-626-4985	Sequence 4985, Ap	475	41	39.8	1746	4	US-10-437-963-159594	Sequence 159594, App
403	41	39.8	123	3	US-09-738-626-5403	Sequence 5403, Ap	476	41	39.8	2106	4	US-10-408-765A-2093	Sequence 2093, Ap
404	41	39.8	148	4	US-10-437-963-172333	Sequence 172333, App	477	41	39.8	2137	5	US-10-756-143-4806	Sequence 4806, Ap
405	41	39.8	149	5	US-10-450-763-60289	Sequence 60289, A	478	41	39.8	4010	6	US-11-097-143-11352	Sequence 11352, A
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407	41	39.8	172	4	US-10-437-963-186763	Sequence 186763, App	480	40.5	39.3	117	4	US-10-437-963-169191	Sequence 169191, App
408	41	39.8	172	4	US-10-425-115-286200	Sequence 286200, App	481	40.5	39.3	160	4	US-10-767-701-59893	Sequence 59893, A
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410	41	39.8	194	5	US-10-450-763-38470	Sequence 38470, A	483	40.5	39.3	297	4	US-10-374-780A-2898	Sequence 2898, Ap
411	41	39.8	209	4	US-10-459-876-4	Sequence 4, Appli	484	40.5	39.3	297	5	US-10-225-066A-494	Sequence 494, App
412	41	39.8	236	5	US-10-450-763-35732	Sequence 35732, A	485	40.5	39.3	403	4	US-10-156-761-8600	Sequence 8600, Ap
413	41	39.8	243	4	US-10-424-599-217250	Sequence 217250, App	486	40.5	39.3	3785	3	US-09-942-025-17	Sequence 17, Appl
414	41	39.8	251	4	US-10-437-963-106292	Sequence 106292, App	487	40.5	39.3	9234	3	US-09-942-025-13	Sequence 13, Appl
415	41	39.8	260	4	US-10-424-599-164163	Sequence 164163, App	488	40	39.3	9234	3	US-10-029-386-33757	Sequence 33757, A
416	41	39.8	260	4	US-10-424-599-231485	Sequence 231485, App	489	40	39.8	30	4	US-10-029-386-33757	Sequence 33757, A
417	41	39.8	262	4	US-10-425-114-54675	Sequence 54675, A	490	40	39.8	77	4	US-10-425-115-305173	Sequence 305173, App
418	41	39.8	271	5	US-10-481-032A-318	Sequence 318, App	491	40	39.8	80	5	US-10-450-763-35101	Sequence 35101, A
419	41	39.8	273	3	US-09-533-029-40	Sequence 40, Appl	492	40	39.8	84	4	US-10-437-963-163833	Sequence 163833, App
420	41	39.8	273	3	US-10-412-699B-162	Sequence 162, App	493	40	39.8	93	4	US-10-437-963-119733	Sequence 119733, App
421	41	39.8	273	4	US-10-425-115-219934	Sequence 219934, App	494	40	39.8	101	3	US-09-773-876-3	Sequence 3, Appli
422	41	39.8	298	4	US-10-437-963-122676	Sequence 122676, App	495	40	39.8	102	5	US-10-984-482-11	Sequence 11, Appl
423	41	39.8	308	4	US-10-156-761-9862	Sequence 9862, Ap	496	40	39.8	117	4	US-10-437-963-195413	Sequence 195413, App
424	41	39.8	316	4	US-10-437-963-102936	Sequence 102936, App	497	40	39.8	125	4	US-10-425-114-53736	Sequence 53736, A
425	41	39.8	316	4	US-10-437-963-145643	Sequence 145643, App	498	40	39.8	127	4	US-10-424-599-165790	Sequence 165790, App
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431	41	39.8	440	5	US-10-450-763-60290	Sequence 60290, A	504	40	39.8	164	4	US-10-424-599-187123	Sequence 187123, App
432	41	39.8	464	5	US-10-450-763-53727	Sequence 53727, A	505	40	39.8	169	3	US-09-768-235B-28	Sequence 28, Appl
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435	41	39.8	562	4	US-10-380-565-33	Sequence 33, Appl	508	40	39.8	173	4	US-10-772-988-8	Sequence 8, Appli
436	41	39.8	623	4	US-10-437-963-148905	Sequence 148905, App	509	40	39.8	173	4	US-10-772-988-10	Sequence 10, Appl
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438	41	39.8	633	3	US-09-815-242-5210	Sequence 5210, Ap	511	40	39.8	188	4	US-10-437-963-175706	Sequence 175706, App
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442	41	39.8	705	4	US-10-369-493-7283	Sequence 7283, Ap	515	40	39.8	193	3	US-09-996-015-47	Sequence 47, Appl
443	41	39.8	715	4	US-10-425-114-58561	Sequence 58561, A	516	40	39.8	196	4	US-10-833-245-1593	Sequence 1593, Ap
444	41	39.8	724	4	US-10-154-419-8	Sequence 8, Appli	517	40	39.8	197	3	US-09-833-245-1593	Sequence 1593, Ap
445	41	39.8	724	5	US-10-772-636-24	Sequence 24, Appl	518	40	39.8	200	4	US-10-437-963-123367	Sequence 123367, App
446	41	39.8	724	5	US-10-506-308-1	Sequence 1, Appli	519	40	39.8	202	3	US-09-996-015-8	Sequence 8, Appli
447	41	39.8	729	4	US-10-123-731-2	Sequence 2, Appli	520	40	39.8	202	4	US-10-287-190-172	Sequence 172, App
448	41	39.8	729	4	US-10-232-759A-20	Sequence 20, Appl	521	40	39.8	202	4	US-10-307-817-160	Sequence 160, App
449	41	39.8	739	4	US-10-425-114-71439	Sequence 71439, A	522	40	39.8	203	4	US-10-369-493-11130	Sequence 11130, A
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451	41	39.8	748	5	US-10-627-373-8	Sequence 8, Appli	524	40	39.8	209	4	US-10-264-237-1788	Sequence 1788, Ap
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453	41	39.8	779	4	US-10-282-122A-47794	Sequence 47794, A	526	40	39.8	218	4	US-10-437-963-143820	Sequence 143820, App
454	41	39.8	818	4	US-10-369-493-5568	Sequence 5568, Ap	527	40	39.8	233	4	US-10-767-701-35932	Sequence 35932, A
455	41	39.8	820	4	US-10-437-963-140417	Sequence 140417, App	528	40	39.8	236	4	US-10-424-599-235357	Sequence 235357, App
456	41	39.8	865	6	US-11-097-143-7842	Sequence 7842, Ap	529	40	39.8	243	5	US-10-644-765-300	Sequence 300, App
457	41	39.8	890	5	US-10-450-763-52296	Sequence 52296, A	530	40	39.8	246	4	US-10-425-115-288583	Sequence 288583, App
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462	41	39.8	1057	4	US-10-425-115-275370	Sequence 275370, App	535	40	39.8	269	6	US-11-097-143-23379	Sequence 23379, A
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465	41	39.8	1088	5	US-10-741-600-933	Sequence 933, App	538	40	39.8	290	4	US-10-425-115-295595	Sequence 295595, App

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543	40	38.8	304	4	US-10-425-114-40677	Sequence 40677, A	616	40	38.8	370	4	US-10-176-978-350	Sequence 350, App
544	40	38.8	314	4	US-10-108-260A-2665	Sequence 2665, App	617	40	38.8	370	4	US-10-179-510-350	Sequence 350, App
545	40	38.8	315	4	US-10-369-493-213	Sequence 213, App	618	40	38.8	370	4	US-10-180-543-350	Sequence 350, App
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547	40	38.8	319	4	US-10-278-173-46	Sequence 46, App1	620	40	38.8	370	4	US-10-180-546-350	Sequence 350, App
548	40	38.8	319	4	US-10-425-114-40269	Sequence 40269, A	621	40	38.8	370	4	US-10-180-547-350	Sequence 350, App
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551	40	38.8	325	4	US-10-225-066A-276	Sequence 276, App	624	40	38.8	370	4	US-10-180-559-350	Sequence 350, App
552	40	38.8	325	4	US-10-374-780A-2564	Sequence 2564, App	625	40	38.8	370	4	US-10-181-000-350	Sequence 350, App
553	40	38.8	325	4	US-10-389-566-1251	Sequence 1251, App	626	40	38.8	370	4	US-10-183-010-350	Sequence 350, App
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555	40	38.8	325	5	US-10-225-066A-276	Sequence 276, App	628	40	38.8	370	4	US-10-184-614-350	Sequence 350, App
556	40	38.8	325	4	US-10-425-114-67506	Sequence 67506, A	629	40	38.8	370	4	US-10-184-623-350	Sequence 350, App
557	40	38.8	328	4	US-10-236-115-1181	Sequence 1181, App	630	40	38.8	370	4	US-10-184-635-350	Sequence 350, App
558	40	38.8	331	4	US-10-425-114-47214	Sequence 47214, A	631	40	38.8	370	4	US-10-184-637-350	Sequence 350, App
559	40	38.8	335	5	US-10-200-545-87	Sequence 87, App1	632	40	38.8	370	4	US-10-184-646-350	Sequence 350, App
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563	40	38.8	364	4	US-10-425-114-38888	Sequence 38888, A	636	40	38.8	370	4	US-10-187-596-350	Sequence 350, App
564	40	38.8	368	4	US-10-437-963-125134	Sequence 125134, App	637	40	38.8	370	4	US-10-187-745-350	Sequence 350, App
565	40	38.8	370	3	US-09-946-374-315	Sequence 315, App	638	40	38.8	370	4	US-10-187-885-350	Sequence 350, App
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567	40	38.8	370	4	US-10-174-590-350	Sequence 350, App	640	40	38.8	370	4	US-10-199-464-350	Sequence 350, App
568	40	38.8	370	4	US-10-176-758-350	Sequence 350, App	641	40	38.8	370	4	US-10-196-756-350	Sequence 350, App
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573	40	38.8	370	4	US-10-176-914-350	Sequence 350, App	646	40	38.8	370	4	US-10-180-542-350	Sequence 350, App
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578	40	38.8	370	4	US-10-176-482-350	Sequence 350, App	651	40	38.8	370	4	US-10-183-013-350	Sequence 350, App
579	40	38.8	370	4	US-10-176-757-350	Sequence 350, App	652	40	38.8	370	4	US-10-184-612-350	Sequence 350, App
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## ALIGNMENTS

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RESULT 1
US-10-197-954-60
; Sequence 60, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K'ster, Hubert
; APPLICANT: Siddiqi, Suhaib
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-197-954-60

Query Match 100.0%; Score 103; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMDP 17
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DB 1 EGPWLEEEEAAYGWMDP 17

RESULT 2
US-10-613-377A-1
; Sequence 1, Application US/10613377A
; Publication No. US20040208920A1
; GENERAL INFORMATION:
; APPLICANT: Aptton Corporation
; TITLE OF INVENTION: Liposomal Vaccine

RESULT 3
US-10-372-917-13
; Sequence 13, Application US/10372917
; Publication No. US20040209799A1
; GENERAL INFORMATION:
; APPLICANT: VASIOS, GEORGE
; TITLE OF INVENTION: JAK/STAT PATHWAY INHIBITORS AND THE USES THEREOF
; FILE REFERENCE: 5004C
; CURRENT APPLICATION NUMBER: US/10/372,917
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/177,872
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-372-917-13

Query Match 100.0%; Score 103; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 EGPWLEEEEAAYGWMDP 17

RESULT 4
US-10-759-832-1
; Sequence 1, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aptton Corporation
; TITLE OF INVENTION: Liposomal vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; FEATURE:
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; LOCATION: (1)..(1)
; NAME/KEY: MOD_RES
; FEATURE:
; OTHER INFORMATION: AMIDATION
US-10-759-832-1

Query Match      100.0%; Score 103; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17
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Db 1 EGPWLEEEERAYGWMDF 17

RESULT 5
US-10-760-085-60
; Sequence 60, Application US/10760085
; Publication No. US2005004271A1
; GENERAL INFORMATION:
; APPLICANT: Hubert K'ster
; APPLICANT: Daniel Paul Little
; APPLICANT: Suhaib Mahmood Siddiqi
; APPLICANT: Matthew Peter Grealish
; APPLICANT: Subramaniam Marappan
; APPLICANT: Chester Frederick Haseman III
; APPLICANT: Ping Yip
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2309
; CURRENT APPLICATION NUMBER: US/10/760,085
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: 60/441,398
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-760-085-60

Query Match      100.0%; Score 103; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17
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Db 1 EGPWLEEEERAYGWMDF 17

RESULT 6
US-10-813-336-1
; Sequence 1, Application US/1081336
; Publication No. US20050069968A1
; GENERAL INFORMATION:
; APPLICANT: Apticon Corporation
; TITLE OF INVENTION: Gastrin Hormone Immunoassays
; FILE REFERENCE: 1102865-0046
; CURRENT APPLICATION NUMBER: US/10/813,336
; PRIOR FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,244
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 17

; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; FEATURE:
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; LOCATION: (1)..(1)
; NAME/KEY: MOD_RES
; FEATURE:
; OTHER INFORMATION: AMIDATION
US-10-813-336-1

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Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17
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Db 1 EGPWLEEEERAYGWMDF 17

RESULT 7
US-10-206-081-2
; Sequence 2, Application US/10206081
; Publication No. US20050100974A1
; GENERAL INFORMATION:
; APPLICANT: SURFACE LOGIX, INC.
; TITLE OF INVENTION: METHODS OF DETECTING IMMOBILIZED BIOMOLECULES
; FILE REFERENCE: 11641/126
; CURRENT APPLICATION NUMBER: US/10/206,081
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/307,839
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: kinase substrate
US-10-206-081-2

Query Match      100.0%; Score 103; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
US-10-770-712-61
; Sequence 61, Application US/10770712
; Publication No. US20050170333A1
; GENERAL INFORMATION:
; APPLICANT: Vojdani, Aristo
; TITLE OF INVENTION: IDENTIFICATION OF ETIOLOGY OF AUTISM
; FILE REFERENCE: IMSCI2.008A
; CURRENT APPLICATION NUMBER: US/10/770,712
; CURRENT FILING DATE: 2004-02-03
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically prepared peptide sequence
US-10-770-712-61

Query Match      100.0%; Score 103; DB 5; Length 17;
```

```
; OTHER INFORMATION: Peptide
US-11-066-697-422

Query Match      100.0%; Score 103; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYGWMDP 17
   |||||
Db 1 EGPWLEEEAYGWMDP 17

RESULT 9
US-11-036-690-1
; Sequence 1, Application US/11036690
; Publication No. US20050169975A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/11/036,690
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-11-036-690-1

Query Match      100.0%; Score 103; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYGWMDP 17
   |||||
Db 1 EGPWLEEEAYGWMDP 17

RESULT 10
US-11-066-697-422
; Sequence 422, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 422
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide
US-11-066-697-422

Query Match      100.0%; Score 103; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYGWMDP 17
   |||||
Db 1 EGPWLEEEAYGWMDP 17

RESULT 11
US-10-613-377A-2
; Sequence 2, Application US/10613377A
; Publication No. US20040208920A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059
; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-613-377A-2

Query Match      100.0%; Score 103; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYGWMDP 17
   |||||
Db 1 EGPWLEEEAYGWMDP 17

RESULT 12
US-10-759-832-2
; Sequence 2, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-759-832-2

Query Match      100.0%; Score 103; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
```

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDP 17  
|||||  
Db 1 EGPWLEEEERAYGWMDP 17

## RESULT 13

US-10-813-336-2  
; Sequence 2, Application US/10813336  
; Publication No. US20050069966A1  
; GENERAL INFORMATION:  
; APPLICANT: Aptton Corporation  
; TITLE OF INVENTION: Gastrin Hormone Immunoassays  
; FILE REFERENCE: 1102865-0046  
; CURRENT APPLICATION NUMBER: US/10/813,336  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US 60/458,244  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-813-336-2

Query Match 100.0%; Score 103; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.8e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDP 17  
|||||  
Db 1 EGPWLEEEERAYGWMDP 17

## RESULT 14

US-11-036-690-2  
; Sequence 2, Application US/11036690  
; Publication No. US20050169979A1  
; GENERAL INFORMATION:  
; APPLICANT: Aptton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059CIP  
; CURRENT APPLICATION NUMBER: US/11/036,690  
; CURRENT FILING DATE: 2005-01-14  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 10/613,377  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-11-036-690-2

Query Match 100.0%; Score 103; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.8e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDP 17  
|||||  
Db 1 EGPWLEEEERAYGWMDP 17

## RESULT 15

US-10-813-336-3  
; Sequence 3, Application US/10813336  
; Publication No. US20050069966A1  
; GENERAL INFORMATION:  
; APPLICANT: Aptton Corporation  
; TITLE OF INVENTION: Gastrin Hormone Immunoassays  
; FILE REFERENCE: 1102865-0046  
; CURRENT APPLICATION NUMBER: US/10/813,336  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US 60/458,244  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (34)..(34)  
; OTHER INFORMATION: AMIDATION  
US-10-813-336-3

Query Match 100.0%; Score 103; DB 5; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDP 17  
|||||  
Db 18 EGPWLEEEERAYGWMDP 34

## RESULT 16

US-10-813-336-4  
; Sequence 4, Application US/10813336  
; Publication No. US20050069966A1  
; GENERAL INFORMATION:  
; APPLICANT: Aptton Corporation  
; TITLE OF INVENTION: Gastrin Hormone Immunoassays  
; FILE REFERENCE: 1102865-0046  
; CURRENT APPLICATION NUMBER: US/10/813,336  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US 60/458,244  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-813-336-4

Query Match 100.0%; Score 103; DB 5; Length 35;  
Best Local Similarity 100.0%; Pred. No. 5.5e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDP 17  
|||||  
Db 18 EGPWLEEEERAYGWMDP 34

## RESULT 17

```
US-10-839-017-3
; Sequence 3, Application US/10839017
; Publication No. US20050058635A1
; GENERAL INFORMATION:
; APPLICANT: DEMUTH, HANS-ULRICH
; APPLICANT: HOFFMANN, TORSTEN
; APPLICANT: NIESTROU, ANDRE J.
; APPLICANT: SCHILLING, STEPHAN
; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL CYCLASE
; FILE REFERENCE: 20488-53
; CURRENT APPLICATION NUMBER: US/10/839,017
; CURRENT FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,043
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/512,038
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/468,014
; PRIOR FILING DATE: 2003-05-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-10-839-017-3

Query Match          97.1%; Score 100; DB 5; Length 17;
Best Local Similarity 94.1%; Pred. No. 6.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMDP 17
   :|||||
Db 1 QGFWLEEEEEEAYGWMDP 17

RESULT 18
US-10-360-101-170
; Sequence 170, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: MOLL, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: S8,C11-sequence of Big Gastrin-1
US-10-360-101-170

Query Match          97.1%; Score 100; DB 4; Length 33;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMDP 17
   :|||||
Db 17 QGPWLEEEEEEAYGWMDP 33

RESULT 19
US-10-728-082-1
; Sequence 1, Application US/10728082
; Publication No. US20040229810A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013CIP
; CURRENT APPLICATION NUMBER: US/10/728,082
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 10/719,450
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USSN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USSN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USSN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 10/691,123
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-719-450-1

Query Match          97.1%; Score 100; DB 5; Length 33;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMDP 17
   :|||||
Db 17 QGPWLEEEEEEAYGWMDP 33

RESULT 20
US-10-719-450-1
; Sequence 1, Application US/10719450
; Publication No. US2004026682A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013
; CURRENT APPLICATION NUMBER: US/10/719,450
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USSN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USSN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USSN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 10/691,123
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-719-450-1
```

Query Match 97.1%; Score 100; DB 5; Length 33;  
Best Local Similarity 94.1%; Pred. No. 1.3e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWMDP 17  
:|||||  
Db 17 QGPWLEEEBAYGWMDP 33

## RESULT 21

US-10-505-239-5  
; Sequence 5, Application US/10505239  
; Publication No. US20050171014A1  
; GENERAL INFORMATION:  
; APPLICANT: TARASOVA, Nadya I  
; APPLICANT: MICHEJDA, Christopher J  
; APPLICANT: DYBA, Marcin  
; APPLICANT: COHRAN, Carolyn  
; TITLE OF INVENTION: CONJUGATES OF LIGAND, LINKER AND CYTOTOXIC AGENT AND RELATED  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE  
; FILE REFERENCE: 229694  
; CURRENT APPLICATION NUMBER: US/10/505,239  
; CURRENT FILING DATE: 2004-08-19  
; PRIOR APPLICATION NUMBER: PCT/US03/06344  
; PRIOR FILING DATE: 2003-02-27  
; PRIOR APPLICATION NUMBER: 60/360,543  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: 60/370,189  
; PRIOR FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-505-239-5

Query Match 97.1%; Score 100; DB 5; Length 33;  
Best Local Similarity 94.1%; Pred. No. 1.3e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWMDP 17  
:|||||  
Db 17 QGPWLEEEBAYGWMDP 33

## RESULT 22

US-10-408-765A-196  
; Sequence 196, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Eoin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Watnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 196  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-196

Query Match 97.1%; Score 100; DB 4; Length 34;  
Best Local Similarity 94.1%; Pred. No. 1.4e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWMDP 17  
:|||||  
Db 18 QGPWLEEEBAYGWMDP 34

## RESULT 23

US-10-770-712-62  
; Sequence 62, Application US/10770712  
; Publication No. US20050170333A1  
; GENERAL INFORMATION:  
; APPLICANT: VOJDNANI, Aristo  
; TITLE OF INVENTION: IDENTIFICATION OF ETIOLOGY OF AUTISM  
; FILE REFERENCE: IMSCI2.008A  
; CURRENT APPLICATION NUMBER: US/10/770,712  
; CURRENT FILING DATE: 2004-02-03  
; NUMBER OF SEQ ID NOS: 133  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 62  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetically prepared peptide sequence  
US-10-770-712-62

Query Match 97.1%; Score 100; DB 5; Length 34;  
Best Local Similarity 94.1%; Pred. No. 1.4e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWMDP 17  
:|||||  
Db 18 QGPWLEEEBAYGWMDP 34

## RESULT 24

US-11-066-697-423  
; Sequence 423, Application US/11066697  
; Publication No. US20050187159A1  
; GENERAL INFORMATION:  
; APPLICANT: Bridon, Dominique P.  
; APPLICANT: Ezrin, Alan M.  
; APPLICANT: Milner, Peter G.  
; APPLICANT: Holmes, Darren L.  
; APPLICANT: Thibadeau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; FILE REFERENCE: 500862002301  
; CURRENT APPLICATION NUMBER: US/11/066,697  
; CURRENT FILING DATE: 2005-02-25  
; PRIOR APPLICATION NUMBER: 09/657,276  
; PRIOR FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-15  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 423  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-11-066-697-423

Query Match 97.1%; Score 100; DB 6; Length 34;  
Best Local Similarity 94.1%; Pred. No. 1.4e-06;

```
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEEEEAYGWMDF 17
    :|||||
Db 18 QGPWLEEEEEEAYGWMDF 34
    :|||||

RESULT 25
US-10-728-082-3
; Sequence 3, Application US/10728082
; Publication No. US20040229810A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013CIP
; CURRENT APPLICATION NUMBER: US/10/728,082
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 10/719,450
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USSN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USSN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USSN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-728-082-3
Query Match 95.1%; Score 98; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPWLEEEEEEAYGWMDF 17
    :|||||
Db 1 GPWLEEEEEEAYGWMDF 16
    :|||||

RESULT 26
US-10-719-450-3
; Sequence 3, Application US/10719450
; Publication No. US2004026682A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013
; CURRENT APPLICATION NUMBER: US/10/719,450
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USSN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USSN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USSN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-728-082-3
Query Match 95.1%; Score 98; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPWLEEEEEEAYGWMDF 17
    :|||||
Db 1 GPWLEEEEEEAYGWMDF 16
    :|||||

RESULT 27
US-10-728-082-2
; Sequence 2, Application US/10728082
; Publication No. US20040229810A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013CIP
; CURRENT APPLICATION NUMBER: US/10/728,082
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 10/719,450
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USSN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USSN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USSN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: variant gastrin peptide M31L as compared to SEQ ID NO:1
US-10-728-082-2
Query Match 94.2%; Score 97; DB 5; Length 33;
Best Local Similarity 88.2%; Pred. No. 3.5e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEEEEAYGWMDF 17
    :|||||
Db 17 QGPWLEEEEEEAYGWMDF 33
    :|||||

RESULT 28
US-10-719-450-2
; Sequence 2, Application US/10719450
; Publication No. US2004026682A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
```

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; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-719-450-3
Query Match 95.1%; Score 98; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPWLEEEEEEAYGWMDF 17
    :|||||
Db 1 GPWLEEEEEEAYGWMDF 16
    :|||||

RESULT 27
US-10-728-082-2
; Sequence 2, Application US/10728082
; Publication No. US20040229810A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013CIP
; CURRENT APPLICATION NUMBER: US/10/728,082
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 10/719,450
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USSN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USSN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USSN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: variant gastrin peptide M31L as compared to SEQ ID NO:1
US-10-728-082-2
Query Match 94.2%; Score 97; DB 5; Length 33;
Best Local Similarity 88.2%; Pred. No. 3.5e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEEEEAYGWMDF 17
    :|||||
Db 17 QGPWLEEEEEEAYGWMDF 33
    :|||||

RESULT 28
US-10-719-450-2
; Sequence 2, Application US/10719450
; Publication No. US2004026682A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
```

```
; TITLE OF INVENTION: Preparation
; FILE REFERENCE: 24492-013
; CURRENT APPLICATION NUMBER: US/10/719,450
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USSN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USSN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USSN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: variant gastrin peptide M31L as compared to SEQ ID NO:1
US-10-719-450-2

Query Match          94.2%; Score 97; DB 5; Length 33;
Best Local Similarity 88.2%; Pred. No. 3.5e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDF 17
Db 17 QGPWLEEEERAYGWLDF 33

RESULT 29
US-10-244-324A-1
; Sequence 1, Application US/10244324A
; Publication No. US20030162795A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Product Inc.
; TITLE OF INVENTION: THIENOPYRIDINE AND THIENOPYRIDINE DERIVATIVES
; FILE REFERENCE: PC9882C
; CURRENT APPLICATION NUMBER: US/10/244,324A
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Description of
; OTHER INFORMATION: Artificial Synthetic
US-10-244-324A-1

Query Match          93.2%; Score 96; DB 4; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.7e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDF 17
Db 3 KGPWLEEEERAYGWLDF 19

RESULT 30
US-10-394-322A-70
; Sequence 70, Application US/10394322A
; Publication No. US2003023391A1
; GENERAL INFORMATION:
```

```
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-70

Query Match          93.2%; Score 96; DB 4; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.7e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDF 17
Db 3 KGPWLEEEERAYGWLDF 19

RESULT 31
US-10-931-348-3
; Sequence 3, Application US/10931348
; Publication No. US20050026219A1
; GENERAL INFORMATION:
; APPLICANT: Birk, Gerald
; APPLICANT: Hadarnovsky, Steffen
; TITLE OF INVENTION: Process for Label-Free Measurement of Modified Substrate
; FILE REFERENCE: 1/1200-2-CIP-1
; CURRENT APPLICATION NUMBER: US/10/931,348
; CURRENT FILING DATE: 2004-09-01
; PRIOR APPLICATION NUMBER: US 09/823,150
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 10/716,125
; PRIOR FILING DATE: 2003-11-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphorylated modified substrate
US-10-931-348-3

Query Match          93.2%; Score 96; DB 5; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.7e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDF 17
Db 3 KGPWLEEEERAYGWLDF 19

RESULT 32
US-10-728-082-4
; Sequence 4, Application US/10728082
; Publication No. US20040229810A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013CIP
; CURRENT APPLICATION NUMBER: US/10/728,082
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 10/719,450
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/ PRIOR FILING DATE: 2003-11-21
/ PRIOR APPLICATION NUMBER: USSN 60/428,562
/ PRIOR FILING DATE: 2002-11-22
/ PRIOR APPLICATION NUMBER: USSN 60/430,590
/ PRIOR FILING DATE: 2002-12-03
/ PRIOR APPLICATION NUMBER: USSN 60/519,933
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: USSN 60/420,187
/ PRIOR FILING DATE: 2002-10-22
/ PRIOR APPLICATION NUMBER: USSN 60/420,399
/ PRIOR FILING DATE: 2002-10-22
/ PRIOR APPLICATION NUMBER: USSN 10/691,123
/ PRIOR FILING DATE: 2003-10-22
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 4
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: artificial
/ FEATURE:
/ OTHER INFORMATION: variant gastrin peptide - M14L as compared to SEQ ID NO:3
US-10-728-082-4

Query Match          92.2%; Score 95; DB 5; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 GPWLEEEEEAYGWMD 17
DB      1 GPWLEEEEEAYGWLD 16

RESULT 33
US-10-719-450-4
/ Sequence 4, Application US/10719450
/ Publication No. US20040266682A1
/ GENERAL INFORMATION:
/ APPLICANT: Cruz, Antonio
/ TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
/ FILE REFERENCE: 24492-013
/ CURRENT APPLICATION NUMBER: US/10/719,450
/ CURRENT FILING DATE: 2003-11-21
/ PRIOR APPLICATION NUMBER: USSN 60/428,100
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: USSN 60/428,562
/ PRIOR FILING DATE: 2002-11-22
/ PRIOR APPLICATION NUMBER: USSN 60/430,590
/ PRIOR FILING DATE: 2002-12-03
/ PRIOR APPLICATION NUMBER: USSN 60/519,933
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: USSN 60/420,187
/ PRIOR FILING DATE: 2002-10-22
/ PRIOR APPLICATION NUMBER: USSN 60/420,399
/ PRIOR FILING DATE: 2002-10-22
/ PRIOR APPLICATION NUMBER: USSN 10/691,123
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 4
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: artificial
/ FEATURE:
/ OTHER INFORMATION: variant gastrin peptide - M14L as compared to SEQ ID NO:3
US-10-719-450-4

Query Match          92.2%; Score 95; DB 5; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 GPWLEEEEEAYGWMD 17
DB      1 GPWLEEEEEAYGWLD 16

RESULT 34
US-10-104-607B-5
/ Sequence 5, Application US/10104607B
/ Publication No. US20030091574A1
/ GENERAL INFORMATION:
/ APPLICANT: Aphton Corporation
/ TITLE OF INVENTION: Combination Treatment of Pancreatic Cancer
/ FILE REFERENCE: 1102865-0052
/ CURRENT APPLICATION NUMBER: US/10/104,607B
/ CURRENT FILING DATE: 2002-03-22
/ PRIOR APPLICATION NUMBER: 60/278,294
/ PRIOR FILING DATE: 2001-03-23
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 5
/ LENGTH: 34
/ TYPE: PRT
/ ORGANISM: homo sapiens
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: XAA = Pyroglutamine
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (34)..(34)
/ OTHER INFORMATION: XAA= Amidated phenylalanine
US-10-104-607B-5

Query Match          91.3%; Score 94; DB 4; Length 34;
Best Local Similarity 93.8%; Pred. No. 9.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 BQWLEEEEEAYGWMD 16
DB      18 QGPWLEEEEEAYGWMD 33

RESULT 35
US-10-104-607B-4
/ Sequence 4, Application US/10104607B
/ Publication No. US20030091574A1
/ GENERAL INFORMATION:
/ APPLICANT: Aphton Corporation
/ TITLE OF INVENTION: Combination Treatment of Pancreatic Cancer
/ FILE REFERENCE: 1102865-0052
/ CURRENT APPLICATION NUMBER: US/10/104,607B
/ CURRENT FILING DATE: 2002-03-22
/ PRIOR APPLICATION NUMBER: 60/278,294
/ PRIOR FILING DATE: 2001-03-23
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (1)..(17)
/ OTHER INFORMATION: Amino acid sequence of Gastrin 17
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: XAA= Pyroglutamic acid or 5-oxoproline
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (17)..(17)
/ OTHER INFORMATION: XAA= Amidated phenylalanine
US-10-104-607B-4

Query Match          89.3%; Score 92; DB 4; Length 17;
```

Best Local Similarity 100.0%; Pred. No. 8.7e-06; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 0;

QY 2 GPWLEEEERAYGWMD 16  
| | | | | | | | | | | | | | | | | |  
DB 2 GPWLEEEERAYGWMD 16

## RESULT 36

US-10-227-012-2  
; Sequence 2, Application US/10227012  
; Publication No. US20040038217A1  
; GENERAL INFORMATION:  
; APPLICANT: Bioarray Solutions, LTD.  
; APPLICANT: Yang, Jiacheng  
; TITLE OF INVENTION: MOLECULAR CONSTRUCTS AND METHODS OF USE FOR DETECTION OF  
; TITLE OF INVENTION: BIOCHEMICAL REACTIONS  
; FILE REFERENCE: 4363-4008  
; CURRENT APPLICATION NUMBER: US/10/227,012  
; CURRENT FILING DATE: 2002-08-22  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: PEPTIDE  
; LOCATION: (12)..(12)  
; OTHER INFORMATION: Tyr (Y) is phosphorylated  
; PUBLICATION INFORMATION:  
; AUTHORS: Baldwin, et al.  
; TITLE: Phosphorylation of gastrin-17 by epidermal growth  
; TITLE: factor-stimulated tyrosine kinase.  
; JOURNAL: Nature  
; VOLUME: 301  
; ISSUE: 5899  
; PAGES: 435-437  
; DATE: 1983-02-03  
; DATABASE ENTRY DATE:  
; RELEVANT RESIDUES: (2)..(18)  
US-10-227-012-2

Query Match 85.9%; Score 88.5; DB 4; Length 18;  
Best Local Similarity 94.1%; Pred. No. 2.8e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 EGPWLEEEERAYGWMD 17  
| | | | | | | | | | | | | | | | | |  
DB 2 EGPWLEEEERAYGWMD 17

## RESULT 37

US-11-066-697-424  
; Sequence 424, Application US/11066697  
; Publication No. US20050187159A1  
; GENERAL INFORMATION:  
; APPLICANT: Bridon, Dominique P.  
; APPLICANT: Ezrin, Alan M.  
; APPLICANT: Milner, Peter G.  
; APPLICANT: Holmes, Darren L.  
; APPLICANT: Thibaut, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 500862002301  
; CURRENT APPLICATION NUMBER: US/11/066,697  
; CURRENT FILING DATE: 2005-02-25  
; PRIOR APPLICATION NUMBER: 09/657,276  
; PRIOR FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783

; PRIOR FILING DATE: 1999-10-15  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 424  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-11-066-697-424

Query Match 75.7%; Score 78; DB 6; Length 17;  
Best Local Similarity 82.4%; Pred. No. 0.00073;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMD 17  
| | | | | | | | | | | | | | | | | |  
DB 1 EGPWLEEEERAYGWMD 17

## RESULT 38

US-10-762-226-1  
; Sequence 1, Application US/10762226  
; Publication No. US20050025770A1  
; GENERAL INFORMATION:  
; APPLICANT: Gavas, Philip C.  
; APPLICANT: Karr, Stephen L.  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Watson, Susan A.  
; TITLE OF INVENTION: Immunological Methods for the Treatment of  
; TITLE OF INVENTION: Gastrointestinal Cancer  
; FILE REFERENCE: 1102865-0031  
; CURRENT APPLICATION NUMBER: US/10/762,226  
; CURRENT FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: 60/011,411  
; PRIOR FILING DATE: 1996-02-08  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Pyroglutamic acid residue  
US-10-762-226-1

Query Match 67.0%; Score 69; DB 5; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0089;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAY 12  
| | | | | | | | | | | | | |  
DB 1 EGPWLEEEERAY 12

## RESULT 39

US-10-343-654-12  
; Sequence 12, Application US/10343654  
; Publication No. US20030204063A1  
; GENERAL INFORMATION:  
; APPLICANT: Denis Gravel (Inventor)  
; APPLICANT: Abdelkrim Habi (Inventor)  
; APPLICANT: Thierry Abribat (Inventor)  
; APPLICANT: Theratechnologies Inc. (Assignee)  
; TITLE OF INVENTION: Modified Biological Peptides with  
; TITLE OF INVENTION: Increased Potency  
; FILE REFERENCE: 12411-22PCT  
; CURRENT APPLICATION NUMBER: US/10/343,654  
; CURRENT FILING DATE: 2003-02-03

```
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 34
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa = para-Glu or para-Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (4)...(4)
; OTHER INFORMATION: Xaa = Pro or Leu
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (6)...(6)
; OTHER INFORMATION: Xaa = Gly or Asp
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)...(7)
; OTHER INFORMATION: Xaa = Pro or Ser
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (8)...(8)
; OTHER INFORMATION: Xoo = Pro or Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa = His or Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)...(10)
; OTHER INFORMATION: Xaa = Leu or Met or Phe or Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (11)...(11)
; OTHER INFORMATION: Xaa = Val or Ile
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (14)...(14)
; OTHER INFORMATION: Xaa = Pro or Leu
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (15)...(15)
; OTHER INFORMATION: Xaa = Ser or Ala
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (18)...(18)
; OTHER INFORMATION: Xaa = Gln or Glu
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (19)...(19)
; OTHER INFORMATION: Xaa = Gly or Arg
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (21)...(21)
; OTHER INFORMATION: Xaa = Trp or Pro or Arg
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (22)...(22)
; OTHER INFORMATION: Xaa = Leu or Val or Met
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)...(24)
; OTHER INFORMATION: Xaa = Glu or Lys
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (27)...(27)
; OTHER INFORMATION: Xaa = Glu or Ala
; US-10-343-654-12
```

Query Match 60.2%; Score 62; DB 4; Length 34;

```
Best Local Similarity 73.3%; Pred. No. 0.23;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PWLLEEEAYGWMDF 17
   | | | | | | | | | |
Db 20 PXXEXAYGWMDF 34

RESULT 40
US-10-613-377A-18
; Sequence 18, Application US/10613377A
; Publication No. US20040208920A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059
; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of GnRH amino acid sequence linked to a spacer
; OTHER INFORMATION: peptide
; US-10-613-377A-18
```

Query Match 57.3%; Score 59; DB 4; Length 17;  
Best Local Similarity 90.9%; Pred. No. 0.3;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 EGPWLEEEEA 11
   | | | | | | | |
Db 1 EGPWLEEEES 11
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```
RESULT 41
US-10-759-832-18
; Sequence 18, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of GnRH amino acid sequence linked to a spacer
; OTHER INFORMATION: peptide
; US-10-759-832-18
```

Query Match 57.3%; Score 59; DB 5; Length 17;  
Best Local Similarity 90.9%; Pred. No. 0.3;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EGPWLEEEEA 11
   | | | | | | | |
Db 1 EGPWLEEEES 11
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RESULT 42  
US-11-036-690-18  
; Sequence 18, Application US/11036690  
; Publication No. US20050169979A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059CIP  
; CURRENT APPLICATION NUMBER: US/11/036.690  
; CURRENT FILING DATE: 2005-01-14  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 10/613,377  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: synthetic peptide of GNRH amino acid sequence linked to a spacer  
; OTHER INFORMATION: peptide  
US-11-036-690-18

Query Match 57.3%; Score 59; DB 6; Length 17;  
Best Local Similarity 90.9%; Pred. No. 0.3;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEER 11  
| | | | | | | | | |  
Db 1 EGPWLEEEER 11

RESULT 43  
US-10-613-377A-8  
; Sequence 8, Application US/10613377A  
; Publication No. US20040208920A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059  
; CURRENT APPLICATION NUMBER: US/10/613.377A  
; CURRENT FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-613-377A-8

Query Match 56.3%; Score 58; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEER 10  
| | | | | | | | | |  
Db 1 EGPWLEEEER 10

RESULT 44  
US-10-759-832-8  
; Sequence 8, Application US/10759832

; Publication No. US20040247661A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059CIP  
; CURRENT APPLICATION NUMBER: US/10/759,832  
; CURRENT FILING DATE: 2004-01-15  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 10/613,377  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; NAME/KEY: MOD RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-759-832-8

Query Match 56.3%; Score 58; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEER 10  
| | | | | | | | | |  
Db 1 EGPWLEEEER 10

RESULT 45  
US-11-036-690-8  
; Sequence 8, Application US/11036690  
; Publication No. US20050169979A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphton Corporation  
; TITLE OF INVENTION: Liposomal Vaccine  
; FILE REFERENCE: 1102865-0059CIP  
; CURRENT APPLICATION NUMBER: US/11/036,690  
; CURRENT FILING DATE: 2005-01-14  
; PRIOR APPLICATION NUMBER: 60/394,179  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 10/613,377  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; NAME/KEY: MOD RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-11-036-690-8

Query Match 56.3%; Score 58; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEER 10  
| | | | | | | | | |  
Db 1 EGPWLEEEER 10

RESULT 46  
US-10-813-336-6

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; Sequence 6, Application US/10813336
; Publication No. US20050069966A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Gastrin Hormone Immunoassays
; FILE REFERENCE: 1102863-0046
; CURRENT APPLICATION NUMBER: US/10/813,336
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,244
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: AMIDATION
US-10-813-336-6

Query Match 53.4%; Score 55; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ERAYGWMDF 17
Db 1 ERAYGWMDF 9

RESULT 47
US-10-505-239-20
; Sequence 20, Application US/10505239
; Publication No. US20050171014A1
; GENERAL INFORMATION:
; APPLICANT: TARASOVA, Nadya I
; APPLICANT: MICHEJDA, Christopher J
; APPLICANT: DYBA, Marcin
; APPLICANT: COHRAN, Carolyn
; TITLE OF INVENTION: CONJUGATES OF LIGAND, LINKER AND CYTOTOXIC AGENT AND RELATED
; FILE REFERENCE: 229694
; CURRENT APPLICATION NUMBER: US/10/505,239
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: PCT/US03/06344
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/360,543
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/370,189
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: Xaa = at position 8 is norleucine
US-10-505-239-20

Query Match 52.4%; Score 54; DB 5; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.85;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 EEEAYGWXDF 17
Db 1 EEEAYGWXDF 10

RESULT 48
US-10-505-239-25
; Sequence 25, Application US/10505239
; Publication No. US20050171014A1
; GENERAL INFORMATION:
; APPLICANT: TARASOVA, Nadya I
; APPLICANT: MICHEJDA, Christopher J
; APPLICANT: DYBA, Marcin
; APPLICANT: COHRAN, Carolyn
; TITLE OF INVENTION: CONJUGATES OF LIGAND, LINKER AND CYTOTOXIC AGENT AND RELATED
; FILE REFERENCE: 229694
; CURRENT APPLICATION NUMBER: US/10/505,239
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: PCT/US03/06344
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/360,543
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/370,189
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Xaa = at position 13 is norleucine
US-10-505-239-25

Query Match 52.4%; Score 54; DB 5; Length 15;
Best Local Similarity 90.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 EEEAYGWXDF 17
Db 6 EEEAYGWXDF 15

RESULT 49
US-10-505-239-26
; Sequence 26, Application US/10505239
; Publication No. US20050171014A1
; GENERAL INFORMATION:
; APPLICANT: TARASOVA, Nadya I
; APPLICANT: MICHEJDA, Christopher J
; APPLICANT: DYBA, Marcin
; APPLICANT: COHRAN, Carolyn
; TITLE OF INVENTION: CONJUGATES OF LIGAND, LINKER AND CYTOTOXIC AGENT AND RELATED
; FILE REFERENCE: 229694
; CURRENT APPLICATION NUMBER: US/10/505,239
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: PCT/US03/06344
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/360,543
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/370,189
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: Xaa = at position 8 is norleucine
US-10-505-239-26

Query Match 52.4%; Score 54; DB 5; Length 15;
Best Local Similarity 90.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 EEEAYGWXDF 17
Db 6 EEEAYGWXDF 15
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Search completed: January 3, 2006, 09:55:24  
Job time : 153.619 secs

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; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: V = at position 1 is conjugated to SPA110
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Xaa = at position 13 is norleucine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: F = at position 15 comprises a C-terminal amide group
US-10-505-239-26

Query Match      52.4%; Score 54; DB 5; Length 15;
Best Local Similarity 90.0%; Pred.No. 1.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 BEEAYGWMDF 17
        |||||
Db       6 BEEAYGWXDF 15

RESULT 50
US-10-505-239-27
; Sequence 27, Application US/10505239
; Publication No. US20050171014A1
; GENERAL INFORMATION:
; APPLICANT: TARASOVA, Nadya I
; APPLICANT: MICHEJDA, Christopher J
; APPLICANT: DYBA, Marcin
; APPLICANT: COHRAN, Carolyn
; TITLE OF INVENTION: CONJUGATES OF LIGAND, LINKER AND CYTOTOXIC AGENT AND RELATED
; FILE REFERENCE: 229694
; CURRENT APPLICATION NUMBER: US/10/505,239
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: PCT/US03/06344
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/360,543
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/370,189
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ-ID NO 27
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = at position 1 is 2-cyclohexyl-L-alanine and is conjugated
; OTHER INFORMATION: to HTI-286
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Xaa = at position 13 is norleucine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: F = at position 15 comprises a C-terminal amide group
US-10-505-239-27

Query Match      52.4%; Score 54; DB 5; Length 15;
Best Local Similarity 90.0%; Pred.No. 1.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 BEEAYGWMDF 17
        |||||
Db       6 BEEAYGWXDF 15
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:06 ; Search time 174.048 Seconds  
(without alignments)  
68.912 Million cell updates/sec

Title: US-10-759-832-1  
Perfect score: 103  
Sequence: 1 EGPWLEBEEBAYGWDPF 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : UniProt 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	97.1	101	1 GAST_HUMAN	P01350 homo sapien
2	98	95.1	104	1 GAST_PIG	P01351 sus scrofa
3	94	91.3	104	1 GAST_FELCA	P01354 felis silve
4	92	89.3	17	1 GAST_MACMU	P33714 macaca mula
5	92	89.3	104	1 GAST_CANFA	P01353 canis famil
6	91	88.3	34	1 GAST_CAPIH	P04564 capra hircu
7	91	88.3	104	1 GAST_BOVIN	P01352 bos taurus
8	91	88.3	104	1 GAST_SHEEP	O02686 ovis aries
9	90	87.4	107	1 GAST_HORSE	P55885 equus cabal
10	84.5	82.0	33	1 GAST_DIDMA	P33713 didelphis m
11	79	76.7	101	1 GAST_MOUSE	P48757 mus musculu
12	76	73.8	101	2 O6GSF5_MOUSE	O6GSF5 mus musculu
13	76	73.8	101	2 Q9CPR2_MOUSE	Q9CPR2 m mus muscu
14	75	72.8	104	1 GAST_RAT	P04563 rattus norv
15	73.5	71.4	33	1 GAST_CAVPO	P06885 cavia porce
16	73.5	71.4	33	1 GAST_CHIBR	P10034 chinchilla
17	58	56.3	354	2 O604V7_METCA	O604V7 methylococc
18	54	52.4	458	2 O8TV13_METKA	O8TV13 methanopyru
19	52	50.5	720	2 Q805X3_CHV1	Q805X3 cercopithe
20	52	50.5	720	2 Q7T5D2_CHV1	Q7T5D2 cercopithe
21	52	50.5	1055	2 O59DP8_DROME	O59DP8 drosophila
22	52	50.5	1118	2 O59DQ0_DROME	O59DQ0 drosophila
23	52	50.5	1141	2 O3V4C7_DROME	O3V4C7 drosophila
24	52	50.5	1190	2 O59DP9_DROME	O59DP9 drosophila
25	51	49.5	255	2 Q6AP34_DESPS	Q6AP34 desulfocale
26	51	49.5	827	2 Q61WN3_USITWA	Q61WN3 ustilago ma
27	51	49.5	827	2 Q4PBV7_USITWA	Q4PBV7 ustilago ma
28	50	48.5	238	2 Q9SCF1_ARATH	Q9SCF1 arabidopsis
29	50	48.5	401	1 ASSY_SYMTH	O67kel symbiobacte
30	50	48.5	442	2 Q9AA10_CAUCR	Q9AA10 caulobacter
31	50	48.5	732	2 Q9DUC7_VIRU	Q9DUC7 torque teno

32	49	47.6	229	2	Q7M4T4_9PEZI	Q7M4T4 scopulariop
33	49	47.6	614	1	ASNO_BACSU	O05272 bacillus su
34	49	47.6	680	2	Q5Y0Q6_9ALPH	Q5Y0Q6 cercopithe
35	49	47.6	751	2	Q560Q5_CRYNE	Q560Q5 cryptococcu
36	49	47.6	751	2	Q5KFP4_CRYNE	Q5KFP4 cryptococcu
37	49	47.6	931	2	Q6LU36_PHOPR	Q6LU36 photobacter
38	49	47.6	1029	2	Q5K800_CRYNE	Q5K800 cryptococcu
39	49	47.6	1133	2	Q6JCJ3_KLULA	Q6JCJ3 kluyveromyc
40	48	46.6	203	2	Q9HXG2_PSEAE	Q9HXG2 pseudomonas
41	48	46.6	225	2	Q6DJG8_XENLA	Q6DJG8 xenopus lae
42	48	46.6	227	2	Q642R0_XENLA	Q642R0 xenopus lae
43	48	46.6	749	2	Q4LT50_9BURK	Q4LT50 burkholderi
44	48	46.6	762	2	Q4WJ47_ASPFU	Q4WJ47 aspergillus
45	48	46.6	971	2	Q6ZAQ9_ORYSA	Q6ZAQ9 oryza sativ
46	48	46.6	1016	2	Q7ULE2_RHOBA	Q7ULE2 rhodopirell
47	47.5	46.1	401	1	ASSY_SYNEL	Q8dky7 synecococc
48	47	45.6	51	2	Q6LLM0_PHOPR	Q6LLM0 photobacter
49	47	45.6	84	2	Q5QC16_9CAUD	Q5QC16 enterobacte
50	47	45.6	274	2	Q92AF3_LISIN	Q92AF3 listeria in
51	47	45.6	335	1	DHYS_PYRAB	Q9V0H5 pyrococcus
52	47	45.6	393	2	Q6SLJ8_BACLD	Q6SLJ8 bacillus li
53	47	45.6	465	2	Q7FYI0_ANOGA	Q7FYI0 anopheles g
54	47	45.6	873	2	Q7WX90_ALCEU	Q7WX90 alcaligenes
55	47	45.6	1209	2	Q8YVK3_ANASP	Q8YVK3 anabaena sp
56	46.5	45.1	372	2	Q4WHR4_ASPFU	Q4WHR4 aspergillus
57	46.5	45.1	1062	2	Q6ZSD7_HUMAN	Q6ZSD7 homo sapien
58	46.5	45.1	1251	2	Q8TB62_HUMAN	Q8TB62 homo sapien
59	46.5	45.1	1563	2	Q8TB61_HUMAN	Q8TB61 homo sapien
60	46.5	45.1	1565	1	DMN_HUMAN	O15061 homo sapien
61	46.5	45.1	5430	1	MACF1_HUMAN	Q9UPH3 homo sapien
62	46.5	45.1	5430	2	Q5VM20_HUMAN	Q5VM20 homo sapien
63	46	44.7	99	2	Q5JK96_ORYSA	Q5JK96 oryza sativ
64	46	44.7	153	2	Q4GSV6_BRARB	Q4GSV6 brachydanio
65	46	44.7	157	2	Q4GSV4_BRARB	Q4GSV4 brachydanio
66	46	44.7	189	2	Q29411_ARCFU	O29411 archaeoglob
67	46	44.7	191	2	Q7XHJ1_QUERO	Q7XHJ1 quercus rob
68	46	44.7	225	2	Q4GSV3_BRARB	Q4GSV3 brachydanio
69	46	44.7	227	2	Q93783_HUMGT	Q93783 humicola gr
70	46	44.7	249	2	Q4GSV2_BRARB	Q4GSV2 brachydanio
71	46	44.7	276	2	Q8YEK4_BRUME	Q8YEK4 bruceella me
72	46	44.7	282	1	PNMT_HUMAN	P11086 homo sapien
73	46	44.7	282	2	Q6FHD9_HUMAN	Q6FHD9 homo sapien
74	46	44.7	287	2	Q57FU5_BRUAB	Q57FU5 bruceella ab
75	46	44.7	287	2	Q8G379_BRUAB	Q8G379 bruceella su
76	46	44.7	296	2	Q8FMN5_COREF	Q8FMN5 corynebacte
77	46	44.7	318	2	Q6FVG1_CANGA	Q6FVG1 candida gla
78	46	44.7	342	2	Q95XX5_CAEEL	Q95XX5 caenorhabdi
79	46	44.7	351	2	Q8THQ8_METAC	Q8THQ8 methanosaer
80	46	44.7	367	2	O04192_ARATH	O04192 arabidopsis
81	46	44.7	374	2	Q9ZSH6_ARATH	Q9ZSH6 arabidopsis
82	46	44.7	378	2	Q4GSV5_BRARB	Q4GSV5 brachydanio
83	46	44.7	384	2	Q7RXA3_NEUCR	Q7RXA3 neurospora
84	46	44.7	428	2	Q74GJ8_GEOSL	Q74GJ8 geobacter s
85	46	44.7	442	2	Q9FZP0_ARATH	Q9FZP0 arabidopsis
86	46	44.7	494	2	Q87NT6_VIBPA	Q87NT6 vibrio para
87	46	44.7	520	1	ATG15_YEAST	P25661 saccharomyc
88	46	44.7	562	2	Q87QEH_VIBPA	Q87QEH vibrio para
89	46	44.7	565	1	DSBD_ECOLI	P58162 escherichia
90	46	44.7	565	1	DSBD_ECOLI	P58162 escherichia
91	46	44.7	565	2	Q7UAM3_SHIFL	Q7UAM3 shigella fl
92	46	44.7	565	2	Q8CVH5_ECOL6	Q8CVH5 escherichia
93	46	44.7	612	2	Q83P44_SHIFL	Q83P44 shigella fl
94	46	44.7	612	2	Q5LP09_BACFN	Q5LP09 bacteroides
95	46	44.7	612	2	Q64W02_BACFR	Q64W02 bacteroides
96	46	44.7	614	2	Q8GW12_ARATH	Q8GW12 arabidopsis
97	46	44.7	658	2	Q68ST5_9AGAR	Q68ST5 pleurotus d
98	46	44.7	700	1	PHLN_BURPS	Q9rga8 burkholderi
99	46	44.7	700	2	Q62LP4_BURNA	Q62LP4 burkholderi
100	46	44.7	818	2	Q4GSV7_BRARB	Q4GSV7 brachydanio
101	46	44.7	827	2	Q9ZS85_ARATH	Q9ZS85 arabidopsis
102	46	44.7	867	2	Q9FZE6_ARATH	Q9FZE6 arabidopsis
103	46	44.7	1017	2	Q8LM12_ORYSA	Q8LM12 oryza sativ
104	46	44.7	1113	2	Q9M180_ARATH	Q9M180 arabidopsis

105	46	44.7	1119	2	Q9LJK04_ARATH	Q9LJK04_arabidopsis	178	44.5	43.2	301	2	Q5QMA0_ORYSA	Q5QMA0_oryza sativ
106	46	44.7	1175	2	Q92FF3_ARATH	Q92FF3_arabidopsis	179	44.5	43.2	316	2	Q4PHK3_USTMA	Q4PHK3_ustilago ma
107	46	44.7	1198	2	Q9C6N9_ARATH	Q9C6N9_arabidopsis	180	44.5	43.2	799	2	Q5KP69_CRYNE	Q5KP69_cryptococcu
108	46	44.7	1201	2	Q9C607_ARATH	Q9C607_arabidopsis	181	44.5	43.2	799	2	Q5SZW1_CRYNE	Q5SZW1_cryptococcu
109	46	44.7	1285	2	Q9Z801_ARATH	Q9Z801_arabidopsis	182	44.5	43.2	814	2	Q5KP68_CRYNE	Q5KP68_cryptococcu
110	46	44.7	1305	2	Q9ZU21_ARATH	Q9ZU21_arabidopsis	183	44.5	43.2	4408	2	Q4RNF0_TETNG	Q4RNF0_tetraodon n
111	46	44.7	1314	2	Q9ML94_ARATH	Q9ML94_arabidopsis	184	44	42.7	63	2	Q69KJ5_ORYSA	Q69KJ5_oryza sativ
112	46	44.7	1444	2	Q9L7G8_ARATH	Q9L7G8_arabidopsis	185	44	42.7	99	1	BXAL_SAMCY	Q9L7G8_pinctada fu
113	46	44.7	1444	2	Q9SFF0_ARATH	Q9SFF0_arabidopsis	186	44	42.7	131	2	Q9TWT2_PINFU	Q9TWT2_pinctada fu
114	46	44.7	1756	2	Q80975_ARATH	Q80975_arabidopsis	187	44	42.7	131	2	Q9TW98_PINFU	Q9TW98_pinctada fu
115	46	44.7	1786	2	Q4UGM4_Thean	Q4UGM4_theileria a	188	44	42.7	203	1	RPOC1_PROSC	P42078_prochiloron
116	46	44.7	1786	2	Q4N888_Thepa	Q4N888_theileria p	189	44	42.7	217	2	Q6ZDL4_ORYSA	Q6ZDL4_oryza sativ
117	45.5	44.2	269	2	Q8C5S5_MOUSE	Q8C5S5_mus musculus	190	44	42.7	251	2	Q4QJS9_HABIR	Q4QJS9_haemophilus
118	45.5	44.2	311	2	Q8VE83_MOUSE	Q8VE83_mus musculus	191	44	42.7	273	2	Q7S3R8_NEUCR	Q7S3R8_neurospora
119	45.5	44.2	311	2	Q9CQD5_MOUSE	Q9CQD5_mus musculus	192	44	42.7	274	2	Q8Y645_LISMF	Q8Y645_listeria mo
120	45.5	44.2	319	2	Q8CCQ4_MOUSE	Q8CCQ4_mus musculus	193	44	42.7	274	2	Q71YGI_LISMF	Q71YGI_listeria mo
121	45.5	44.2	353	2	Q916J6_PSEAE	Q916J6_pseudomonas	194	44	42.7	307	2	Q93JF6_STRCO	Q93JF6_streptomyce
122	45.5	44.2	402	2	Q6S850_ORYSA	Q6S850_oryza sativ	195	44	42.7	308	2	Q9K642_BACHD	Q9K642_bacillus ha
123	45.5	44.2	439	2	Q5CAG7_ORYSA	Q5CAG7_oryza sativ	196	44	42.7	311	2	Q4IRA3_GIBZE	Q4IRA3_gibberella
124	45.5	44.2	704	2	Q7X6U9_ORYSA	Q7X6U9_oryza sativ	197	44	42.7	341	2	Q5PE26_SALPA	Q5PE26_salmonella
125	45	43.7	83	2	Q8LKG4_LOLPR	Q8LKG4_lolium pere	198	44	42.7	342	2	Q7UIH4_RHOBA	Q7UIH4_rhodopirell
126	45	43.7	98	2	Q80B34_9FLAV	Q80B34_dengue viru	199	44	42.7	356	2	Q4ZNZ0_PSESY	Q4ZNZ0_pseudomonas
127	45	43.7	100	1	BX32_SAMCY	P33719_samia cynth	200	44	42.7	371	2	Q6H6C0_ORYSA	Q6H6C0_oryza sativ
128	45	43.7	106	2	P74093_SYNY3	P74093_synectocyst	201	44	42.7	381	2	Q8PT45_METMA	Q8PT45_methanosarc
129	45	43.7	160	2	Q8S415_MAIZE	Q8S415_zea mays (m	202	44	42.7	383	1	AROC_THET2	Q7X1W3_thermus the
130	45	43.7	173	2	Q27189_STYLE	Q27189_stylonychia	203	44	42.7	383	1	AROC_THET2	Q5S1I5_thermus the
131	45	43.7	173	2	Q7TUJ0_PROMM	Q7TUJ0_prochiloro	204	44	42.7	385	2	Q7XW33_ORYSA	Q7XW33_oryza sativ
132	45	43.7	207	2	Q96U05_NEUCR	Q96U05_neurospora	205	44	42.7	408	1	ASSY_METCA	Q609X7_methyllococ
133	45	43.7	210	2	Q52VK7_9HIV1	Q52VK7_human immun	206	44	42.7	428	2	Q9LH89_ARATH	Q9LH89_arabidopsis
134	45	43.7	249	1	MGUP_BAC25	P82597_bacillus sp	207	44	42.7	483	2	Q4HVB0_GIBZE	Q4HVB0_gibberella
135	45	43.7	252	2	Q7NKKV5_GLOVI	Q7NKKV5_gloeobacter	208	44	42.7	503	2	Q5BAZ8_EMENI	Q5BAZ8_aspergillus
136	45	43.7	277	2	Q8IL82_PLAF7	Q8IL82_plasmodium	209	44	42.7	520	2	Q6CCC4_YARLI	Q6CCC4_yarrowia li
137	45	43.7	292	2	Q5SYJ8_MOUSE	Q5SYJ8_mus musculus	210	44	42.7	520	2	Q67N47_SYMTH	Q67N47_symbiodacte
138	45	43.7	295	2	Q7RUQ1_NEUCR	Q7RUQ1_neurospora	211	44	42.7	523	2	Q5LLB6_SILPO	Q5LLB6_silicibacte
139	45	43.7	325	2	Q4HVP1_GIBZE	Q4HVP1_gibberella	212	44	42.7	532	2	Q9WBL0_BPKU1	Q9WBL0_bacterioph
140	45	43.7	334	2	Q74NP7_BAC1	Q74NP7_bacillus ce	213	44	42.7	618	2	Q5ZLI4_XENLA	Q5ZLI4_xenopus lae
141	45	43.7	340	2	Q7F9M1_ORYSA	Q7F9M1_oryza sativ	214	44	42.7	637	2	Q5WSS5_LEGPL	Q5WSS5_legionella
142	45	43.7	352	2	Q8X0P7_NEUCR	Q8X0P7_neurospora	215	44	42.7	637	2	Q5X0Z9_LEGPA	Q5X0Z9_legionella
143	45	43.7	356	2	Q4K6J3_PSEF5	Q4K6J3_pseudomonas	216	44	42.7	637	2	Q5ZJRJ3_LEGPH	Q5ZJRJ3_legionella
144	45	43.7	358	2	Q587D3_9TRYP	Q587D3_trypanosoma	217	44	42.7	685	2	Q66JB6_XENTR	Q66JB6_xenopus tro
145	45	43.7	359	1	MURG_PSEPK	Q88N76_pseudomonas	218	44	42.7	720	2	Q5S5W8_CRYNE	Q5S5W8_cryptococcu
146	45	43.7	416	2	Q8GS46_ORYSA	Q8GS46_oryza sativ	219	44	42.7	724	2	Q5KJZ0_CRYNE	Q5KJZ0_cryptococcu
147	45	43.7	575	2	Q7MXZ2_PHOLL	Q7MXZ2_photorhabd	220	44	42.7	754	2	Q4RXIC_TETNG	Q4RXIC_tetraodon n
148	45	43.7	577	1	Q6D9J6_ERWCT	Q6D9J6_erwinia car	221	44	42.7	871	2	Q8LPR8_ARATH	Q8LPR8_arabidopsis
149	45	43.7	595	1	DSBD_YERPE	Q8Z1Y9_yersinia pe	222	44	42.7	931	2	Q5ILR3_MAGGR	Q5ILR3_magnaporthe
150	45	43.7	595	2	Q66FE1_YERPS	Q66FE1_yersinia ps	223	44	42.7	942	2	Q9FNJ7_ARATH	Q9FNJ7_arabidopsis
151	45	43.7	648	2	Q9NDS8_BONMO	Q9NDS8_bombay mori	224	44	42.7	1086	1	POL_OMVVS	P16901_o pol poly
152	45	43.7	808	1	YNF8_CABEL	P34561_caenorhabdi	225	44	42.7	1100	2	Q5J355_PPRKO	Q5J355_pyrococcus
153	45	43.7	849	2	Q520N2_MAGGR	Q520N2_magnaporthe	226	44	42.7	1101	1	POL_VILVK	P35956_v pol poly
154	45	43.7	906	2	Q51YI6_MAGGR	Q51YI6_magnaporthe	227	44	42.7	1103	2	Q4SZ09_TETNG	Q4SZ09_tetraodon n
155	45	43.7	1068	2	Q7N9T0_PHOLL	Q7N9T0_photorhabd	228	44	42.7	1105	1	POL_VILV1	P03370_v pol poly
156	45	43.7	1316	2	Q4SDE1_TETNG	Q4SDE1_tetraodon n	229	44	42.7	1105	1	POL_VILV1	P23426_v pol poly
157	45	43.7	1424	2	Q5RGA8_BRARE	Q5RGA8_brachydanio	230	44	42.7	1105	1	POL_VILV2	P23427_v pol poly
158	45	43.7	2005	2	Q51J11_MAGGR	Q51J11_magnaporthe	231	44	42.7	1109	2	Q6HIV5_9RETR	Q6HIV5_small rumin
159	45	43.7	3392	2	Q5RIT6_9FLAV	Q5RIT6_dengue viru	232	44	42.7	1181	2	Q8KYZ4_9PROT	Q8KYZ4_uncultured
160	45	43.7	3392	2	Q5UCB9_9FLAV	Q5UCB9_dengue viru	233	44	42.7	1281	2	Q8TSN6_METAC	Q8TSN6_methanosarc
161	45	43.7	3392	2	Q689G2_9FLAV	Q689G2_dengue viru	234	44	42.7	1337	2	Q9Y8I8_THEHY	Q9Y8I8_thermococcu
162	45	43.7	3392	2	Q689G3_9FLAV	Q689G3_dengue viru	235	44	42.7	1480	2	Q96Q04_HUMAN	Q96Q04_homo sapien
163	45	43.7	3392	2	Q8VBS2_9FLAV	Q8VBS2_dengue viru	236	44	42.7	2768	2	Q751J3_ASHGO	Q751J3_aeshya gos
164	45	43.7	3392	2	Q8VBS3_9FLAV	Q8VBS3_dengue viru	237	44	42.7	3251	2	Q8K4B0_MOUSE	Q8K4B0_mus musculu
165	45	43.7	3392	2	Q91NH2_9FLAV	Q91NH2_dengue viru	238	44	42.7	3392	2	Q75N59_9FLAV	Q75N59_dengue viru
166	45	43.7	3392	2	Q91NH1_9FLAV	Q91NH1_dengue viru	239	44	42.7	3393	2	Q5IK03_9FLAV	Q5IK03_dengue viru
167	45	43.7	3392	2	P89313_9FLAV	P89313_dengue viru	240	44	42.7	3883	2	Q7Q120_ANOGA	Q7Q120_anopheles g
168	45	43.7	3392	2	P89314_9FLAV	P89314_dengue viru	241	43.5	42.2	52	1	ANTR_TRASC	P80110_trachemys g
169	45	43.7	3392	2	P89315_9FLAV	P89315_dengue viru	242	43.5	42.2	110	2	Q42454_TRASC	Q42454_trachemys s
170	45	43.7	3392	2	Q8B104_9FLAV	Q8B104_dengue viru	243	43.5	42.2	212	2	Q966H1_CABEL	Q966H1_caenorhabdi
171	45	43.7	3392	2	Q8B105_9FLAV	Q8B105_dengue viru	244	43.5	42.2	248	2	Q4WFX1_ASPFU	Q4WFX1_aspergillus
172	45	43.7	3392	2	Q8B106_9FLAV	Q8B106_dengue viru	245	43.5	42.2	251	2	Q7MSP6_WOLSU	Q7MSP6_wolfinella s
173	45	43.7	3392	2	Q98Y40_9FLAV	Q98Y40_dengue viru	246	43.5	42.2	426	2	Q881B1_PSESM	Q881B1_pseudomonas
174	45	43.7	3396	1	POLQ_DEN1S	P33478_d genome po	247	43.5	42.2	711	2	Q6FT96_CANGA	Q6FT96_candida gla
175	44.5	43.2	121	2	Q6ZVY1_HUMAN	Q6ZVY1_homo sapien	248	43.5	42.2	829	2	Q7XMP5_ORYSA	Q7XMP5_oryza sativ
176	44.5	43.2	188	2	Q5LX69_SILPO	Q5LX69_silicibacte	249	43.5	42.2	985	2	Q59773_SCHPO	Q59773_schizosacch
177	44.5	43.2	251	2	Q8R681_FUSNN	Q8R681_fusobacteri	250	43.5	42.2	1143	2	Q6P0N6_HUMAN	Q6P0N6_homo sapien

251	43.5	42.2	3060	1	BPAB8_HUMAN	Q8wxt8	homo sapien	324	43	41.7	444	2	Q5X8T8_LEGPA	Q5x8t8	legionella
252	43.5	42.2	3060	2	Q5TF24_HUMAN	Q5tf24	homo sapien	325	43	41.7	444	2	Q5Z271_LEGPH	Q5z271	legionella
253	43.5	42.2	3214	1	BPAL1_HUMAN	Q03001	homo sapien	326	43	41.7	447	2	Q5UXI8_HALMA	Q5uxi8	halorcula
254	43.5	42.2	5171	1	BPAA3_HUMAN	Q94833	homo sapien	327	43	41.7	448	2	Q4N443_THEPA	Q4n443	thelleria p
255	43.5	42.2	5457	2	Q5TBT1_HUMAN	Q5tbt1	homo sapien	328	43	41.7	460	2	Q5QU72_IDILO	Q5qu72	idionarina
256	43.5	42.2	6846	2	Q4ROA7_TETNG	Q4rse7	tetradodon n	329	43	41.7	464	2	Q7NTP1_CHRVO	Q7ntp1	chromobacte
257	43.5	42.2	7543	2	Q5TBT2_HUMAN	Q5tbt2	homo sapien	330	43	41.7	483	2	Q9AA32_CAUCR	Q9aa32	caulobacter
258	43	41.7	111	2	Q7U3D4_SYNPX	Q7u3d4	synchococc	331	43	41.7	491	2	Q8TXK9_METKA	Q8txk9	methanopyru
259	43	41.7	142	2	Q6NER3_CORDI	Q6ner3	corynebacte	332	43	41.7	510	2	Q9NX92_HUMAN	Q9nx92	homo sapien
260	43	41.7	157	2	Q8S416_MAI2E	Q8s416	zea mays (m	333	43	41.7	510	2	Q53RE7_HUMAN	Q53re7	homo sapien
261	43	41.7	157	2	Q8VRA1_ECOLI	Q8vra1	escherichia	334	43	41.7	543	2	Q6P5A5_HUMAN	Q6p5a5	homo sapien
262	43	41.7	157	2	Q83JP0_SHIFL	Q83jp0	shigella fl	335	43	41.7	555	2	Q6YRH6_ONYPE	Q6yrh6	onion yello
263	43	41.7	159	2	Q8X3C0_ECOS7	Q8x3c0	escherichia	336	43	41.7	556	2	Q5MZA9_SYNP6	Q5mza9	synchococc
264	43	41.7	161	2	Q6KD14_ECOLI	Q6kd14	escherichia	337	43	41.7	578	1	DSBD_PANCI	Q9xdb2	pantoea cit
265	43	41.7	161	2	Q707F5_ECOLI	Q707f5	escherichia	338	43	41.7	580	1	SCSA7_MOUSE	Q8b3y9	mus musculus
266	43	41.7	161	2	Q83W78_ECOLI	Q83w78	escherichia	339	43	41.7	580	1	SCSA7_MOUSE	Q9jmd7	rattus norv
267	43	41.7	161	2	Q8G9U0_ECOLI	Q8g9u0	escherichia	340	43	41.7	594	1	TIRI_ARATH	Q570c0	arabidopsis
268	43	41.7	161	2	Q8GA17_ECOLI	Q8ga17	escherichia	341	43	41.7	613	2	Q65L12_BACLD	Q65l12	bacillus li
269	43	41.7	161	2	Q4F8C9_ECOLI	Q4fbc9	escherichia	342	43	41.7	622	2	Q86VG2_HUMAN	Q86vg2	homo sapien
270	43	41.7	161	2	Q721R5_LISMP	Q721r5	listeria mo	343	43	41.7	627	2	Q9TL11_NEPOL	Q9tl11	nephroelimi
271	43	41.7	161	2	Q8FAS2_ECOL6	Q8fas2	escherichia	344	43	41.7	628	2	Q5F3H0_AZOSE	Q5f3h0	azarcus sp
272	43	41.7	161	2	Q8FBZ3_ECOL6	Q8fbz3	escherichia	345	43	41.7	640	2	Q7RW79_NEUCR	Q7rw79	neurospora
273	43	41.7	161	2	Q8FDR9_ECOL6	Q8fdr9	escherichia	346	43	41.7	643	2	Q7Z2V4_HUMAN	Q7z2v4	homo sapien
274	43	41.7	161	2	Q8FG65_ECOL6	Q8fg65	escherichia	347	43	41.7	654	2	Q96DY5_MOUSE	Q96dy5	mus musculus
275	43	41.7	161	2	Q8X9K5_ECOS7	Q8x9k5	escherichia	348	43	41.7	657	2	Q8R3D4_MOUSE	Q8r3d4	mus musculus
276	43	41.7	162	2	Q9LPP0_ARATH	Q9lpp0	arabidopsis	349	43	41.7	667	2	Q8BTM4_MOUSE	Q8btm4	mus musculus
277	43	41.7	176	2	Q5I3Q1_MBLGA	Q5i3q1	meleagris g	350	43	41.7	669	2	Q55GK3_DICD1	Q55gk3	dictyostell
278	43	41.7	177	2	Q8B0V0_PSESM	Q8b0v0	pseudomonas	351	43	41.7	702	1	ZN282_HUMAN	Q9udv7	homo sapien
279	43	41.7	181	2	Q8FTU3_ECOL6	Q8ftu3	escherichia	352	43	41.7	671	2	Q6DKK0_HUMAN	Q6dkk0	homo sapien
280	43	41.7	181	2	Q8FKM6_ECOL6	Q8fkm6	escherichia	353	43	41.7	679	2	Q8JZT5_MOUSE	Q8jzt5	mus musculus
281	43	41.7	185	2	Q4UMC7_RICPE	Q4umc7	rickettsia	354	43	41.7	699	2	Q5AX91_EMENI	Q5ax91	aspergillus
282	43	41.7	200	1	SEPI5_SCHPO	Q94646	schizosacch	355	43	41.7	702	2	Q6CF82_YARLI	Q6cf82	yarrowia li
283	43	41.7	213	2	Q91041_9HIV1	Q91041	human immun	356	43	41.7	704	2	Q7A8N5_ECOS7	Q7a8n5	escherichia
284	43	41.7	230	2	Q4UJA8_RICPE	Q4uj8	homo sapien	357	43	41.7	704	2	Q8XC70_ECOS7	Q8xc70	escherichia
285	43	41.7	264	2	NNMT_HUMAN	P40261	homo sapien	358	43	41.7	721	1	Q84BK5_ENTFC	Q84bk5	enterococcu
286	43	41.7	264	2	Q6FHA9_HUMAN	Q6fha9	homo sapien	359	43	41.7	744	1	JPH3_MOUSE	Q9et77	mus musculus
287	43	41.7	271	2	Q9AL46_SHIFL	Q9al46	shigella fl	360	43	41.7	744	2	Q8BR43_MOUSE	Q8br43	mus musculus
288	43	41.7	272	2	Q89LR4_BRAJL	Q89lr4	bradyrhizob	361	43	41.7	760	2	Q8BNM7_MOUSE	Q8bnm7	mus musculus
289	43	41.7	278	2	Q7SBH1_NEUCR	Q7sbh1	neurospora	362	43	41.7	786	2	Q9F271_ARATH	Q9f271	arabidopsis
290	43	41.7	282	2	Q4SBG5_TETNG	Q4sbg5	tetradodon n	363	43	41.7	833	1	SEM4C_HUMAN	Q9c0c4	homo sapien
291	43	41.7	292	2	Q8NMJ7_CORGL	Q8nmj7	corynebacte	364	43	41.7	887	2	Q7XT48_ORYZA	Q7xt48	oryza sativ
292	43	41.7	296	2	Q7WU30_STAAU	Q7wu30	staphylococ	365	43	41.7	896	2	Q93YS3_ARATH	Q93ys3	arabidopsis
293	43	41.7	301	2	Q6ZHS5_ORISA	Q6zhs5	oryza sativ	366	43	41.7	910	2	Q9C520_ARATH	Q9c520	arabidopsis
294	43	41.7	303	1	VANY_ENTFC	P37711	enterococcu	367	43	41.7	970	2	Q51YM6_MAGGR	Q51ym6	magnaportha
295	43	41.7	304	1	PRMA_SYMTH	Q67851	syntrobacte	368	43	41.7	974	2	Q7PRK3_ANOGA	Q7prk3	anopheles g
296	43	41.7	314	2	Q5BC64_EMENI	Q5bc64	aspergillus	369	43	41.7	1012	2	Q4ICG3_GIBZE	Q4icg3	gibberella
297	43	41.7	318	2	Q69LP9_ORYZA	Q69lp9	oryza sativ	370	43	41.7	1095	2	Q7Q269_GIALA	Q7q269	giardia lam
298	43	41.7	330	2	Q8ZZR8_PYRAE	Q8zzr8	pyrobaculum	371	43	41.7	1122	2	Q8JAV1_9RETR	Q8jav1	viana/maedi
299	43	41.7	333	2	Q759Z3_ASHGO	Q759z3	ashbya goss	372	43	41.7	1159	2	Q5HQJ5_STABQ	Q5hqj5	staphylococ
300	43	41.7	341	2	Q57MC1_SALCH	Q57mc1	salmonella	373	43	41.7	1163	2	Q8CPU0_DICD1	Q8cpu0	dictyostell
301	43	41.7	341	2	Q8Z584_SALTI	Q8z584	salmonella	374	43	41.7	1163	2	Q54DM6_DICD1	Q54dm6	dictyostell
302	43	41.7	341	2	Q8ZNJ9_SALTI	Q8znj9	salmonella	375	43	41.7	1170	2	Q7VBU2_PROMA	Q7vbu2	prochloroco
303	43	41.7	357	2	Q560P8_CRYNE	Q560p8	cryptococcu	376	43	41.7	1172	2	Q6QR22_TRYCP	Q6qr22	trypanosoma
304	43	41.7	362	2	Q5KPF6_CRYNE	Q5kpf6	cryptococcu	377	43	41.7	1236	2	Q5CPL9_CRYPV	Q5cpl9	cryptospori
305	43	41.7	363	2	Q51LX7_WAGGR	Q51lx7	magnaportha	378	43	41.7	1580	2	Q6ZPH3_MOUSE	Q6zph3	mus musculus
306	43	41.7	384	2	Q4S4V8_TETNG	Q4s4v8	tetradodon n	379	43	41.7	2154	2	Q4S7Z6_TETNG	Q4s7z6	tetradodon n
307	43	41.7	388	2	Q8B0C4_PSESM	Q8b0c4	pseudomonas	380	43	41.7	2206	2	Q5B7N7_EMENI	Q5b7n7	aspergillus
308	43	41.7	395	2	Q582R5_STRYP	Q582r5	trypanosoma	381	43	41.7	3036	2	Q4PAT2_USTNA	Q4pat2	ustilago ma
309	43	41.7	396	1	ASSY_STRAS	Q8e7l1	streptococc	382	43	41.7	3391	2	Q9WDA2_9FLAV	Q9wda2	dengue viru
310	43	41.7	396	1	ASSY_STRAS	Q8e272	streptococc	383	43	41.7	3391	2	Q9WDA4_9FLAV	Q9wda4	dengue viru
311	43	41.7	396	1	ASSY_STRMU	Q8cw20	streptococc	384	43	41.7	3392	2	Q91ND2_9FLAV	Q91nd2	dengue viru
312	43	41.7	398	1	ASSY_STRR6	Q8dr15	streptococc	385	42.5	41.3	113	2	Q4VCM4_MOUSE	Q4vcn4	mus musculus
313	43	41.7	399	1	ASSY_STRT1	Q8d15	streptococc	386	42.5	41.3	134	2	Q853Z6_9CAUD	Q853z6	mycobacteri
314	43	41.7	399	1	ASSY_STRT2	Q5m2k2	streptococc	387	42.5	41.3	137	2	Q4VCN1_MOUSE	Q4vcn1	mus musculus
315	43	41.7	402	2	Q4TM76_9SPHN	Q4tm76	erythrobact	388	42.5	41.3	137	2	Q4VCN2_MOUSE	Q4vcn2	mus musculus
316	43	41.7	406	2	Q87MU7_VIBPA	Q87mu7	vibrio para	389	42.5	41.3	158	2	Q4VCM5_MOUSE	Q4vcn5	mus musculus
317	43	41.7	413	2	Q6AN53_DESPS	Q6ans3	desulfotale	390	42.5	41.3	158	2	Q4VCM7_MOUSE	Q4vcn7	mus musculus
318	43	41.7	414	2	Q4IAO9_GIBZE	Q4iao9	gibberella	391	42.5	41.3	158	2	Q4VCM8_MOUSE	Q4vcn8	mus musculus
319	43	41.7	417	2	Q98LNI_RHILO	Q98lni	rhizobium l	392	42.5	41.3	158	2	Q4VCM9_MOUSE	Q4vcn9	mus musculus
320	43	41.7	437	2	Q20871_CAEBL	Q20871	caenorhabdi	393	42.5	41.3	158	2	Q4VCN0_MOUSE	Q4vcn0	mus musculus
321	43	41.7	442	2	Q519V1_ENTHI	Q519v1	entamoeba h	394	42.5	41.3	158	2	Q4VCN5_MOUSE	Q4vcn5	mus musculus
322	43	41.7	443	2	Q59940_NEUCR	Q59940	neurospora	395	42.5	41.3	158	2	Q4VCP1_MOUSE	Q4vcp1	mus musculus
323	43	41.7	443	2	Q7RV11_NEUCR	Q7rv11	neurospora	396	42.5	41.3	181	2	Q95409_9PRIM	Q95409	gorilla gor

397	42.5	41.3	201	2	Q8W5X2_9CAUD	Q8W5x2 bacterioph	470	42	40.8	310	2	Q9FJP2_ARYATH	Q9fjp2 arabidopsis
398	42.5	41.3	243	2	Q740K7_MYCPA	Q740k7 mycobacteri	471	42	40.8	311	2	Q67WF6_ORYSA	Q67wf6 oryza sativ
399	42.5	41.3	246	2	Q4VCP2_MOUSE	Q4vcnp2 mus musculu	472	42	40.8	312	2	Q513L6_ECOLI	Q513l6 escherichia
400	42.5	41.3	257	2	Q4VCN4_MOUSE	Q4vcn4 mus musculu	473	42	40.8	312	2	Q87KB7_VIBPA	Q87kb7 vibrio para
401	42.5	41.3	264	2	Q6MP98_PARUM	Q6mp98 parachlamyd	474	42	40.8	318	2	Q9X5F7_ZYMMO	Q9x5f7 zymomonas m
402	42.5	41.3	275	2	Q4L214_MAIZE	Q4l214 zea mays (m	475	42	40.8	322	2	Q4N9F6_THEPA	Q4n9f6 theileria p
403	42.5	41.3	297	1	TRI52_HUMAN	Q96a61 homo sapien	476	42	40.8	326	2	Q585J4_9TRYP	Q585j4 trypanosoma
404	42.5	41.3	305	2	Q6BG17_PARTE	Q6bg17 paramycocu	477	42	40.8	330	1	DHYS_METJA	Q58224 methanococ
405	42.5	41.3	309	2	Q55ZW3_CRYNE	Q55zw3 cryptococcu	478	42	40.8	336	2	Q585J4_9TRYP	Q585j4 trypanosoma
406	42.5	41.3	309	2	Q5KP72_CRYNE	Q5kp72 cryptococcu	479	42	40.8	341	1	YBJE_ECOLI	Q585u0 tupaia glis
407	42.5	41.3	311	2	Q5SG66_HUMAN	Q5sg66 homo sapien	480	42	40.8	341	1	YBJE_ECOLI	Q585u0 tupaia glis
408	42.5	41.3	324	1	CBP21_HORVU	P55747 hordeum vul	481	42	40.8	341	2	Q7AC70_ECO57	Q7ac70 escherichia
409	42.5	41.3	329	2	Q9FG68_ARYATH	P55747 hordeum vul	482	42	40.8	341	2	Q83QV7_SHIFL	Q83qv7 snigella fl
410	42.5	41.3	331	2	Q6QMF4_MOUSE	Q9f968 arabidopsis	483	42	40.8	341	2	Q8FFS5_ECOL6	Q8ffs5 escherichia
411	42.5	41.3	331	2	Q6QMF2_MOUSE	Q6gmf4 mus musculu	484	42	40.8	341	2	Q8XE79_ECO57	Q8xe79 escherichia
412	42.5	41.3	338	2	Q6PEB5_MOUSE	Q6peb5 mus musculu	484	42	40.8	349	2	Q8PXT8_METMA	Q8pxt8 methanogarc
413	42.5	41.3	348	2	Q6SDV6_BACLD	Q6peb5 mus musculu	485	42	40.8	349	2	Q9SPG8_ARYATH	Q9spg8 arabidopsis
414	42.5	41.3	349	2	Q4VCN9_MOUSE	Q65dv6 bacillus li	486	42	40.8	350	2	Q8Y0H6_RALSO	Q8y0h6 ralstonia s
415	42.5	41.3	349	2	Q4VCN9_MOUSE	Q4vcn9 mus musculu	487	42	40.8	360	2	Q8GWF0_ARYATH	Q8gwf0 arabidopsis
416	42.5	41.3	355	2	Q30896_PITPI	O19440 mus musculu	488	42	40.8	361	2	Q5ZIO5_CHICK	Q5zi05 gallus gall
417	42.5	41.3	357	2	Q30896_PITPI	Q30896 pithecia pi	489	42	40.8	365	2	Q7YID9_CRYPV	Q7yid9 cryptospori
418	42.5	41.3	365	1	LA02_GORGO	Q78205 gorilla gor	490	42	40.8	365	2	Q5CK77_CRYHO	Q5ck77 cryptospori
419	42.5	41.3	365	1	LA03_GORGO	P30376 gorilla gor	491	42	40.8	381	2	Q8LNJ6_ORYSA	Q8lnj6 oryza sativ
420	42.5	41.3	365	1	LA04_GORGO	P30377 gorilla gor	492	42	40.8	382	1	MYB_AVIMB	P01104 avian myelo
421	42.5	41.3	365	1	LA80_HUMAN	P30378 gorilla gor	493	42	40.8	397	2	Q6F556_MOUSE	Q6f556 mus musculu
422	42.5	41.3	365	1	LA80_HUMAN	Q95h89 pan troglod	494	42	40.8	403	1	ASSY_BUCAI	P57158 buchnera ap
423	42.5	41.3	365	2	Q95H90_PANTR	Q95h89 pan troglod	495	42	40.8	403	2	Q7S9C9_NEUCR	Q7s9c9 neurospora
424	42.5	41.3	365	2	Q95H88_PANTR	Q95h88 pan troglod	496	42	40.8	436	2	Q8MPH5_OXYTR	Q8mph5 oxytricha t
425	42.5	41.3	365	2	Q95H88_PANTR	Q95h88 pan troglod	497	42	40.8	436	2	Q8MPH7_OXYTR	Q8mph7 oxytricha t
426	42.5	41.3	442	2	Q7MRP0_WOLSU	Q7mrp0 wolinsella s	498	42	40.8	441	2	Q64644_RAT	Q64644 rattus norv
427	42.5	41.3	533	2	Q5CKS4_CRYHO	Q5ckr8 cryptospori	499	42	40.8	442	2	Q6LNU9_PROPR	Q6lnu9 photobacter
428	42.5	41.3	534	2	Q5CTR8_CRYPV	Q5ctr8 cryptospori	500	42	40.8	455	2	Q8LNU9_PROPR	Q8lnu9 photobacter
429	42.5	41.3	726	2	Q4X1Z5_ASPFU	Q4x1z5 aspergillus	501	42	40.8	463	1	GLP1R_HUMAN	P43220 homo sapien
430	42.5	41.3	964	2	Q5SPB2_BRARE	Q5spb2 brachydanio	502	42	40.8	463	1	GLP1R_HUMAN	P43220 homo sapien
431	42.5	41.3	1096	2	Q8GRF3_9ACTO	Q8grf3 streptomyce	503	42	40.8	472	1	ZIM3_HUMAN	Q9spe6 homo sapien
432	42.5	41.3	1897	2	Q4SY99_TETNG	Q4sy99 tetraodon n	504	42	40.8	472	1	ZIM3_HUMAN	Q9spe6 homo sapien
433	42.5	41.3	1831	2	Q5AW24_EMENI	Q5aw24 aspergillus	505	42	40.8	472	1	ZIM3_HUMAN	Q9spe6 homo sapien
434	42	40.8	98	1	BXA3_SAMCY	P33720 samia cynth	506	42	40.8	476	2	Q4S697_TETNG	Q4s697 tetraodon n
435	42	40.8	98	1	FER2_PHYAM	P00231 phytoacca	507	42	40.8	481	2	Q51F02_ENTHI	Q51fu2 entamoeba h
436	42	40.8	128	1	CION_CIOIN	P16240 ciona intes	508	42	40.8	481	2	Q9SFV8_ARYATH	Q9sfv8 arabidopsis
437	42	40.8	129	2	Q97048_PINFU	P16240 ciona intes	509	42	40.8	481	2	Q4IVQ2_AZOVI	Q4ivq2 azotobacter
438	42	40.8	130	2	Q9UAH3_PINFU	Q9uah3 pictada fu	510	42	40.8	490	2	Q6EQ30_ORYSA	Q6eq30 oryza sativ
439	42	40.8	139	2	Q95LQ5_HORSE	Q95lq5 equus cabal	511	42	40.8	494	1	ENP2_CHICK	P79784 gallus gall
440	42	40.8	143	2	Q56ZH9_ARYATH	Q56zh9 arabidopsis	512	42	40.8	495	2	Q8BIU1_MOUSE	Q8biu1 mus musculu
441	42	40.8	143	2	Q6WCX0_PARUM	Q6wcx0 parachlamyd	513	42	40.8	502	2	Q626C9_CAEBR	Q626c9 caenorhabdi
442	42	40.8	159	2	Q9HYU1_PSEAE	Q9hyu1 pseuodomonas	514	42	40.8	510	2	Q8ZQ00_ANASP	Q8z0q0 anabaena sp
443	42	40.8	161	2	Q51J33_ECOLI	Q51j33 escherichia	515	42	40.8	512	2	Q7QG25_ANOGA	Q7qg25 anopheles g
444	42	40.8	161	2	Q5K5S2_ECOLI	Q5k5s2 escherichia	516	42	40.8	519	2	Q52DS6_MAGGR	Q52ds6 magnaporthe
445	42	40.8	179	2	Q78AY6_NEUCR	Q78ay6 neurospora	517	42	40.8	530	2	Q922Q2_MOUSE	Q922q2 mus musculu
446	42	40.8	179	2	Q4S352_TETNG	Q4s352 tetraodon n	518	42	40.8	533	2	Q7X711_ORYSA	Q7x711 oryza sativ
447	42	40.8	180	2	Q5K5L7_ECOLI	Q5k5l7 escherichia	519	42	40.8	538	2	Q6LW55_PROPR	Q6lw55 photobacter
448	42	40.8	183	2	Q5WFE7_BACSK	Q5wfe7 bacillus cl	520	42	40.8	552	2	Q875K8_COPCI	Q875k8 coprinus ci
449	42	40.8	203	2	Q883Z0_SORBI	Q883z0 sorghum bic	521	42	40.8	555	2	Q56PB9_PHOSU	Q56pb9 phodopus au
450	42	40.8	204	2	Q5WHH4_BACSK	Q5whh4 bacillus cl	522	42	40.8	559	2	Q73XJ5_MYCPA	Q73xj5 mycobacteri
451	42	40.8	208	2	Q8USW8_9HIV1	Q8usw8 human immun	523	42	40.8	580	1	SC5A7_HUMAN	Q9szv3 homo sapien
452	42	40.8	209	2	Q58519_TRYPA	Q58519 trypanosoma	524	42	40.8	580	2	Q53TF2_HUMAN	Q53tf2 homo sapien
453	42	40.8	220	2	Q6TGS1_ORYSA	Q6tgs1 oryza sativ	525	42	40.8	587	1	MCCB_ARYATH	Q81dd8 arabidopsis
454	42	40.8	221	2	Q6TGS1_ORYSA	Q6tgs1 oryza sativ	526	42	40.8	596	1	CHDH_MOUSE	Q8bj64 mus musculu
455	42	40.8	232	2	Q6FK80_CANGA	Q6fk80 candida gla	527	42	40.8	597	2	Q5JN42_ORYSA	Q5jn42 oryza sativ
456	42	40.8	242	2	Q5SG22_EMENI	Q5sg22 aspergillus	528	42	40.8	599	2	Q6UPE0_RAT	Q6upe0 rattus norv
457	42	40.8	254	2	Q9LD63_ADIRA	Q9ld63 adiantum ra	529	42	40.8	601	2	Q4NJZ3_9MICC	Q4njz3 arthrobacte
458	42	40.8	268	2	P81394_ANTMA	P81394 antirrhinum	530	42	40.8	633	2	Q4KMF7_BRARE	Q4kmf7 brachydanio
459	42	40.8	268	2	Q8NSY4_CORGL	Q8nsy4 corynebacte	531	42	40.8	634	2	Q4IU88_AZOVI	Q4iu88 azotobacter
460	42	40.8	273	2	Q7Q0E5_ANOGA	Q7q0e5 anopheles g	532	42	40.8	643	2	Q9HEW2_CRYNE	Q9hew2 cryptococcu
461	42	40.8	276	2	Q56UT4_ORYSA	Q56ut4 oryza sativ	533	42	40.8	643	2	Q9HEW3_CRYNE	Q9hew3 cryptococcu
462	42	40.8	283	1	PNMT_RAT	Q5ypw3 nocardia fa	534	42	40.8	644	2	Q9HEW5_CRYNE	Q9hew5 cryptococcu
463	42	40.8	285	1	PNMT_RAT	P10337 rattus norv	535	42	40.8	644	2	Q9UV59_CRYNV	Q9uv59 cryptococcu
464	42	40.8	286	2	Q6HC33_BACHK	Q6hc33 bacillus th	536	42	40.8	644	2	Q6TG16_CRIGA	Q6tg16 cryptococcu
465	42	40.8	288	2	Q7URF9_RHOBA	Q7urf9 rhodospirell	537	42	40.8	644	2	Q5KHP3_CRYNE	Q5khp3 cryptococcu
466	42	40.8	295	1	PNMT_MOUSE	P40935 mus musculu	538	42	40.8	644	2	Q55UP8_CRYNE	Q55up8 cryptococcu
467	42	40.8	301	2	Q9SN12_ARYATH	Q9sn12 arabidopsis	539	42	40.8	645	2	Q5Y224_CRYGA	Q5y224 cryptococcu
468	42	40.8	304	2	Q8K3A6_MOUSE	Q8k3a6 mus musculu	540	42	40.8	668	2	Q5X5X8_CRYNE	Q5x5x8 cryptococcu
469	42	40.8	304	2	Q39155_ARYATH	Q39155 arabidopsis	541	42	40.8	668	2	Q5KMS4_CRYNE	Q5kms4 cryptococcu
			304	2	Q49745_ARYATH	Q49745 arabidopsis	542	42	40.8	671	2	Q58ES2_BRARE	Q58es2 brachydanio

543	42	40.8	686	2	Q4PIC6_USTWA	Q4pic6	ustilago ma
544	42	40.8	697	2	Q4LUV1_9BURK	Q4lUV1	burkholderi
545	42	40.8	698	2	Q8TP40_METAC	Q8tp40	methanosarc
546	42	40.8	737	2	Q8BV00_MOUSE	Q8bv00	mus musculus
547	42	40.8	743	1	COGB_CABEL	Q44502	caenorhabdi
548	42	40.8	743	1	MYBB_XENLA	P52551	xenopus lae
549	42	40.8	744	2	Q8UC67_AGR75	Q8uc67	agrobacteri
550	42	40.8	745	2	Q23618_ARATH	Q23618	arabidopsis
551	42	40.8	748	2	Q6NRE6_XENLA	Q6nre6	xenopus lae
552	42	40.8	761	2	Q8DYO0_NITRU	Q8dyv0	nitrosomona
553	42	40.8	764	2	Q7D045_AGR75	Q7d045	agrobacteri
554	42	40.8	772	2	Q8BVJ3_MOUSE	Q8bvj3	m mus muscu
555	42	40.8	814	2	Q4WNA8_ASPFU	Q4wn48	aspergillus
556	42	40.8	827	2	Q8BHX2_MOUSE	Q8bhx2	mus musculus
557	42	40.8	834	2	Q8S065_9BROM	Q8s065	peanut stun
558	42	40.8	941	1	VDP_MOUSE	Q9z1z0	mus musculus
559	42	40.8	952	2	Q9LYE0_ARATH	Q9lye0	arabidopsis
560	42	40.8	959	2	Q91WE7_MOUSE	Q91we7	mus musculus
561	42	40.8	961	2	Q94FL9_ARATH	Q94fl9	arabidopsis
562	42	40.8	1129	2	Q4HU48_GIBZE	Q4hu48	gibberella
563	42	40.8	1134	2	Q5V729_HALMA	Q5v729	haloarcula
564	42	40.8	1134	2	Q5V7W1_HALMA	Q5v7w1	haloarcula
565	42	40.8	1145	2	Q72CL7_DESVH	Q72cl7	desulfovibr
566	42	40.8	1149	1	HDAC6_MOUSE	Q922v5	mus musculus
567	42	40.8	1152	2	Q8CSC3_MOUSE	Q8csc3	mus musculus
568	42	40.8	1277	2	Q17517_CABEL	Q17517	caenorhabdi
569	42	40.8	1352	2	Q899D3_CLOTE	Q899d3	clostridium
570	42	40.8	1363	2	Q9VFD3_DROME	Q9vfd3	drosophila
571	42	40.8	1421	2	Q84ZR6_ORYSA	Q84zr6	oryza sativ
572	42	40.8	1424	2	Q5XJV6_MOUSE	Q5xjv6	mus musculus
573	42	40.8	1424	2	Q52KF1_MOUSE	Q52kf1	mus musculus
574	42	40.8	1550	2	Q7TNC6_MOUSE	Q7tnc6	mus musculus
575	42	40.8	1588	2	Q55WX4_CRYNE	Q55wx4	cryptococcu
576	42	40.8	1588	2	Q5KJCS_CRYNE	Q5kjcs	cryptococcu
577	42	40.8	1622	2	Q7RQ89_PLAYO	Q7rgr9	plasmodium
578	42	40.8	2174	2	Q92JUH_RHIME	Q92juh	rhizobium m
579	42	40.8	5105	2	Q7RJO9_ANOGA	Q7rjg9	anopheles g
580	42	40.8	5105	2	Q7PMK5_ANOGA	Q7pmk5	anopheles g
581	41.5	40.3	113	2	Q8ZVH7_PYRAE	Q8zv7	pyrobaculum
582	41.5	40.3	126	2	Q8W4T5_9SOLN	Q8w4t5	solanum phu
583	41.5	40.3	176	2	Q5TWF8_ANOGA	Q5tmf8	anopheles g
584	41.5	40.3	178	2	Q7YMN0_PIG	Q7ymn0	sus scrofa
585	41.5	40.3	194	2	Q6CWE2_KLULA	Q6cwe2	kluyveromyc
586	41.5	40.3	286	2	Q8H257_9ROSI	Q8h257	gossypioide
587	41.5	40.3	288	2	Q4WMP7_ASPFU	Q4wmp7	aspergillus
588	41.5	40.3	314	2	Q860F6_MACNE	Q860f6	macaca neme
589	41.5	40.3	358	2	Q1012_SAGFU	Q1012	saginus fu
590	41.5	40.3	365	2	Q617A3_MACFA	Q617a3	macaca fasc
591	41.5	40.3	427	2	Q91673_PSEAB	Q91673	pseudomonas
592	41.5	40.3	441	2	Q92Q44_RHIME	Q92q44	rhizobium m
593	41.5	40.3	445	2	Q7SC88_NEUCR	Q7sc88	neurospora
594	41.5	40.3	448	1	GUN_CLOSA	P15704	clostridium
595	41.5	40.3	456	2	Q6BJH0_DEBHA	Q6bjh0	debaromyce
596	41.5	40.3	496	2	Q856N2_9CAUD	Q856n2	mycobacteri
597	41.5	40.3	499	2	Q5ART0_EMENI	Q5art0	aspergillus
598	41.5	40.3	511	2	Q5KSN5_9ACTO	Q5kns	streptomyce
599	41.5	40.3	524	2	Q872Q8_NEUCR	Q872q8	neurospora
600	41.5	40.3	529	2	Q4S1N8_TETNG	Q4s1n8	tetradodon n
601	41.5	40.3	531	2	Q9ACN7-STROI	Q9acn7	streptomyce
602	41.5	40.3	579	2	Q9RBS3_DEIRA	Q9rrs3	deinococcus
603	41.5	40.3	586	2	Q9FJ99_ARATH	Q9fj99	arabidopsis
604	41.5	40.3	588	2	Q61U58_CABER	Q61u58	caenorhabdi
605	41.5	40.3	644	2	Q82AM8_STRAW	Q82am8	streptomyce
606	41.5	40.3	683	2	Q7PYW1_ANOGA	Q7pyw1	anopheles g
607	41.5	40.3	720	1	GLGB_CHLPN	Q9z876	chlamydia p
608	41.5	40.3	773	2	Q8MR70_DROME	Q8mr70	drosophila
609	41.5	40.3	776	1	SYM_NANEQ	Q74m41	nanorchaeu
610	41.5	40.3	786	2	Q503P9_BRARE	Q503p9	brachydanio
611	41.5	40.3	836	2	Q4YTE9_FLABE	Q4yte9	plasmodium
612	41.5	40.3	864	2	Q7RGL6_PLAYO	Q7rgl6	plasmodium
613	41.5	40.3	872	2	Q9VH20_DROME	Q9vh20	drosophila
614	41.5	40.3	895	2	Q51HW1_MAGGR	Q51hw1	magnaporthe
615	41.5	40.3	930	1	ATSS_HUMAN	Q9una0	homo sapien

616	41.5	40.3	930	2	Q52LV4_HUMAN	Q52lv4	homo sapien
617	41.5	40.3	1375	2	Q4RUK8_TETNG	Q4ruk8	tetradodon n
618	41.5	40.3	2611	1	BPABA_MOUSE	Q91zu8	mus musculus
619	41.5	40.3	7389	1	BPABA_MOUSE	Q91zu8	mus musculus
620	41	39.8	42	2	Q9LE12_9TRAC	Q91e12	equisetum s
621	41	39.8	42	2	Q9LE64_ADIRA	Q91e64	adiantum ra
622	41	39.8	42	2	Q9LE26_PSINU	Q91e26	peilotum nu
623	41	39.8	42	2	Q8XZ29_EC057	Q8xz29	escherichia
624	41	39.8	66	2	Q9XA12-STRCO	Q9xa12	streptomyce
625	41	39.8	69	2	Q5I712_BACNO	Q5i712	bacteroides
626	41	39.8	85	2	Q9KV47_VIECH	Q9kv47	vibrio chol
627	41	39.8	92	2	Q8KGA1_CHLTE	Q8kgav	condylactis
628	41	39.8	110	2	Q9GVV9_CONGI	Q9gvv9	homo sapien
629	41	39.8	111	2	Q96RH9_HUMAN	Q96rh9	homo sapien
630	41	39.8	119	2	Q5FK70_LACAC	Q5fk70	lactobacilli
631	41	39.8	123	2	Q8NPT6_CORGL	Q8npt6	corynebacte
632	41	39.8	123	2	Q8NQTO_CORGL	Q8nqt0	corynebacte
633	41	39.8	125	2	Q6D7N3_ERWCT	Q6d7n3	erwinia car
634	41	39.8	131	2	Q6ILM6_DROME	Q6ilm6	drosophila
635	41	39.8	139	2	Q5C312_SCHJA	Q5c312	schistosoma
636	41	39.8	159	2	Q98309_MCV1	Q98309	molluscum c
637	41	39.8	176	2	Q57J17_SALCH	Q57j17	salmonella
638	41	39.8	176	2	Q8ZLT6_SALTY	Q8zlt6	trypanosoma
639	41	39.8	183	2	Q9GPL4_TRYCR	Q9gpl4	trypanosoma
640	41	39.8	185	2	Q32435_BACUS	Q32435	bacillus su
641	41	39.8	208	2	Q875J7_CRYNV	Q875j7	cryptococcu
642	41	39.8	208	2	Q96VN8_CRYNE	Q96vn8	cryptococcu
643	41	39.8	226	1	YODN_BACSU	Q34414	bacillus su
644	41	39.8	226	2	Q65IE3_BACLD	Q65ie3	bacillus li
645	41	39.8	227	2	Q6TBL8_9CHRO	Q6tbl8	microcycatis
646	41	39.8	227	2	Q6TBL9_MICAE	Q6tbl9	microcycatis
647	41	39.8	233	2	Q4SJB1_TETNG	Q4sjb1	tetradodon n
648	41	39.8	248	2	Q8X4R9_EC057	Q8x4r9	escherichia
649	41	39.8	260	2	Q5ZTS9_LEGPH	Q5zts9	legionella
650	41	39.8	261	2	Q9JNW3_STRPY	Q9jnw3	streptococc
651	41	39.8	263	2	Q8XKL5_CLOPE	Q8xkl5	clostridium
652	41	39.8	268	2	Q5ABX1_CANAL	Q5abx1	candida alb
653	41	39.8	270	2	Q9PLE5_ARATH	Q9ple5	arabidopsis
654	41	39.8	273	2	Q941F8_ARATH	Q941f8	arabidopsis
655	41	39.8	273	2	Q941F9_ARATH	Q941f9	arabidopsis
656	41	39.8	273	2	Q39028_ARATH	Q39028	arabidopsis
657	41	39.8	273	2	Q93VZ0_ARATH	Q93vz0	arabidopsis
658	41	39.8	273	2	Q93V46_ARATH	Q93v46	arabidopsis
659	41	39.8	276	2	Q8LGV5_ARATH	Q8lgv5	arabidopsis
660	41	39.8	286	2	Q8H261_GOSHI	Q8h261	gossypium h
661	41	39.8	287	2	Q8H259_9ROSI	Q8h259	gossypium x
662	41	39.8	287	2	Q8H259_9ROSI	Q8h259	gossypium x
663	41	39.8	287	2	Q8H258_9ROSI	Q8h258	gossypium h
664	41	39.8	287	2	Q8TA39_HETGL	Q8ta39	heterodera
665	41	39.8	288	2	Q14725_HUMAN	Q14725	homo sapien
666	41	39.8	289	2	Q9JNW6_STRPY	Q9jnw6	streptococc
667	41	39.8	290	2	Q9JNW9_STRPY	Q9jnw9	streptococc
668	41	39.8	290	2	Q9JNV0_STRPY	Q9jnv0	streptococc
669	41	39.8	290	2	Q9JF08_STRPY	Q9jfp8	streptococc
670	41	39.8	290	2	Q9JF08_STRPY	Q9jfp8	streptococc
671	41	39.8	290	2	Q9JF08_STRPY	Q9jfp8	streptococc
672	41	39.8	290	2	Q9JF23_STRPY	Q9jfp3	streptococc
673	41	39.8	293	2	Q9LXG9_ARATH	Q9lxg9	arabidopsis
674	41	39.8	293	2	Q94020_GOSHI	Q94020	gossypium h
675	41	39.8	293	2	Q94JN4_GOSHI	Q94jns	gossypium h
676	41	39.8	293	2	Q94JN5_GOSHI	Q94jns	gossypium h
677	41	39.8	294	2	Q4UIW3_PANTH	Q4uiw3	paenibacilli
678	41	39.8	295	2	Q8L145_9CHRO	Q8l145	microcycatis
679	41	39.8	296	2	Q7PVN3_ANOGA	Q7pvn3	anopheles g
680	41	39.8	296	2	Q924P2-STROI	Q924p2	streptomyce
681	41	39.8	296	2	Q51MR4_MAGGR	Q51mr4	magnaporthe
682	41	39.8	298	2	Q8H7R9_ORYSA	Q8h7r9	oryza sativ
683	41	39.8	298	2	Q4UIV5_9BACL	Q4uiv5	paenibacilli
684	41	39.8	299	2	Q30284_ARCFU	Q30284	archaeoglob
685	41	39.8	305	2	Q82KP8_STRAW	Q82kp8	streptomyce
686	41	39.8	312	2	Q57WG5_9TRYP	Q57wg5	trypanosoma
687	41	39.8	312	2	Q8NC15_HUMAN	Q8nc15	homo sapien
688	41	39.8	314	2	Q8NC15_HUMAN	Q8nc15	homo sapien

689	41	39.8	314	2	Q8XM80_CLOPE	Q8xm80 clostridium	762	41	39.8	645	2	Q7WR95_BORBR	Q7wr95 bordetella
690	41	39.8	316	2	Q8H8G2_ORYSA	Q8h8g2 oryza sativ	763	41	39.8	652	2	Q72IA2_THET2	Q72ia2 thermus the
691	41	39.8	317	2	Q94J08_ORYSA	Q94j08 oryza sativ	764	41	39.8	652	2	Q5SHY6_THET8	Q5shy6 thermus the
692	41	39.8	317	2	Q75LP7_ORYSA	Q75lp7 oryza sativ	765	41	39.8	655	2	Q4T812_TETNG	Q4t812 tetraodon n
693	41	39.8	318	2	Q8Z2Z6_PYRAE	Q8z2z6 pyrobaculum	766	41	39.8	662	2	Q8YML4_ANASP	Q8yml4 anabaena ap
694	41	39.8	319	2	Q9UNZ2_STRPY	Q9unj2 streptococc	767	41	39.8	663	2	Q8PE50_XANCP	Q8pe50 xanthomonas
695	41	39.8	319	2	Q9JF21_STRPY	Q9jnz2 streptococc	768	41	39.8	665	2	Q6CWM0_KULUA	Q6cwm0 kluyveromyc
696	41	39.8	322	2	Q95LM1_MACFA	Q95lm1 macaca fasc	769	41	39.8	683	2	Q5LXF8_SILPO	Q5lxf8 silicibacte
697	41	39.8	323	2	Q8R6X1_THETN	Q8r6x1 thermoaer	770	41	39.8	686	2	Q6INQ5_XENLA	Q6inq5 xenopus lae
698	41	39.8	325	2	Q8YXT2_ANASP	Q8yxt2 anabaena ap	771	41	39.8	685	2	Q9V6K7_DROME	Q9v6k7 drosophila
699	41	39.8	326	2	Q4R410_MACFA	Q4r410 macaca fasc	772	41	39.8	691	2	Q5KFT1_CRYNE	Q5kft1 cryptococcu
700	41	39.8	330	2	Q9NIV4_TRYCR	Q9niv4 trypanosoma	773	41	39.8	694	2	Q55QD6_CRYNE	Q55qd6 cryptococcu
701	41	39.8	330	2	Q8H829_ORYSA	Q8h829 oryza sativ	774	41	39.8	700	2	Q5F3N6_CHICK	Q5f3n6 gallus gall
702	41	39.8	343	2	Q63BH8_BACCC	Q63bh8 bacillus ce	775	41	39.8	719	2	Q8S616_ORYSA	Q8s616 oryza sativ
703	41	39.8	343	2	Q6HIY5_BACCK	Q6hiy5 bacillus th	776	41	39.8	724	2	Q86UG5_HUMAN	Q86ug5 homo sapien
704	41	39.8	343	2	Q738H3_BACCL	Q738h3 bacillus th	777	41	39.8	724	2	Q6ZQN7_HUMAN	Q6zqn7 homo sapien
705	41	39.8	343	2	Q81QNI_BACAN	Q81qni bacillus an	778	41	39.8	728	1	BAP1_MOUSE	Q8pnu7 mus musculu
706	41	39.8	344	2	Q9JF07_STRPY	Q9jp07 streptococc	779	41	39.8	729	1	BAP1_HUMAN	Q92560 homo sapien
707	41	39.8	348	2	Q9JF11_STRPY	Q9jp11 streptococc	780	41	39.8	729	1	SYG_HUMAN	Q23627 arabidopsis
708	41	39.8	352	2	Q4XTD8_PLACH	Q4xtd8 plasmodium	781	41	39.8	733	2	Q7UT57_RHOBA	Q7ut57 rhodospirell
709	41	39.8	361	2	Q75IY9_ORYSA	Q75iy9 oryza sativ	782	41	39.8	734	2	Q9LNZ0_ARATH	Q9lnz0 arabidopsis
710	41	39.8	368	2	Q98QJ0_MYCPU	Q98qj0 mycoplasma	783	41	39.8	735	2	Q5B638_EMENI	Q5b638 aspergillus
711	41	39.8	372	2	Q5LM61_SILPO	Q5lm61 silicibacte	784	41	39.8	742	2	Q4F8A7_XENTR	Q4f8a7 xenopus tro
712	41	39.8	375	2	Q6W119_RHISN	Q6w119 rhizobium s	785	41	39.8	745	2	Q8LM40_ORYSA	Q8lm40 oryza sativ
713	41	39.8	376	2	Q6YX17_ORYSA	Q6yx17 oryza sativ	786	41	39.8	748	1	JPH3_HUMAN	Q8wxh2 homo sapien
714	41	39.8	377	2	Q9JF10_STRPY	Q9jp10 streptococc	787	41	39.8	772	2	Q54J94_DICDI	Q54j94 dictyostell
715	41	39.8	381	2	Q01888_CABEL	Q01888 caenorhabdi	788	41	39.8	809	2	Q4Y5N8_PLACH	Q4y5n8 plasmodium
716	41	39.8	388	2	Q5GZ9V_XANOR	Q5gz9v xanthomonas	789	41	39.8	817	2	Q9P588_NEUCR	Q9p588 neurospora
717	41	39.8	398	1	ASSY_GLOVI	Q7ncp5 gloebacter	790	41	39.8	844	2	Q59891_CRYNE	Q59891 cryptococcu
718	41	39.8	403	2	Q9K7Q2_BACHD	Q9k7q2 bacillus ha	791	41	39.8	850	2	Q7MVD9_PORGI	Q7mvd9 porphyromon
719	41	39.8	407	2	Q4HZ92_GIBBE	Q4hz92 gibberella	792	41	39.8	881	2	Q55MX0_CRYNE	Q55mx0 cryptococcu
720	41	39.8	413	2	Q4Q8E3_LEIMA	Q4q8e3 leishmania	793	41	39.8	882	2	Q5KB99_CRYNE	Q5kb99 cryptococcu
721	41	39.8	416	2	Q58GE8_9CUCU	Q58ge8 ips pini (n	794	41	39.8	891	2	Q8H8T8_ORYSA	Q8h8t8 oryza sativ
722	41	39.8	417	2	Q4WB58_ASPFU	Q4wb58 aspergillus	795	41	39.8	892	2	Q55HB3_CRYNE	Q55hb3 cryptococcu
723	41	39.8	423	2	Q5SPP9_CRYNE	Q5spp9 cryptococcu	796	41	39.8	908	2	Q55HB3_CRYNE	Q55hb3 cryptococcu
724	41	39.8	423	2	Q5KQD9_CRYNE	Q5kdq9 cryptococcu	797	41	39.8	934	1	KGP25_DROME	P32023 drosophila
725	41	39.8	424	2	Q824T7_CHLCV	Q824t7 chlamydompi	798	41	39.8	958	2	Q5N7Y8_ORYSA	Q5n7y8 oryza sativ
726	41	39.8	427	2	Q4WX25_ASPFU	Q4wx25 aspergillus	799	41	39.8	998	2	Q4WK70_ASPFU	Q4wk70 aspergillus
727	41	39.8	463	2	Q8TOH4_DROME	Q8toh4 drosophila	800	41	39.8	1019	2	Q9C699_ARATH	Q9c699 arabidopsis
728	41	39.8	470	2	Q8C0S0_MOUSE	Q8c0s0 mus musculu	801	41	39.8	1028	2	Q51VL2_MAGGR	Q51vl2 magnaporthe
729	41	39.8	484	2	Q41KN8_GIBBE	Q41kn8 gibberella	802	41	39.8	1033	2	Q4V0E4_XANCP	Q4v0e4 xanthomonas
730	41	39.8	494	2	Q85YR1_9ROSI	Q85yr1 euphorbia s	803	41	39.8	1042	2	Q948S5_TOBAC	Q948s5 nicotiana t
731	41	39.8	496	2	Q98R26_ARATH	Q98r26 arabidopsis	804	41	39.8	1062	2	Q65OV5_ORYSA	Q65ov5 oryza sativ
732	41	39.8	498	2	Q9A588_CAUCR	Q9a588 caulobacter	805	41	39.8	1076	2	Q9NS13_HUMAN	Q9ns13 homo sapien
733	41	39.8	499	2	Q55174_SYNY3	Q55174 synechocyst	806	41	39.8	1088	2	Q9NPJ9_HUMAN	Q9npj9 homo sapien
734	41	39.8	505	2	Q94CC4_ARATH	Q94cc4 arabidopsis	807	41	39.8	1095	2	Q9LJZ5_ARATH	Q9ljz5 arabidopsis
735	41	39.8	505	2	Q9M652_ARATH	Q9m652 arabidopsis	808	41	39.8	1106	2	Q6XDB6_RAT	Q6xdb6 rattus norv
736	41	39.8	505	2	Q8H1P9_ARATH	Q8h1p9 arabidopsis	809	41	39.8	1119	1	RPOB_THETAQ	Q9kwu7 thermus aqu
737	41	39.8	514	2	Q86AR8_DICDI	Q86ar8 dictyostell	810	41	39.8	1120	2	Q6FXC5_CANGA	Q6fxc5 candida gla
738	41	39.8	526	2	Q8YCP1_BRUME	Q8ycp1 bruceella me	811	41	39.8	1121	1	CARB_MYCUE	Q9ccr2 mycobacteri
739	41	39.8	527	2	Q554U9_DICDI	Q554u9 dictyostell	812	41	39.8	1122	2	Q69YG6_HUMAN	Q69yg6 homo sapien
740	41	39.8	531	2	Q8STU6_ENCCU	Q8stue encephalito	813	41	39.8	1171	2	Q7V1M5_PROMP	Q7v1m5 prochloroco
741	41	39.8	532	2	Q7S1R5_NEUCR	Q7s1r5 neurospora	814	41	39.8	1221	2	Q741V0_MYCPA	Q741v0 mycobacteri
742	41	39.8	558	2	Q59A29_BOVIN	Q59a29 bos taurus	815	41	39.8	1233	2	Q6ZU35_HUMAN	Q6zu35 homo sapien
743	41	39.8	560	1	DONS_MOUSE	Q9gxp4 mus musculu	816	41	39.8	1266	2	Q4WU40_ASPFU	Q4wu40 aspergillus
744	41	39.8	565	2	Q75LV4_ORYSA	Q75lv4 oryza sativ	817	41	39.8	1270	2	Q8UGR8_AGRTS	Q8ugr8 agrobacteri
745	41	39.8	566	1	DONS_HUMAN	Q9nyp3 homo sapien	818	41	39.8	1272	2	Q53QX7_HUMAN	Q53qx7 homo sapien
746	41	39.8	566	2	Q8NC53_HUMAN	Q8nc53 homo sapien	819	41	39.8	1349	2	Q93QX7_STRCO	Q93qx7 streptomyc
747	41	39.8	578	2	Q7UR11_RHOBA	Q7ur11 rhodospirell	820	41	39.8	1406	1	TOP2_CANGA	Q93794 candida gla
748	41	39.8	613	2	Q5ALL3_CANAL	Q5all3 candida alb	821	41	39.8	1474	2	Q4SE63_TETNG	Q4se63 tetraodon n
749	41	39.8	615	2	Q9LU67_ARATH	Q9lu67 arabidopsis	822	41	39.8	1568	2	Q95785_HUMAN	Q95785 homo sapien
750	41	39.8	616	2	Q74Z91_ASHGO	Q74z91 ashbya gos	823	41	39.8	1572	2	Q4PHA0_USTMA	Q4pha0 ustilago ma
751	41	39.8	622	2	Q6BS64_DEBHA	Q6bs64 debaryomyce	824	41	39.8	1676	2	Q8A6R7_BACTN	Q8a6r7 bacteroides
752	41	39.8	628	2	Q9SAZ1_ARATH	Q9saz1 arabidopsis	825	41	39.8	1700	2	Q5UQE4_MIMIV	Q5uqe4 mimivirus
753	41	39.8	632	2	Q5O0P9_PSESY	Q5o0p9 pseudomonas	826	41	39.8	1744	2	Q7Q3N4_ANOGA	Q7q3n4 anopheles g
754	41	39.8	632	2	Q4K3Y5_PSEFS	Q4k3y5 pseudomonas	827	41	39.8	1749	2	Q51IP5_MAGGR	Q51ip5 magnaporthe
755	41	39.8	632	2	Q88B78_PSESM	Q88b78 pseudomonas	828	41	39.8	2127	1	SPTB1_MOUSE	P15508 mus musculu
756	41	39.8	633	2	Q9HTU6_PSEAE	Q9htu6 pseudomonas	829	41	39.8	2136	1	SPTB1_HUMAN	P11277 homo sapien
757	41	39.8	634	2	Q8A5N8_BACTN	Q8a5n8 bacteroides	830	41	39.8	2137	2	Q6XDA0_RAT	Q6xda0 rattus norv
758	41	39.8	639	2	Q65PF2_BACLD	Q65pf2 bacillus li	831	41	39.8	2238	2	Q4N8M2_THEPA	Q4n8m2 theileria p
759	41	39.8	642	2	Q9HEM4_CRYNV	Q9hem4 cryptococcu	832	41	39.8	2332	2	Q59FP5_HUMAN	Q59fp5 homo sapien
760	41	39.8	645	2	Q7VTA4_BORPE	Q7vt44 bordetella	833	41	39.8	2443	2	Q96J17_HUMAN	Q96j17 homo sapien
761	41	39.8	645	2	Q7W2C7_BORPA	Q7w2c7 bordetella	834	41	39.8	2497	2	Q4P9F1_USTMA	Q4p9f1 ustilago ma
										3121	2	Q42269_BRARE	Q42269 brachydanio

835	41	39.8	3391	2	Q9Q4T2_9FLAV	Q9q4t2	dengue viru	908	40	38.8	115	2	Q986E7_RHILO	Q986e7	rhizobium 1
836	41	39.8	3392	2	Q6WP56_9FLAV	Q6wp56	dengue viru	909	40	38.8	115	2	Q4S6K6_TERNG	Q4s6k8	tetraodon n
837	41	39.8	3392	2	Q6WP57_9FLAV	Q6wp57	dengue viru	910	40	38.8	125	2	Q886Q6_PSESM	Q886q6	pseudomonas
838	41	39.8	3392	2	Q6WP58_9FLAV	Q6wp58	dengue viru	911	40	38.8	128	2	Q7N3J5_PSHOL	Q7n3j5	photorehabdu
839	41	39.8	3392	2	Q80KC7_9FLAV	Q80kc7	dengue viru	912	40	38.8	129	2	Q7XKD8_ORYSA	Q7xkd8	oryza sativ
840	41	39.8	3392	2	Q80RP0_9FLAV	Q80rp0	dengue viru	913	40	38.8	131	2	Q9PLC1_HUMAN	Q9plc1	homo sapien
841	41	39.8	3392	2	Q8B646_9FLAV	Q8b646	dengue viru	914	40	38.8	131	2	Q4PNA8_IKOSC	Q4pna8	ixodes scap
842	41	39.8	3392	2	Q8B647_9FLAV	Q8b647	dengue viru	915	40	38.8	135	2	Q5QT29_ORYSA	Q5qt29	oryza sativ
843	41	39.8	3392	2	Q8B648_9FLAV	Q8b648	dengue viru	916	40	38.8	136	2	Q9AIH8_MAGMG	Q9aih8	magnetospir
844	41	39.8	3392	2	Q8B665_9FLAV	Q8b665	dengue viru	917	40	38.8	137	2	Q7PL19_ANOCA	Q7pl19	anopheles g
845	41	39.8	3392	2	Q8JQD9_9FLAV	Q8jqd9	dengue viru	918	40	38.8	138	2	Q603Z5_METCA	Q603z5	methylococc
846	41	39.8	3392	2	Q8JQK3_9FLAV	Q8jqk3	dengue viru	919	40	38.8	139	2	Q8WXX0_BOVIN	Q8wx0	bos taurus
847	41	39.8	3392	2	Q8JQJ0_9FLAV	Q8jqj0	dengue viru	920	40	38.8	144	2	Q6WXX2_NEUCR	Q6wx2	neurospora
848	41	39.8	3392	2	Q8JQF2_9FLAV	Q8jqf2	dengue viru	921	40	38.8	145	2	Q45943_CORBU	Q45942	coxiella bu
849	41	39.8	3392	2	Q91101_9FLAV	Q91101	dengue viru	922	40	38.8	148	2	Q9KKG5_PSEAD	Q9kk95	pseudomonas
850	41	39.8	3392	2	Q91102_9FLAV	Q91102	dengue viru	923	40	38.8	154	2	Q9TIE2_GSEAD	Q9tie2	lactobacill
851	41	39.8	3392	2	Q9J7C5_9FLAV	Q9j7c5	dengue viru	924	40	38.8	158	2	Q6LVB8_PHOPR	Q6lvb8	photobacter
852	41	39.8	3392	2	Q9J7C6_9FLAV	Q9j7c6	dengue viru	925	40	38.8	160	2	Q9PLB9_HUMAN	Q9plb9	homo sapien
853	41	39.8	4010	2	Q9VJC6_DROME	Q9vjc6	drosophila	926	40	38.8	160	2	Q83010_PORGI	Q83010	porphyrcmon
854	41	39.8	4024	2	Q8WXX0_HUMAN	Q8wx0	homo sapien	927	40	38.8	171	2	Q5Z076_NOCFA	Q5z076	nocardia fa
855	41	39.8	4031	2	Q9Y2F3_HUMAN	Q9y2f3	homo sapien	928	40	38.8	175	2	Q6ADC4_LEIXX	Q6adc4	leifsonia x
856	40.5	39.3	165	2	Q7YPH7_GALSB	Q7yph7	galago sene	929	40	38.8	177	2	Q4KBB5_PSEF5	Q4kbb5	pseudomonas
857	40.5	39.3	174	2	Q7YNZ2_PIG	Q7ynz2	sus scrofa	930	40	38.8	189	2	Q59EQ2_HUMAN	Q59eq2	homo sapien
858	40.5	39.3	177	2	Q7YPX1_AOTVO	Q7ypx1	aotus vocif	931	40	38.8	189	2	Q5UTAI_FELCA	Q5utai	felis silve
859	40.5	39.3	206	2	Q80U11_MOUSE	Q80u11	mus musculus	932	40	38.8	192	2	Q9Y329_HUMAN	Q9y329	homo sapien
860	40.5	39.3	207	2	Q63561_9HIVI	Q63561	human immun	933	40	38.8	198	2	Q8VDX0_MOUSE	Q8vdx0	mus musculus
861	40.5	39.3	207	2	Q62LE9_BURMA	Q62le9	burkholderi	934	40	38.8	198	2	Q8CFT9_MOUSE	Q8cft9	mus musculus
862	40.5	39.3	207	2	Q63W99_BURPS	Q63w99	burkholderi	935	40	38.8	199	1	T5312_RAT	Q8ctm3	rattus norv
863	40.5	39.3	207	2	Q5BBM8_EMENI	Q5bbm8	aspergillus	936	40	38.8	200	2	Q6ZLF1_ORYSA	Q6zlf1	oryza sativ
864	40.5	39.3	219	2	Q4M094_9BURK	Q4m094	burkholderi	937	40	38.8	200	2	Q88613_MERUN	Q88613	meriones un
865	40.5	39.3	249	2	Q5KY38_GEOKA	Q5ky38	geobacillus	938	40	38.8	201	2	Q5DSE3_9PEZI	Q5dse3	sarcosphaer
866	40.5	39.3	251	2	Q7P2N0_FUSNV	Q7p2n0	fusobacteri	939	40	38.8	204	2	Q5IWP0_MAGGR	Q5iwp0	magnaporth
867	40.5	39.3	258	2	Q4NFZ0_5MICC	Q4nfz0	arthrobacte	940	40	38.8	204	2	Q5DSE4_9PEZI	Q5dse4	sarcosphaer
868	40.5	39.3	273	1	YGF0_YEAST	P53177	saccharomyc	941	40	38.8	208	2	Q8SU10_ENCCU	Q8su10	encephalito
869	40.5	39.3	286	2	Q6W2G0_RHTSN	Q6w2g0	rhizobium s	942	40	38.8	217	2	Q5Z2Q0_PEA	Q5z2q0	pisum sativ
870	40.5	39.3	297	2	Q9M213_ARATH	Q9m213	arabidopsis	943	40	38.8	218	2	Q5VPQ5_ORYSA	Q5vpq5	oryza sativ
871	40.5	39.3	340	2	Q7MZH7_SAGOE	Q7mzh7	saguinus oe	944	40	38.8	220	2	Q5DSE9_9PEZI	Q5dse9	boudiera de
872	40.5	39.3	343	2	Q9QOQ2_RAT	Q9qoq2	rattus norv	945	40	38.8	221	1	T5312_MOUSE	Q8ctf8	mus musculus
873	40.5	39.3	343	2	Q9ROV0_RAT	Q9rov0	rattus norv	946	40	38.8	225	2	Q7NB46_MYCGA	Q7nb46	mycoplasma
874	40.5	39.3	344	2	Q9BCZ1_MOUSE	Q9bcz1	rattus musculus	947	40	38.8	226	2	Q7SEQ4_NEUCR	Q7seq4	neurospora
875	40.5	39.3	353	2	Q7JJ65_RAT	Q7jj65	rattus norv	948	40	38.8	227	2	Q4VKA9_9PEZI	Q4vka9	sarcosphaer
876	40.5	39.3	358	2	Q4Q6V8_LEIMA	Q4q6v8	leishmania	949	40	38.8	230	2	Q67231_AQUAE	Q67231	aquifex aeo
877	40.5	39.3	363	2	Q78105_RAT	Q78105	rattus norv	950	40	38.8	241	2	Q5IJ31_MAGGR	Q5ij31	magnaporth
878	40.5	39.3	379	2	Q31615_MOUSE	Q31615	mus musculus	951	40	38.8	246	2	Q8ETG1_OCRSH	Q8etg1	oceanobacil
879	40.5	39.3	383	2	Q7MPK9_VIBVY	Q7mpk9	vibrio vuln	952	40	38.8	249	2	Q8HZU2_ORYSA	Q8hzu2	oryza sativ
880	40.5	39.3	400	2	Q5WZAT7_THEMA	Q5wzat7	thermotoga	953	40	38.8	251	1	Y1664_HABIN	P45305	haemophilus
881	40.5	39.3	403	2	Q5NYS7_AZOSE	Q5nys7	azocarcus sp	954	40	38.8	251	1	Y989_SVNY3	P74514	synschochet
882	40.5	39.3	403	2	Q8P272_STRAM	Q8p272	streptomyce	955	40	38.8	256	2	Q6BRZ7_DEBHA	Q6brz7	debaromyce
883	40.5	39.3	416	2	Q53U08_STRFR	Q53u08	streptomyce	956	40	38.8	257	1	LIVG_ARCFC	Q28881	archaeoglob
884	40.5	39.3	423	2	Q7UGH9_RHOBA	Q7ugh9	rhodopirell	957	40	38.8	257	2	Q60BZ2_METCA	Q60b22	methylococc
885	40.5	39.3	428	2	Q4V7U4_XENILA	Q4v7u4	xenopus lae	958	40	38.8	258	2	Q8SZY6_DROME	Q8szy6	drosophila
886	40.5	39.3	429	2	Q6NTX5_XENILA	Q6ntx5	xenopus lae	959	40	38.8	260	2	Q9V7G4_DROME	Q9v7g4	drosophila
887	40.5	39.3	464	2	Q58507_PYROHO	Q58507	pyrococcus	960	40	38.8	261	2	Q6D444_ERWCT	Q6d444	erwinia car
888	40.5	39.3	847	2	Q6R029_ARATH	Q6r029	arabidopsis	961	40	38.8	261	2	Q8FS61_COREF	Q8fs61	corynebacte
889	40.5	39.3	847	2	Q9LV31_ARATH	Q9lv31	arabidopsis	962	40	38.8	263	1	INMT_HUMAN	Q95050	homo sapien
890	40.5	39.3	930	2	Q8RLT7_CLOCE	Q8rlt7	clostridium	963	40	38.8	263	1	INMT_PONPY	Q5rfr7	pongo pygma
891	40.5	39.3	930	2	Q59290_CLOJO	Q59290	clostridium	964	40	38.8	263	1	INMT_RABIT	Q97972	oryctolagus
892	40.5	39.3	938	2	Q4Q1P3_LEIMA	Q4q1p3	leishmania	965	40	38.8	264	1	TEMT_MOUSE	P40936	mus musculus
893	40.5	39.3	1009	2	Q07971_HALSA	Q07971	halobacteri	966	40	38.8	266	2	Q73011_TREDE	Q73011	treponema d
894	40.5	39.3	1028	2	Q6C542_YARLI	Q6c542	yarrowia li	967	40	38.8	269	2	Q9V929_DROME	Q9v929	drosophila
895	40.5	39.3	1073	2	Q51965_HALSA	Q51965	halobacteri	968	40	38.8	269	2	Q9RHU4_STRTL	Q9rhu4	streptomyce
896	40.5	39.3	1150	2	Q4P018_9DELT	Q4p018	anaeromyxob	969	40	38.8	271	2	Q7R775_PLAYO	Q7r775	plasmodium
897	40.5	39.3	1369	2	Q63WB6_BURPS	Q63wb6	burkholderi	970	40	38.8	275	2	Q5CTX3_SCHJA	Q5ctx3	schistosoma
898	40.5	39.3	1403	2	Q9QXG1_MOUSE	Q9qxg1	mus musculus	971	40	38.8	276	2	Q96CG9_HUMAN	Q96cg9	homo sapien
899	40.5	39.3	2252	2	Q48595_TETNG	Q48595	tetraodon n	972	40	38.8	277	2	Q4NNY9_9DELT	Q4nny9	anaeromyxob
900	40.5	39.3	3443	2	Q8JZM8_MOUSE	Q8jzm8	mus musculus	973	40	38.8	278	2	P93391_TORAC	P93391	nicotiana t
901	40	38.8	88	2	Q8S423_ZEAIZE	Q8s423	zea mays (m	974	40	38.8	285	2	Q5WE74_BACSK	Q5we74	bacillus cl
902	40	38.8	92	2	Q7SBY9_NEUCR	Q7sby9	neurospora	975	40	38.8	291	2	Q80XS8_MOUSE	Q80xs8	mus musculus
903	40	38.8	94	2	Q5VBG0_9FLAV	Q5vbg0	dengue viru	976	40	38.8	292	2	Q7RC51_PLAYO	Q7rc51	plasmodium
904	40	38.8	103	2	Q6NB07_RHOBA	Q6nb07	rhodopseudo	977	40	38.8	294	2	Q7VE40_PROMA	Q7ve40	prochloroco
905	40	38.8	109	2	Q710H1_PEA	Q710h1	pisum sativ	978	40	38.8	295	2	Q622T8_BACLD	Q622t8	bacillus li
906	40	38.8	110	1	26SI_BRANA	P24565	brassica na	979	40	38.8	296	2	Q600E5_MYCHY	Q600e5	mycoplasma
907	40	38.8	113	2	Q75UW1_STRHI	Q75uw1	streptoallo	980	40	38.8	296	2	Q67QK8_SWTWH	Q67qk8	symbiobacte

981 40 38.8 296 2 Q65PE9 BACLD  
982 40 38.8 299 2 Q9M2D9 ARATH  
983 40 38.8 300 1 RME1 YEAST  
984 40 38.8 300 2 Q7V4E3 PROCHLORO  
985 40 38.8 301 2 Q66HF0 RAT  
986 40 38.8 303 2 Q798J5 BACSU  
987 40 38.8 315 2 Q5N44 CRYNE  
988 40 38.8 315 2 Q5KBH3 CRYNE  
989 40 38.8 316 2 Q4LGN3 BURKHOLDERI  
990 40 38.8 319 2 Q6R043 ARATH  
991 40 38.8 319 2 Q9SPG6 ARATH  
992 40 38.8 321 2 Q5WVG4 LEGPL  
993 40 38.8 321 2 Q5X424 LEGPA  
994 40 38.8 321 2 Q5ZUB8 LEGPH  
995 40 38.8 322 2 Q67VZ4 ORYSA  
996 40 38.8 323 2 Q9AB36 CAUCR  
997 40 38.8 325 2 Q9LFEI ARATH  
998 40 38.8 325 2 Q6R054 ARATH  
999 40 38.8 330 2 Q5RYN6 NOCFA  
1000 40 38.8 333 2 Q8ZY26 PYRAE

## ALIGNMENTS

RESULT 1  
GAST\_HUMAN  
ID GAST\_HUMAN STANDARD; PRT; 101 AA.  
AC P01350; P78463; P78464;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 23-OCT-1986 (Rel. 02, Last sequence update)  
DE GASTRIN precursor (Contains: Gastrin 71 (Component I); Gastrin 52; Big  
DE Gastrin (Gastrin 34) (Component II); Gastrin (Gastrin 17) (Component  
DE III); Gastrin 14; Gastrin 61.  
GN Name=GAST; Synonyms=GAS;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=87219893; PubMed=3034736; DOI=10.1016/0378-1119(86)90338-0;  
RA Kariya Y., Kato K., Hayashizaki Y., Himeno S., Tarui S., Matsubara K.;  
RT "Expression of human gastrin gene in normal and gastrinoma tissues.";  
RL Gene 50:345-352(1986).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=84272693; PubMed=6087340;  
RA Ito R., Sato K., Helmer T., Jay G., Agarwal K.L.;  
RT "Structural analysis of the gene encoding human gastrin: the large  
RT intron contains an Alu sequence.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:4662-4666(1984).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=84169471; PubMed=6324077;  
RA Kato K., Hayashizaki Y., Takahashi Y., Himeno S., Matsubara K.;  
RT "Molecular cloning of the human gastrin gene.";  
RL Nucleic Acids Res. 11:8197-8203(1983).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=83221503; PubMed=6574456;  
RA Boel E., Vuust J., Norris F., Norris K., Wind A., Rehfeld J.F.,  
RA Marcker K.A.;  
RT "Molecular cloning of human gastrin cDNA: evidence for evolution of  
RT gastrin by gene duplication.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:2866-2869(1983).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=84144842; PubMed=6322186;  
RA Wiborg O., Berglund L., Boel E., Norris F., Norris K., Rehfeld J.F.,  
RA Marcker K.A., Vuust J.;

RT "Structure of a human gastrin gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:1067-1069(1984).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=84159488; PubMed=6689486; DOI=10.1016/0378-1119(83)90035-5;  
RA Kato K., Himeno S., Takahashi Y., Wakabayashi T., Tarui S.,  
RA Matsubara K.;  
RT "Molecular cloning of human gastrin precursor cDNA.";  
RL Gene 26:53-57(1983).  
RN [7]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [8]  
RP PROTEIN SEQUENCE OF 22-101, AND CHARACTERIZATION OF GASTRIN 71.  
RC TISSUE=Antal mucosa;  
RX MEDLINE=94333379; PubMed=8055952;  
RA Renfeld J.F., Johnson A.H.;  
RT "Identification of gastrin component I as gastrin-71. The largest  
RT possible bioactive progastrin product.";  
RL Eur. J. Biochem. 223:765-773(1994).  
RN [9]  
RP PROTEIN SEQUENCE OF 76-92.  
RX MEDLINE=67021327; PubMed=5921183;  
RA Bentley P.H., Kenner G.W., Sheppard R.C.;  
RT "Structures of human gastrins I and II.";  
RL Nature 209:583-585(1966).  
RN [10]  
RP PROTEIN SEQUENCE OF 59-68.  
RX MEDLINE=89273602; PubMed=2730647;  
RA Higashimoto Y., Himeno S., Shinomura Y., Nagao K., Tamura T.,  
RA Tarui S.;  
RT "Purification and structural determination of urinary NH2-terminal big  
RT gastrin fragments.";  
RL Biochem. Biophys. Res. Commun. 160:1364-1370(1989).  
RN [11]  
RP PROTEIN SEQUENCE OF 76-92.  
RX MEDLINE=69298172; PubMed=5822140;  
RA Gregory R.A., Tracy H.J., Agarwal K.L., Grossman M.I.;  
RT "Amino acid constitution of two gastrins isolated from Zollinger-  
RT Ellison tumour tissue.";  
RL Gut 10:603-608(1969).  
RN [12]  
RP CHARACTERIZATION OF GASTRIN 6, AND SULFATION OF TYR-87.  
RX MEDLINE=95137019; PubMed=7530658;  
RA Rehfeld J.F., Hansen C.P., Johnsen A.H.;  
RT "Post-poly(Glu) cleavage and degradation modified by O-sulfated  
RT tyrosine: a novel post-translational processing mechanism.";  
RL EMBO J. 14:389-396(1995).  
RN [13]  
RP PROCESSING AND SULFATION OF TYR-87.  
RX MEDLINE=20508341; PubMed=11052986;  
RA Palmaes Hansen C., Stadil F., Rehfeld J.F.;  
RT "Metabolism and acid secretory effect of sulfated and nonsulfated

RT gastrin-6 in humans.";

RL An. J. Physiol. 279:G503-G509(2000).

CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and

CC secrete hydrochloric acid and the pancreas to secrete its

CC digestive enzymes. It also stimulates smooth muscle contraction

CC and increases blood circulation and water secretion in the stomach

CC and intestine.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- PTM: Two different processing pathways probably exist in antral G-

CC cells. In the dominant pathway progastrin is cleaved at three

CC sites resulting in two major bioactive gastrins, gastrin-34 and

CC gastrin-17. In the putative alternative pathway, progastrin may be

CC processed only at the most C-terminal dibasic site resulting in

CC the synthesis of gastrin-71.

CC -1- PTM: Sulfation of Tyr-87 blocks peptide degradation and enhances

CC activity.

CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC EMBL; X00183; CAA25005.1; -; Genomic DNA.

CC EMBL; X00183; CAA25006.1; -; Genomic DNA.

CC EMBL; X00183; CAA25007.1; -; Genomic DNA.

CC EMBL; V00511; CAA23769.1; -; mRNA.

CC EMBL; M15958; AAA52520.1; -; Genomic DNA.

CC EMBL; K01254; AAB59533.1; -; Genomic DNA.

CC EMBL; BC069724; AAH69724.1; -; mRNA.

CC EMBL; BC069762; AAH69762.1; -; mRNA.

CC PIR; A93997; GMHUB.

CC EMBL; ENSG00000184502; Homo sapiens.

CC HGNC; HGNC:4164; GAST.

CC MIM; 137250; -.

CC GO; GO:0005179; P:hormone activity; TAS.

CC GO; GO:0007165; P:signal transduction; NAS.

CC InterPro; IPR001651; Gastrin.

CC Pfam; PF00918; Gastrin; 1.

CC SMART; SM00029; GASTRIN; 1.

CC PROSITE; PS00259; GASTRIN; 1.

CC Amidation; cleavage on pair of basic residues;

CC Direct protein sequencing; Hormone; Phosphorylation;

CC Pyrrolidone carboxylic acid; Signal; Sulfation.

FT SIGNAL 1 21

FT PEPTIDE 22 92 Gastrin 71.

FT PEPTIDE 41 92 Gastrin 52.

FT PEPTIDE 59 92 Big Gastrin.

FT PEPTIDE 76 92 Gastrin.

FT PEPTIDE 79 92 Gastrin 14.

FT PEPTIDE 87 92 Gastrin 6.

FT PROPEP 96 101 Removed in mature form.

FT SITE 40 41 Cleavage.

FT SITE 58 59 Cleavage.

FT SITE 75 76 Cleavage.

FT SITE 95 96 Cleavage.

FT MOD\_RES 59 59 Pyrrolidone carboxylic acid.

FT MOD\_RES 76 76 Pyrrolidone carboxylic acid.

FT MOD\_RES 87 87 Sulfotyrosine (partial).

FT MOD\_RES 92 92 Phenylalanine amide (G-93 provides amide group).

FT MOD\_RES 96 96 Phosphoserine (By similarity).

FT SEQUENCE 101 AA; 11394 MW; A03C847FCFB7216C CRC64;

Query Match 97.18; Score 100; DB 1; Length 101;

Best Local Similarity 94.11; Pred. No. 1.8e-06;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWDF 17

:|||||

Db 76 QGPWLEEEBAYGWDF 92

RESULT 2

GAST\_PIG STANDARD; PRT; 104 AA.

ID P01351;

AC 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].

GN Name=GAST; Synonyms=GAS;

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;

OC Sus.

OX NCBI\_TaxID=9823;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=82174533; PubMed=6951161;

RA Yoo O.J., Powell C.T., Agarwal K.L.;

RT "Molecular cloning and nucleotide sequence of full-length of cDNA

RT coding for porcine gastrin.";

RL Proc. Natl. Acad. Sci. U.S.A. 79:1049-1053(1982).

RN [2]

RP NUCLEOTIDE SEQUENCE OF 56-82.

RX MEDLINE=80240380; PubMed=6930858;

RA Agarwal K.L., Noyes B.E.;

RT "Studies on gastrin mRNA structure using an oligonucleotide probe.";

RL Ann. N. Y. Acad. Sci. 343:433-442(1980).

RN [3]

RP PROTEIN SEQUENCE OF 76-92.

RX PubMed=14248711;

RA Gregory H., Hardy P.M., Jones D.S., Kenner G.W., Sheppard R.C.;

RT "The antral hormone gastrin.";

RL Nature 204:931-933(1964).

RN [4]

RP SYNTHESIS.

RX PubMed=14248712;

RA Anderson J.C., Barton M.A., Gregory R.A., Hardy P.M., Kenner G.W.,

RA McLeod J.K., Preston J., Sheppard R.C., Morley J.S.;

RT "Synthesis of gastrin.";

RL Nature 204:933-934(1964).

CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and

CC secrete hydrochloric acid and the pancreas to secrete its

CC digestive enzymes. It also stimulates smooth muscle contraction

CC and increases blood circulation and water secretion in the stomach

CC and intestine.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

CC -----

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CC use as long as its content is in no way modified and this statement is not

CC removed.

CC EMBL; V01303; CAA24610.1; -; mRNA.

CC EMBL; M25036; AAA31111.1; -; mRNA.

CC PIR; A93903; GMPGB.

CC InterPro; IPR001651; Gastrin.

CC Pfam; PF00918; Gastrin; 1.

CC SMART; SM00029; GASTRIN; 1.

CC PROSITE; PS00259; GASTRIN; 1.

CC Amidation; cleavage on pair of basic residues;

CC Direct protein sequencing; Hormone; Phosphorylation;

CC Pyrrolidone carboxylic acid; Signal; Sulfation.

FT SIGNAL 1 21

FT PROPEP 22 58

FT PEPTIDE 59 92 Big gastrin.

FT PEPTIDE 76 92 Gastrin.

FT PROPEP 96 104

FT MOD\_RES 59 59 Pyrrolidone carboxylic acid.

FT MOD\_RES 76 76 Pyrrolidone carboxylic acid.

FT MOD\_RES 87 87 Sulfotyrosine (partial).

```
FT MOD_RES 92 92 Phenylalanine amide (G-93 provides amide
FT MOD_RES 96 96 group).
FT MOD_RES 96 96 Phosphoserine (By similarity).
SQ SEQUENCE 104 AA; 11558 MW; B0BD1D7E05304B79 CRC64;

Query Match 95.1%; Score 98; DB 1; Length 104;
Best Local Similarity 88.2%; Pred. No. 3.6e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMDF 17
Db :||||:|||||
76 QGPWMEEEEAAYGWMDF 92

RESULT 3
GAST_FELCA
ID_GAST_FELCA STANDARD; PRT; 104 AA.
AC P01354;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92127058; PubMed=1773057;
RA Kim S.-J., Uhm K.N., Kang Y.K., Yoo O.-J.;
RT "Bovine and feline gastrin cDNA sequences and the amino acid and
RT nucleotide sequence homologies among mammalian species.";
RL DNA Seq. 1:181-187(1991).
RN [2]
RP PROTEIN SEQUENCE OF 76-92.
RX MEDLINE=69206035; PubMed=5784957;
RA Agarwal K.L., Kenner G.W., Sheppard R.C.;
RT "Feline gastrin. An example of peptide sequence analysis by mass
RT spectrometry.";
RL J. Am. Chem. Soc. 91:3096-3097(1969).
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
-----
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-----
EMBL; X16582; CAA34599.1; -, mRNA.
PIR; S14401; GMCT.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00918; Gastrin; 1.
DR SMART; SM00029; GASTRIN; 1.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Phosphorylation;
KW Pyrrolidone carboxylic acid; Signal; Sulfation.
FT SIGNAL 1 21
FT PROPEP 22 58
FT PEPTIDE 59 92 Big gastrin.
FT PEPTIDE 76 92 Gastrin.
FT PROPEP 96 104
FT MOD_RES 59 59 Pyrrolidone carboxylic acid.
FT MOD_RES 76 76 Pyrrolidone carboxylic acid.
FT MOD_RES 87 87 Sulfotyrosine.
```

```
FT MOD_RES 92 92 Phenylalanine amide (G-93 provides amide
FT MOD_RES 96 96 group).
FT MOD_RES 96 96 Phosphoserine (By similarity).
SQ SEQUENCE 104 AA; 11482 MW; 4DB92E4416A7AC9F CRC64;

Query Match 91.3%; Score 94; DB 1; Length 104;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMDF 17
Db :||||:|||||
76 QGPWLEEEEAAYGWMDF 92

RESULT 4
GAST_MACMU
ID_GAST_MACMU STANDARD; PRT; 17 AA.
AC P33714;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin.
GN Name=GAST; Synonyms=GAS;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=91164506; PubMed=2003150; DOI=10.1016/0167-0115(91)90005-2;
RA Yu J.-H., Xin Y., Eng J., Yalow R.S.;
RT "Rhesus monkey gastroenteropancreatic hormones: relationship to human
RT sequences.";
RL Regul. Pept. 32:39-45(1991).
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
-----
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-----
PIR; A60071; A60071.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Hormone;
KW Pyrrolidone carboxylic acid; Sulfation.
FT MOD_RES 1 1
FT MOD_RES 12 12 Sulfotyrosine.
FT MOD_RES 17 17 Phenylalanine amide.
SQ SEQUENCE 17 AA; 2076 MW; 6F6E92C73611D39A CRC64;

Query Match 89.3%; Score 92; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.7e-06;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMDF 17
Db :||||:|||||
1 QGPWMEEEEAAYGWMDF 17

RESULT 5
GAST_CANFA
ID_GAST_CANFA STANDARD; PRT; 104 AA.
AC P01353;
DT 21-JUL-1986 (Rel. 01, Created)
```

DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].  
 GN Name=GAST; Synonyms=GAS;  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 OC Canis.  
 OX NCBI\_TaxID=9615;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Antral mucosa;  
 RX MEDLINE=91085716; PubMed=2262079;  
 RA Gantz I., Takeuchi T., Yamada T.;  
 RT "Cloning of canine gastrin cDNA's encoding variant amino acid  
 sequences";  
 RL Digestion 46:99-104(1990).  
 RN (2)  
 RP PROTEIN SEQUENCE OF 59-92.  
 RC TISSUE=Antral mucosa;  
 RX MEDLINE=87016557; PubMed=3763441; DOI=10.1016/0196-9781(86)90045-8;  
 RA Bonato C., Eng J., Hulmes J.D., Miedel M., Pan Y.-C.E., Yalow R.S.;  
 RT "Sequences of gastrins purified from a single antrum of dog and of  
 goat";  
 RL Peptides 7:689-693(1986).  
 RN (3)  
 RP PROTEIN SEQUENCE OF 76-92, AND PHOSPHORYLATION.  
 RX MEDLINE=69253357; PubMed=5799207;  
 RA Agarwal K.L., Kenner G.W., Sheppard R.C.;  
 RT "Structure and synthesis of canine gastrin";  
 RL Experimentia 25:346-348(1969).  
 RN (4)  
 RP PROTEIN SEQUENCE OF 96-104.  
 RC TISSUE=Antral mucosa;  
 RX MEDLINE=89331947; PubMed=2756156; DOI=10.1016/0167-0115(89)90264-4;  
 RA Desmond H., Varro A., Young J., Gregory H., Nemeth J., Dockray G.J.;  
 RT "The constitution and properties of phosphorylated and  
 unphosphorylated C-terminal fragments of progastrin from dog and  
 ferret antrum";  
 RL Regul. Pept. 25:223-233(1989).  
 CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and  
 secrete hydrochloric acid and the pancreas to secrete its  
 digestive enzymes. It also stimulates smooth muscle contraction  
 and increases blood circulation and water secretion in the stomach  
 and intestine.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 CC -----  
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 removed.  
 CC -----  
 DR PIR; B61053; GMDG.  
 DR Ensembl; ENSCARG0000015924; Canis familiaris.  
 DR InterPro; IPR001651; Gastrin.  
 DR Pfam; PF00918; Gastrin; 1.  
 DR SMART; SM00029; GASTRIN; 1.  
 DR PROSITE; PS00259; GASTRIN; 1.  
 DR Amidation; Cleavage on pair of basic residues;  
 KW Direct protein sequencing; Hormone; Phosphorylation;  
 FT Pyroglutamate carboxylic acid; Signal; Sulfation.  
 FT SIGNAL 1 21  
 FT PROPEP 22 58  
 FT PEPTIDE 59 92 Big gastrin.  
 FT PEPTIDE 76 92 Gastrin.  
 FT PROPEP 96 104  
 FT MOD\_RES 59 59  
 FT MOD\_RES 76 76 Pyroglutamate carboxylic acid.  
 FT MOD\_RES 87 87 Sulfotyrosine.  
 FT MOD\_RES 92 92 Phenylalanine amide (G-93 provides amide  
 group).

FT MOD\_RES 96 96 Phosphoserine.  
 FT VARIANT 85 85 A -> T. AEE (in Ref. 3).  
 FT CONFLICT 83 85 EEA -> AEE (in Ref. 3).  
 SQ SEQUENCE 104 AA; 11519 MW; 73BF72A18DFE78CA CRC64;  
 Query Match 89.3%; Score 92; DB 1; Length 104;  
 Best Local Similarity 82.4%; Pred. No. 2.6e-05;  
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEEAAYGWMDF 17  
 Db 76 QGFWVEEEEAAYGWMDF 92  
 :|||:|||||  
 RESULT 6  
 GAST\_CAPHI  
 ID GAST\_CAPHI STANDARD; PRT; 34 AA.  
 AC P04564;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].  
 GN Name=GAST; Synonyms=GAS;  
 OS Capra hircus (Goat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Caprinae; Capra.  
 OX NCBI\_TaxID=9925;  
 RN (1)  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Antral mucosa;  
 RX MEDLINE=87016557; PubMed=3763441; DOI=10.1016/0196-9781(86)90045-8;  
 RA Bonato C., Eng J., Hulmes J.D., Miedel M., Pan Y.-C.E., Yalow R.S.;  
 RT "Sequences of gastrins purified from a single antrum of dog and of  
 goat";  
 RL Peptides 7:689-693(1986).  
 CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and  
 secrete hydrochloric acid and the pancreas to secrete its  
 digestive enzymes. It also stimulates smooth muscle contraction  
 and increases blood circulation and water secretion in the stomach  
 and intestine.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 CC -----  
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 removed.  
 CC -----  
 DR PIR; JS0426; JS0426.  
 DR InterPro; IPR001651; Gastrin.  
 DR Pfam; PF00918; Gastrin; 1.  
 DR PROSITE; PS00259; GASTRIN; 1.  
 KW Amidation; Cleavage on pair of basic residues;  
 KW Direct protein sequencing; Hormone; Pyroglutamate carboxylic acid;  
 KW Sulfation.  
 FT PEPTIDE 1 34 Big gastrin.  
 FT PEPTIDE 18 34 Gastrin.  
 FT MOD\_RES 1 1 Pyroglutamate carboxylic acid.  
 FT MOD\_RES 18 18 Pyroglutamate carboxylic acid.  
 FT MOD\_RES 29 29 Sulfotyrosine.  
 FT MOD\_RES 34 34 Phenylalanine amide.  
 SQ SEQUENCE 34 AA; 3903 MW; 67501111E76D0CF4 CRC64;  
 Query Match 88.3%; Score 91; DB 1; Length 34;  
 Best Local Similarity 82.4%; Pred. No. 1.1e-05;  
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEEAAYGWMDF 17  
 Db 18 QGFWVEEEEAAYGWMDF 34  
 :|||:|||||

FT	CONFLICT	48	48	N -> T (in Ref. 1).
FT	CONFLICT	74	74	K -> N (in Ref. 1).
FT	CONFLICT	81	81	E -> G (in Ref. 1).
FT	CONFLICT	96	96	S -> M (in Ref. 1).
FT	CONFLICT	99	99	E -> G (in Ref. 1).
SQ	SEQUENCE	104 AA;	11573 MW;	54D03BF200F299F2 CRC64;
Query Match				
Best Local Similarity 88.3%; Score 91; DB 1; Length 104;				
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;				
QY	1 EGPWLEEEAYGWDF	17		
DB	76 QGPWVEEEAYGWDF	92		
RESULT 8				
ID	GAST_SHEEP	STANDARD;	PRT;	104 AA.
AC	002686;			
DT	15-JUL-1998	(Rel. 36, Created)		
DT	15-JUL-1998	(Rel. 36, Last sequence update)		
DT	13-SEP-2005	(Rel. 48, Last annotation update)		
DE	Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].			
GN	Name=GAST; Synonyms=GAS;			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;			
OC	Pecora; Bovidae; Caprinae; Ovis.			
OX	NCBI_TaxID=9940;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=9818586; PubMed=9522119;			
RA	Moore C., Jie R., Shulkes A., Baldwin G.S.;			
RT	"Molecular cloning and sequence of the ovine gastrin gene.";			
RL	Nature 219:614-615 (1997).			
RN	[2]			
RP	PROTEIN SEQUENCE OF 76-92.			
RX	MEDLINE=68357500; PubMed=5665711;			
RA	Agarwal K.L., Beacham J., Bentley P.H., Gregory R.A., Kenner G.W.,			
RA	Sheppard R.C., Tracy H.J.;			
RT	"Isolation, structure and synthesis of ovine and bovine gastrins.";			
RL	Nature 219:614-615 (1968).			
CC	-!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and			
CC	secrete hydrochloric acid and the pancreas to secrete its			
CC	digestive enzymes. It also stimulates smooth muscle contraction			
CC	and increases blood circulation and water secretion in the stomach			
CC	and intestine.			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
DR	EMBL; M31657; AAA30537.1; -; Genomic_DNA.			
DR	EMBL; X16581; CA34598.1; -; mRNA.			
DR	PIR; S14400; GNBO.			
DR	InterPro; IPR001651; Gastrin.			
DR	Pfam; PF00918; Gastrin; 1.			
DR	SMART; SM00029; GASTRIN; 1.			
DR	PROSITE; PS00259; GASTRIN; 1.			
KW	Amidation; Cleavage on pair of basic residues;			
KW	Direct protein sequencing; Hormone; Phosphorylation;			
KW	Pyrrolidone carboxylic acid; Signal; Sulfation.			
FT	SIGNAL	1	21	
FT	PROPEP	22	58	
FT	PEPTIDE	59	92	Big gastrin.
FT	PEPTIDE	76	92	Gastrin.
FT	PROPEP	96	104	
FT	MOD_RES	59	59	Pyrrolidone carboxylic acid.
FT	MOD_RES	76	76	Pyrrolidone carboxylic acid.
FT	MOD_RES	87	87	Sulfoxyrosine.
FT	MOD_RES	92	92	Phenylalanine amide (G-93 provides amide
FT	MOD_RES	96	96	group).
FT	MOD_RES	96	96	Phosphoserine (By similarity).
FT	CONFLICT	32	32	A -> L (in Ref. 1).
FT	CONFLICT	37	37	G -> R (in Ref. 1).

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FT MOD_RES 92 92 Phenylalanine amide (G-93 provides amide
FT MOD_RES 96 96 Phosphoserine (By similarity).
FT MOD_RES 104 AA; 624063D4B5CE5AFD CRC64;
SQ SEQUENCE 104 AA; 11532 MW; 624063D4B5CE5AFD CRC64;

Query Match 88.3%; Score 91; DB 1; Length 104;
Best Local Similarity 82.4%; Pred. No. 3.6e-05;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEBEEAYGWMDF 17
Db 76 QGPWLEEEBEEAYGWMDF 92

RESULT 9
GAST_HORSE
ID GAST_HORSE STANDARD; PRT; 107 AA.
AC P5585;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Antral mucosa;
RX MEDLINE=98380242; PubMed=9716385;
RA Johnson A.H., Sandin A., Rourke I.J., Bundgaard J.R., Nilsson G.,
RA Rehfeld J.F.;
RT 'Unique progastrin processing in equine G-cells suggests marginal
RT tyrosyl sulfotransferase activity.';
RL Eur. J. Biochem. 255:432-438 (1998).
CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC

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CC
EMBL; Y09440; CAA70590.1; -; mRNA.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00918; Gastrin; 1.
DR SMART; SM00029; GASTRIN; 1.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues; Hormone;
KW Phosphorylation; Pyrrolidone carboxylic acid; Signal; Sulfation.
FT SIGNAL 1 21
FT PROPEP 22 61 Big gastrin.
FT PEPTIDE 62 95 Gastrin.
FT PROPEP 79 95
FT PROPEP 99 107
FT MOD_RES 62 62 Pyrrolidone carboxylic acid (Potential).
FT MOD_RES 79 79 Pyrrolidone carboxylic acid (Potential).
FT MOD_RES 90 90 Sulfotyrosine.
FT MOD_RES 95 95 Phenylalanine amide (G-96 provides amide
FT MOD_RES 99 99 group).
FT MOD_RES 107 AA; 11884 MW; 104166CAAE5C234F CRC64;
SQ SEQUENCE 107 AA; 11884 MW; 104166CAAE5C234F CRC64;

Query Match 87.4%; Score 90; DB 1; Length 107;
Best Local Similarity 82.4%; Pred. No. 5.2e-05;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 EGPWLEEEBEEAYGWMDF 17
Db 79 QGPWLEKEBEEAYGWMDF 95

RESULT 10
GAST_DIDMA
ID GAST_DIDMA STANDARD; PRT; 33 AA.
AC P33713;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 33); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90298616; PubMed=2361360;
RA Shinomura Y., Eng J., Rattan S.C., Yalow R.S.;
RT "Opossum (Didelphis virginiana) 'little' and 'big' gastrins.";
RL Comp. Biochem. Physiol. 96B:239-242 (1990).
CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC

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use as long as its content is in no way modified and this statement is not
removed.
CC
PIR; A60506; A60506.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00918; Gastrin; 1.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Pyrrolidone carboxylic acid;
KW Sulfation.
FT PEPTIDE 1 33 Big gastrin.
FT PEPTIDE 18 33 Gastrin.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 18 18 Pyrrolidone carboxylic acid.
FT MOD_RES 28 28 Sulfotyrosine.
FT MOD_RES 33 33 Phenylalanine amide.
SQ SEQUENCE 33 AA; 3856 MW; 217D28C15027B661 CRC64;

Query Match 82.0%; Score 84.5; DB 1; Length 33;
Best Local Similarity 88.2%; Pred. No. 8.9e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EGPWLEEEBEEAYGWMDF 17
Db 18 QGPWLEKEBEEAYGWMDF 33

RESULT 11
GAST_MOUSE
ID GAST_MOUSE STANDARD; PRT; 101 AA.
AC P48757; P70334; Q64295;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Gastrin 71; Big gastrin (Gastrin 34);
DE Gastrin].
GN Name=Gast; Synonyms=Gas;

```

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=129/Sv;  
RX MEDLINE=96067529; PubMed=7488110;  
RA Koh T.J., Wang T.C.;  
RT "Molecular cloning and sequencing of the murine gastrin gene.";  
RL Biochem. Biophys. Res. Commun. 216:34-41 (1995).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BA1B/C;  
RX MEDLINE=96114738; PubMed=7492958;  
RA Noh M.J., Kim S.J., Kang Y.K., Yoo O.J.;  
RT "Sequences responsible for transcription termination of the mouse gastrin gene.";  
RL Biochem. Mol. Biol. Int. 35:1205-1213 (1995).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=129/SvJ; TISSUE=Stomach;  
RX MEDLINE=96228048; PubMed=8647286; DOI=10.1016/0014-5793(96)00430-9;  
RA Friis-Hansen L., Rourke I.J., Bundgaard J.R., Rehfeld J.F., Samuelson L.C.;  
RT "Molecular structure and genetic mapping of the mouse gastrin gene.";  
RL FEBS Lett. 386:128-132 (1996).  
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stomach and intestine.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
-----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
-----  
DR EMBL; U34293; AAB97872.1; -; Genomic DNA.  
DR EMBL; U58136; AAB06947.1; -; Genomic DNA.  
DR EMBL; X94760; CAA64386.1; -; Genomic DNA.  
DR EMBL; X94758; CAA64385.1; -; mRNA.  
DR PIR; S68861; S68861.  
DR Ensembl; ENSMUSG00000017165; Mus musculus.  
DR MGI; MGI:104768; Gast.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR InterPro; IPR001651; Gastrin.  
DR Pfam; PF00918; Gastrin; 1.  
DR SMART; SM00029; GASTRIN; 1.  
DR PROSITE; PS00259; GASTRIN; 1.  
KW Amidation; Cleavage on pair of basic residues; Hormone;  
KW Phosphorylation; Pyrrolidone carboxylic acid; Signal; Sulfation.  
FT SIGNAL 1 21 Potential.  
FT PEPTIDE 22 92 Gastrin 71.  
FT PEPTIDE 59 92 Big gastrin.  
FT PEPTIDE 76 92 Gastrin.  
FT PROPEP 96 101  
FT MOD\_RES 59 59  
FT MOD\_RES 87 87 Pyrrolidone carboxylic acid (By similarity).  
FT MOD\_RES 92 92 Sulfotyrosine (By similarity).  
FT MOD\_RES 92 92 Phenylalanine amide (G-93 provides amide group).  
FT MOD\_RES 96 96 Phosphoserine (By similarity).  
FT CONFLICT 45 45 R -> G (in Ref. 2).  
FT CONFLICT 76 76 E -> Q (in Ref. 3).  
SQ SEQUENCE 101 AA; 11607 MW; 2AA6F8D54DBFB69F CRC64;

Query Match 76.7%; Score 79; DB 1; Length 101;  
Best Local Similarity 82.4%; Pred. No. 0.0018;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 EGPWLEEEEEEAYGWMDP 17  
DB 76 ERPRMEEEEEEAYGWMDP 92  
RESULT 12  
Q6GSF5 MOUSE  
ID Q6GSF5 MOUSE PRELIMINARY; PRT; 101 AA.  
AC Q6GSF5  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Gastrin.  
GN Name=Gast;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Pancreas;  
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richardson D., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heltan E., Kettman M., Madan A.A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalios D.E., Scherch A., Schein J.E., Jones S.J.W., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Pancreas;  
RG NIH MGC Project;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC064791; AAH64791.1; -; mRNA.  
DR Ensembl; ENSMUSG00000017165; Mus musculus.  
DR MGI; MGI:104768; Gast.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR InterPro; IPR001651; Gastrin.  
DR Pfam; PF00918; Gastrin; 1.  
DR SMART; SM00029; GASTRIN; 1.  
DR PROSITE; PS00259; GASTRIN; UNKNOWN 1.  
SQ SEQUENCE 101 AA; 11606 MW; 2AB3B9814DBFB69F CRC64;  
Query Match 73.8%; Score 76; DB 2; Length 101;  
Best Local Similarity 86.7%; Pred. No. 0.0049;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 3 PWLEEEEEEAYGWMDP 17  
DB 78 PRMEEEEEEAYGWMDP 92  
RESULT 13  
Q6CPR2 MOUSE  
ID Q6CPR2 MOUSE PRELIMINARY; PRT; 101 AA.  
AC Q6CPR2;

DT 01-JUN-2001 (TEMBUREL 17, Created)  
 DT 01-JUN-2001 (TEMBUREL 17, Last sequence update)  
 DE Mus musculus adult male stomach cDNA, RIKEN full-length enriched  
 DE library, clone:2200008H06 product:GASTRIN, full insert sequence (Mus  
 DE musculus adult male small intestine cDNA, RIKEN full-length enriched  
 DE library, clone:2010003E11 product:GASTRIN, full insert sequence) (Mus  
 DE musculus adult male small intestine cDNA, RIKEN full-length enriched  
 DE library, clone:2010008H15 product:GASTRIN, full insert sequence) (Mus  
 DE musculus adult male small intestine cDNA, RIKEN full-length enriched  
 DE library, clone:2010104K23 product:GASTRIN, full insert sequence) (Mus  
 DE musculus adult male small intestine cDNA, RIKEN full-length enriched  
 DE library, clone:2010203E02 product:GASTRIN, full insert sequence) (Mus  
 DE musculus adult male small intestine cDNA, RIKEN full-length enriched  
 DE library, clone:2010300J04 product:GASTRIN, full insert sequence)  
 GN NamesCast;  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Small intestine, and Stomach;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44 (1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Small intestine, and Stomach;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukuishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Brownstein M.J., Sult C., Fletcher C., Fujita M., Gariboldi M.F.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Saeki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontecki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Small intestine, and Stomach;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Otsu N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tonaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Sult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Brad D., Brucic V., Chothia C., Corbani L.B., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,  
 RA Grimond S., Guatinchich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zaslavskiy M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Small intestine, and Stomach;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630 (2000).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Small intestine, and Stomach;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hazada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771 (2000).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Small intestine, and Stomach;  
 RA Adachi J., Aizawa K., Akimura S., Akimura T., Arai A., Aono H.,  
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
 RA Hatanaka T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 RA Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK008649; BAB25807.1; -; mRNA.  
 DR EMBL; AK008062; BAB25437.1; -; mRNA.  
 DR EMBL; AK008159; BAB25501.1; -; mRNA.  
 DR EMBL; AK008420; BAB25658.1; -; mRNA.  
 DR EMBL; AK008494; BAB25699.1; -; mRNA.  
 DR EMBL; AK008313; BAB25596.1; -; mRNA.  
 DR Ensembl; ENSMUSG00000017165; Mus musculus.  
 DR MGI; MGI:104768; Gast.  
 DR GO; GO:0005615; Extracellular space; TAS.  
 DR InterPro; IPR001651; Gastrin.  
 DR Pfam; PF00918; Gastrin; 1.  
 DR SMART; SM00029; Gastrin; 1.  
 DR PROSITE; PS00259; GASTRIN; UNKNOWN 1.  
 SQ SEQUENCE 101 AA; 11590 MW; 41DE15814DBF68E CRC64;

Query Match 73.8%; Score 76; DB 2; Length 101;  
 Best Local Similarity 86.7%; Pred. No. 0.0049; Indels 0; Gaps 0;  
 Matches 13; Conservative 1; Mismatches 1;  
 QY 3 PWLEEEBAYGWMDP 17  
 DB 78 PRNEEBEAYGWMDP 92

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RESULT 14
GAST_RAT
ID _GAST_RAT STANDARD; PRT; 104 AA.
AC P04553.
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big Gastrin (Gastrin 34); Gastrin].
GN Name=Gast; Synonyms=Gas;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX MEDLINE=88288206; PubMed=3453895;
RA Fuller P.J., Stone D.L., Brand S.J.;
RT "Molecular cloning and sequencing of a rat preprogastrin complementary
deoxyribonucleic acid.";
RL Mol. Endocrinol. 1:306-311(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Gastric antrum;
RX MEDLINE=83039009; PubMed=6897117; DOI=10.1016/0196-9781(82)90172-3;
RA Schaffer M.H., Agarwal K.L., Noyes B.E.;
RT "Rat gastrin's amino acid sequence determined from the nucleotide
sequence of the mRNA.";
RL Peptides 3:693-696(1982).
RN [3]
RP PROCESSING, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=91072336; PubMed=1701434;
RA Varró A., Nemeth J., Bridson J., Lee C., Moore S., Dockray G.J.;
RT "Processing of the gastrin precursor. Modulation of phosphorylated,
sulfated, and amidated products.";
RL J. Biol. Chem. 265:21476-21481(1990).
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
secrete hydrochloric acid and the pancreas to secrete its
digestive enzymes. It also stimulates smooth muscle contraction
and increases blood circulation and water secretion in the stomach
and intestine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; M25459; AAA41195.1; -; mRNA.
CC EMBL; M38653; AAA41919.1; -; mRNA.
CC F01R; A40910; A40910.
CC Ensembl; ENSRNOG00000014740; Rattus norvegicus.
CC GO; GO:0005179; F:hor-mone activity; IDA.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
CC GO; GO:0007165; P:signal transduction; IDA.
CC InterPro; IPR001651; Gastrin.
CC Pfam; PF00318; Gastrin; 1.
CC SMART; SM00029; GASTRIN; 1.
CC PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues; Hormone;
Phosphorylation; Pyroglutamate; Pyroglutamate; Signal; Sulfation.
FT SIGNAL 1 21
FT PROPEP 22 58
FT PEPTIDE 59 92
FT PROPEP 76 92
FT PROPEP 96 104
FT MOD_RES 59 59
FT MOD_RES 76 76
FT MOD_RES 87 87
FT MOD_RES 92 92
Phenylalanine amide (G-93 provides amide

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FT MOD_RES 96
FT MOD_RES 103
SQ SEQUENCE 104 AA; 11832 MW; 973FD06276BF1E21 CRC64;
group).
Phosphoserine.
Sulfotyrosine.
Query Match 72.8%; Score 75; DB 1; Length 104;
Best Local Similarity 86.7%; Pred. No. 0.007;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 PVLREEREAYGWMDF 17
DB 78 PPMEEEREAYGWMDF 92
:|||||
RESULT 15
GAST_CAVPO STANDARD; PRT; 33 AA.
AC P06885;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 33); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=86309993; PubMed=3747718; DOI=10.1016/0024-3205(86)90283-3;
RA Bonato C., Eng J., Pan Y.-C.E., Miedel M., Hulmes J.D., Yalow R.S.;
RT "Guinea pig 33-amino acid gastrin.";
RL Life Sci. 39:959-964(1986).
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
secrete hydrochloric acid and the pancreas to secrete its
digestive enzymes. It also stimulates smooth muscle contraction
and increases blood circulation and water secretion in the stomach
and intestine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC PIR; A26089; GMGPB.
CC InterPro; IPR001651; Gastrin.
CC Pfam; PF00918; Gastrin; 1.
CC PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues;
Direct protein sequencing; Hormone; Pyroglutamate; Pyroglutamate; Signal.
FT PEPTIDE 1 33
FT PEPTIDE 18 33
FT MOD_RES 1 1
FT MOD_RES 18 18
FT MOD_RES 33 33
FT MOD_RES 33 33
SQ SEQUENCE 33 AA; 3757 MW; B37C251CD40EB30C CRC64;
Query Match 71.4%; Score 73.5; DB 1; Length 33;
Best Local Similarity 76.5%; Pred. No. 0.0033;
Matches 13; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
QY 1 EGPVLEEREAYGWMDF 17
DB 18 QGPV-ABEEAYGWMDF 33
:|||||
RESULT 16
GAST_CHIBR STANDARD; PRT; 33 AA.
ID _GAST_CHIBR

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AC P10034;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Gastrin precursor [Contains: Big gastrin (Gastrin 33); Gastrin].  
 GN Names=CASP; Synonyms=GAS;  
 OS Chinchilla brevicaudata (Chinchilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 OC Hystricognathi; Chinchillidae; Chinchilla.  
 OX NCBI\_TaxID=10152;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=87156784; PubMed=3827930;  
 RA Shinomura Y., Eng J., Yalow R.S.;  
 RT "Chinchilla 'big' and 'little' gastrins.";  
 RL Biochem. Biophys. Res. Commun. 143:7-14(1987).  
 CC -I- FUNCTION: Gastrin stimulates the stomach mucosa to produce and  
 CC secrete hydrochloric acid and the pancreas to secrete its  
 CC digestive enzymes. It also stimulates smooth muscle contraction  
 CC and increases blood circulation and water secretion in the stomach  
 CC and intestine.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC PIR; A29541; A29541.  
 DR PIR; B29541; B29541.  
 DR InterPro; IPR001651; Gastrin.  
 DR Pfam; PF00918; Gastrin; 1.  
 DR PROSITE; PS00259; GASTRIN; 1.  
 DR Annotation: Cleavage on pair of basic residues;  
 KW Direct protein sequencing; Hormone; Pyrrolidone carboxylic acid;  
 KW Sulfation.  
 FT PEPTIDE 1 33 Big gastrin.  
 FT PEPTIDE 18 33 Gastrin.  
 FT MOD\_RES 18 18 Pyrrolidone carboxylic acid.  
 FT MOD\_RES 28 28 Sulfotyrosine.  
 FT MOD\_RES 33 33 Phenylalanine amide.  
 SQ SEQUENCE 33 AA; 3715 MW; 6711F5CDC50FAA2D CRC64;  
 Query Match 71.4%; Score 73.5; DB 1; Length 33;  
 Best Local Similarity 76.5%; Pred. No. 0.0033;  
 Matches 13; Conservative 1; Mismatches 2; Indels 1; Gaps 1;  
 QY 1 EGPWLEEEERAYGWMDP 17  
 DB 18 QGFW-AEEERAYGWMDP 33  
 RESULT 17  
 Q604V7 METCA  
 ID Q604V7 METCA PRELIMINARY; PRT; 354 AA.  
 AC Q604V7;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE UDP-N-acetylglucosamine-N-acetylmuramyl-(Pentapeptide)  
 DE Diphosphoryl-undecaprenol N-acetylglucosamine transferase  
 DE (EC 2.4.1.-)  
 GN Name=murG; OrderedLocusNames=MCA2429;  
 OS Methylococcus capsulatus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;  
 OC Methylococcaceae; Methylococcus.  
 OX NCBI\_TaxID=414;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Bath / NCIMB 11132;

RX PubMed=15383840; DOI=10.1371/journal.pbio.0020303;  
 RA Ward N.L., Larsen O., Sakwa J., Brubach L., Khouri H.M., Durkin A.S.,  
 RA Dimitrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E.,  
 RA Methe B.A., Wu M., Heidelberg J.F., Paulsen I.T., Fouts D.E.,  
 RA Ravel J., Tettelin H., Ren Q., Read T.D., DeBoy R.T., Seshadri R.,  
 RA Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J.,  
 RA Grindhaug S.H., Holt I.E., Bidhammer I., Jonassen I., Vanaken S.,  
 RA Utterback T.R., Feldblyum T.V., Fraser C.M., Lilienhaug J.R.,  
 RA Eissen J.A.;  
 RT "Genomic insights into methanotrophy: the complete genome sequence of  
 RT Methylococcus capsulatus (Bath).";  
 RL PLoS Biol. 2:1616-1628(2004).  
 DR EMBL; AS017282; AAU91479.1; -; Genomic\_DNA.  
 DR TIGR; MCA2429; -;  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0030246; P:carbohydrate binding; IEA.  
 DR GO; GO:0016758; P:transferase activity, transferring hexosyl . . ; IEA.  
 DR GO; GO:0050511; P:undecaprenyldiphospho-muramoylpentapeptide . . ; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR GO; GO:0030259; P:lipid glycosylation; IEA.  
 DR GO; GO:0019277; P:UDP-N-acetylgalactosamine biosynthesis; IEA.  
 DR InterPro; IPR004276; Glyco\_tran\_28.  
 DR InterPro; IPR006009; MurG.  
 DR Pfam; PF03033; Glyco\_transf\_28; 1.  
 DR Pfam; PF04101; Glyco\_tran\_28\_C; 1.  
 DR TIGRFAMs; TIGR01133; murG; 1.  
 KW Complete proteome; Glycosyltransferase; Transferase.  
 SQ SEQUENCE 354 AA; 37457 MW; 6F4F3508287E8252 CRC64;  
 Query Match 56.3%; Score 58; DB 2; Length 354;  
 Best Local Similarity 64.3%; Pred. No. 7;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 PWLEEEERAYGWMD 16  
 DB 238 PFIEDNEERAYGWAD 251  
 RESULT 18  
 Q8TVI3 METKA  
 ID Q8TVI3 METKA PRELIMINARY; PRT; 458 AA.  
 AC Q8TVI3;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Terpene cyclase/mutase family protein.  
 GN OrderedLocusNames=MK1406;  
 OS Methanopyrus kandleri.  
 OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;  
 OC Methanopyrus.  
 OX NCBI\_TaxID=2320;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AV19 / DSM 6324 / JCM 9639;  
 RX MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;  
 RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,  
 RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,  
 RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,  
 RA Malykh A.G., Koonin E.V., Kozlovskiy S.A.;  
 RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19  
 RT and monophyly of archaeal methanogens.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).  
 DR EMBL; AF010433; AA02619.1; -; Genomic\_DNA.  
 KW Complete proteome.  
 SQ SEQUENCE 458 AA; 51683 MW; 8C3B515050B5C940 CRC64;  
 Query Match 52.4%; Score 54; DB 2; Length 458;  
 Best Local Similarity 47.1%; Pred. No. 34;  
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEERAYGWMDP 17  
 DB 18 QGFW-AEEERAYGWMDP 33

Db 195 EGNLQKEDKGYCWIDY 211

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RESULT 19
QB05Y3 CHV1
ID Q805Y3_CHV1 PRELIMINARY; PRT; 720 AA.
AC Q805Y3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tegument protein.
GN Name=UL46;
OS Cercopithecine herpesvirus 1 (CeHV-1) (Simian herpes B virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10325;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22607624; PubMed=12721804; DOI=10.1007/s00705-003-0011-2;
RA Ohsawa K., Black D.H., Sato H., Rogers K., Eberle R.;
RT "Sequence and genetic arrangement of the UL region of the monkey B
RT virus (Cercopithecine herpesvirus 1) genome and comparison with the UL
RT region of other primate herpesviruses.";
RL Arch. Virol. 148:989-997(2003).
DR EMBL; AB096160; BACS0806.1; -; Genomic DNA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR005051; Herpes UL46.
DR Pfam; PF03387; Herpes UL46; 1.
SQ SEQUENCE 720 AA; 77571 MW; E6F4991C4F5D7BD6 CRC64;
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Query Match 50.5%; Score 52; DB 2; Length 720;  
Best Local Similarity 61.5%; Pred. No. 1.1e+02;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 WLEEEEAAYGWD 16

Db 629 WVEENPIYGWGD 641

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RESULT 20
QT75D2 CHV1
ID Q775D2_CHV1 PRELIMINARY; PRT; 720 AA.
AC Q775D2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tegument phosphoprotein.
GN Name=UL46;
OS Cercopithecine herpesvirus 1 (CeHV-1) (Simian herpes B virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10325;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E2490;
RX DOI=10.1128/JVI.77.11.6167-6177.2003;
RA Perelygina L., Zhu L., Zurkuhlen H., Mills R., Borodovsky M.,
RA Hilliard J.K.;
RT "Complete Sequence and Comparative Analysis of the Genome of Herpes B
RT Virus (Cercopithecine Herpesvirus 1) from a Rhesus Monkey.";
RL J. Virol. 77:6167-6177(2003).
DR EMBL; AF533768; AAP41464.1; -; Genomic DNA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR005051; Herpes UL46.
DR Pfam; PF03387; Herpes UL46; 1.
SQ SEQUENCE 720 AA; 77628 MW; F4BE81497B73715A CRC64;
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Query Match 50.5%; Score 52; DB 2; Length 720;  
Best Local Similarity 61.5%; Pred. No. 1.1e+02;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 WLEEEEAAYGWD 16

Db 629 WVEENPIYGWGD 641

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RESULT 21
Q59DP8 DROME
ID Q59DP8_DROME PRELIMINARY; PRT; 1055 AA.
AC Q59DP8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE CG2165-PE, isoform E.
GN Name=CG2165; ORFNames=CG2165;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Fostler A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Havel D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
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RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RA Berkeley Drosophila Genome Project;  
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirska R., Smith E.,  
RA Yu C., Rubin G.;  
RT "Drosophila melanogaster release 4 sequence.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RG FlyBase;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003844; AX52514.1; -; Genomic\_DNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0003388; F:calcium-transporting ATPase activity; IEA.  
DR GO; GO:0003824; F:catalytic activity; IEA.  
DR GO; GO:0018820; F:hydrolase activity, acting on acid anhydrid. . .; IEA.  
DR GO; GO:0008816; P:calcium ion transport; IEA.  
DR GO; GO:0006812; P:calcium ion transport; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR006408; ATPase-IIB Ca.  
DR InterPro; IPR001757; ATPase\_E1-E2.  
DR InterPro; IPR006088; Cation\_ATPase\_C.  
DR InterPro; IPR004014; Cation\_ATPase\_N.  
DR InterPro; IPR005834; Dehal-like hydro.  
DR InterPro; IPR008250; E1-E2\_ATPase reg.  
DR Pfam; PF00689; Cation\_ATPase\_C; 1.  
DR Pfam; PF00690; Cation\_ATPase\_N; 1.  
DR Pfam; PF00122; E1-E2\_ATPase; 1.  
DR Pfam; PF00702; Hydrolase; 1.  
DR PRINTS; PR00119; CATATPASE.  
DR TIGRFAMs; TIGR01517; ATPase-IIB Ca; 1.  
DR TIGRFAMs; TIGR01494; ATPase\_P-type; 4.  
DR PROSITE; PS00154; ATPASE\_E1\_E2; UNKNOWN 1.  
SQ SEQUENCE 1118 AA; 123213 MW; 3495117F17DDB1 CRC64;  
Query Match 50.5%; Score 52; DB 2; Length 1118;  
Best Local Similarity 50.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
QY 1 EGPWLEEEEAAGWMD 16  
Db 116 DAPVLQEEHEHGWIE 131  
ID Q9V4C7 DROME PRELIMINARY; PRT; 1141 AA.  
AC Q9V4C7;  
RESULT 23  
QY Q9V4C7 DROME  
ID Q9V4C7 DROME PRELIMINARY; PRT; 1141 AA.  
AC Q9V4C7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)  
DE CG2165-PA, isoform A (CG2165-pb, isoform b).  
GN Name=CG2165; ORfName=CG2165;  
OS Drosophila melanogaster (fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
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RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo S.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,  
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin M., Houston K.A., Howland T.J., Wei M.-H., Ibegwa C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan N., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
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RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirska R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
RT melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirska R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin:  
RT a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RN [5]

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RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[6]
RN NUCLEOTIDE SEQUENCE.
RP FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR ENBL; AE003944; AF59350.3; -, Genomic DNA.
DR Ensemble; CG2165; Drosophila melanogaster.
DR FlyBase; FBgn0025704; CG2165.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005388; F:calcium-transporting ATPase activity; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid. .; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR GO; GO:000612; P:cation transport; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR006408; ATPase-IIB_Ca.
DR InterPro; IPR001757; ATPase_EI-E2.
DR InterPro; IPR006068; Cation ATPase_C.
DR InterPro; IPR004014; Cation ATPase_N.
DR InterPro; IPR005834; Dehal like hydro.
DR InterPro; IPR008250; EI-E2_ATPase_reg.
DR Pfam; PF00689; Cation_ATPase_C; 1.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; EI-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR TIGRPFAMS; TIGR01517; ATPase-IIB_Ca; 1.
DR TIGRPFAMS; TIGR01494; ATPase_P-type; 4.
DR PROSITE; PS00154; ATPASE_EI-E2; UNKNOWN 1.
SQ SEQUENCE 1141 AA; 125710 MW; 9D48BCDDEB132F14 CRC64;

Query Match 50.59; Score 52; DB 2; Length 1141;
Best Local Similarity 50.08; Pred. No. 1.8e+02;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EGPWLEEEBAYGMD 16
Db 116 DAPVLQEEBHHGWIE 131

RESULT 24
Q59DP9 DROME
ID Q59DP9 DROME PRELIMINARY; PRT; 1190 AA.
AC Q59DP9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE CG2165-PC, Isoform C.
GN Name=CG2165; ORFNames=CG2165;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazei R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cayley S., Dahke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin C.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin M., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kaulush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.R., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusakern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reineert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupeki M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[2]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Taber P.B., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Ruso S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[5]
RN NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

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RN NUCLEOTIDE SEQUENCE.
RP FlyBase,
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003844; AX52515.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005388; F:calcium-transporting ATPase activity; IEA.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0015820; F:hydrolase activity; acting on acid anhydrid. . .; IEA.
DR GO; GO:0008816; P:calcium ion transport; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR006408; ATPase-IIB Ca.
DR InterPro; IPR001757; ATPase-E1-E2.
DR InterPro; IPR006088; Cation_ATPase_C.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Dehal_like_hydro.
DR InterPro; IPR008250; E1-E2_ATPase_reg.
DR Pfam; PF00689; Cation_ATPase_C; 1.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR TIGRPFAM; TIGR01517; ATPase-IIB Ca; 1.
DR TIGRPFAM; TIGR01494; ATPase_P-type; 4.
DR PROSITE; PS00154; ATPase_E1-E2; UNKNOWN 1.
SQ SEQUENCE 1190 AA; 131439 MW; 684FCBE483A184B9 CRC64;

Query Match 50.5%; Score 52; DB 2; Length 1190;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEAYGWD 16
:|:|||||:|:|:
DB 116 DAPVLQEEEHGWIE 131

RESULT 25
Q6APG4 DRSPS
ID Q6APG4_DRSPS PRELIMINARY; PRT; 255 AA.
AC Q6APG4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Probable amino acid ABC transporter, periplasmic substrate-binding protein.
GN OrderedLocusNames=DP1031;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
OC Desulfobulbaceae; Desulfotalea.
OX NCBI_TaxID=84980;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=LSv54 / DSM 12343;
RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
RA Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium from permanently cold Arctic sediments.";
RL Environ. Microbiol. 6:887-902(2004).
DR EMBL; CH522870; CAG35760.1; -; Genomic_DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001311; SBP/glu receptor.
DR InterPro; IPR001638; SBP_bac_3.
DR Pfam; PF00497; SBP_bac_3; 1.
DR SMART; SM00062; PBPb; 1.
KW Complete proteome.

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SQ SEQUENCE 255 AA; 28171 MW; 6C01A3F260481D7D CRC64;

Query Match 49.5%; Score 51; DB 2; Length 255;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEAYGW 14
:|:|:|:|:|:
DB 149 DGKWLDKENKAGW 162

RESULT 26
Q6IWN3_USTMA
ID Q6IWN3_USTMA PRELIMINARY; PRT; 827 AA.
AC Q6IWN3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE P21-activated kinase Cla4.
OS Ustilago maydis (Smut fungus).
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=5270;
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15469512; DOI=10.1111/j.1365-2958.2004.04296.x;
RA Leveleki L., Mahlert M., Sandrock B., Bolker M.;
RT "The PAK family kinase Cla4 is required for budding and morphogenesis in Ustilago maydis.";
RL Mol. Microbiol. 54:396-406(2004).
DR EMBL; AY616187; AAT39367.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000955; PAK_box_Rho_bd.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH type.
DR InterPro; IPR00719; Prot_Kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00220; S_TKG; 1.
DR SMART; SM00219; TyrKG; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 827 AA; 88136 MW; 515A3E18PACF20C8 CRC64;

Query Match 49.5%; Score 51; DB 2; Length 827;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 LEEEEEAYGWD 16
:|:|:|:|:|:
DB 181 LKSDSELYGWD 192

RESULT 27
Q4PBV7_USTMA
ID Q4PBV7_USTMA PRELIMINARY; PRT; 827 AA.
AC Q4PBV7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

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DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=U02406.1;  
 OS Ustilago maydis 521.  
 CC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;  
 CC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.  
 OX NCBI\_TaxID=237631;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=521;  
 RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,  
 RA Alt-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,  
 RA Arachi H., Ambuster J., Bachantang P., Baldwin J., Barry A.,  
 RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,  
 RA Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,  
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,  
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,  
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,  
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,  
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,  
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,  
 RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,  
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,  
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,  
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseleis M., Karlsson E.,  
 RA Kells C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,  
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,  
 RA Lindblad-toh K., Liu X., Lokityang T., Lokitysang Y., Lucien O.,  
 RA Lui A., Ma L., J., Mabbitt R., Macdonald J., Maclean C., Major J.,  
 RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,  
 RA McCarthy M., McDonough S., Mcghee T., Meldrum J., Meneus L.,  
 RA Mesirov J., Mihalav L., Mihova T., Mikkelsen T., Mlenga V., Moru K.,  
 RA Mozes J., Mulrain L., Munson G., Naylor J., Neues C., Nguyen C.,  
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,  
 RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,  
 RA O'neil K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,  
 RA Purcell S., Rachupka T., Ramesay U., Rameau R., Ray V., Raymond C.,  
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,  
 RA Rutman M., Schupbach R., Seaman C., Settippalli S., Sharpe T.,  
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,  
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,  
 RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuina K.,  
 RA Tenzing P., Testaye S., Theodore J., Thoulutsang Y., Topham K.,  
 RA Towey S., Teamlu T., Tsomo N., Vallée D., Vassiliev H.,  
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,  
 RA Wangdi T., Whittraker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,  
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,  
 RA Zimmer A., Zody M., Lander E.;  
 RT "The genome sequence of Ustilago maydis.";  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC -1- SIMILARITY: Contains 1 PH domain.  
 CC EMBL; AACP01000083; EAK83444.1; -; Genomic\_DNA.  
 DR InterPro; IPR000095; PAK\_Box\_Rho\_bd.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR00719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00169; PH; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR SMART; SM00219; Tyrc; 1.  
 DR PROSITE; PS0108; CRIB; 1.  
 DR PROSITE; PS0003; PH\_DOMAIN; 1.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;  
 KW Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 827 AA; 98136 MW; 515A3E18FACF20C8 CRC64;  
 Query Match 49.5%; Score 51; DB 2; Length 827;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 LEEEREAYGWM 16  
 DB 181 LKSDDELYGWM 192  
 RESULT 28  
 Q9SCPL ARATH PRELIMINARY; PRT; 238 AA.  
 ID Q9SCPL ARATH PRELIMINARY; PRT; 238 AA.  
 AC Q9SCPL;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Putative transcription factor MYB27 (At3G53200) (MYB transcription factor).  
 GN Names=T4D2.130; Synonyms=At3G53200/T4D2.130; ORFNames=At3G53200;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 CC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.,  
 RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quettier F.,  
 RA Salanoubat M.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,  
 RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,  
 RA Hayashizaki Y., Shinozaki K.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,  
 RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Heuan V.W.,  
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,  
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,  
 RA Palm C.C., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
 RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,  
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Qu L., Gu H.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL; AL132958; CAB64223.1; -; Genomic\_DNA.  
 DR EMBL; AK117256; BAC41931.1; -; mRNA.  
 DR EMBL; AY519599; AAS10069.1; -; mRNA.  
 DR EMBL; BT005257; AAO63321.1; -; mRNA.  
 DR PIR; T46166; T46166.  
 DR HSSP; P06876; LMBK.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; P:DNA binding; IEA.  
 DR GO; GO:0045449; P:regulation of transcription; IEA.  
 DR InterPro; IPR012287; Homeodomain-rel.  
 DR InterPro; IPR001005; Myb\_DNA\_bd.

```

DR Pfam, PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00090; MYB_3; 2.
KW Nuclear protein; Repeat.
SQ SEQUENCE 238 AA; 27996 MW; B6DDCF70E22D562E CRC64;

Query Match 48.5%; Score 50; DB 2; Length 238;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPWLEEEER 10
Db |||||:|
12 GPWLEEEDE 20

RESULT 29
ASSY_SYMTH
ID_ASSY_SYMTH STANDARD; PRT; 401 AA.
AC Q67KEI;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Argininosuccinate synthase (EC 6.3.4.5) (Citruiline--aspartate
ligase).
GN Name=argG; OrderedLocusNames=STH2874;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=T / IAM 14863;
RX PubMed=15383646; DOI=10.1093/nar/gkh830;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Genome sequence of Symbiobacterium thermophilum, an uncultivable
bacterium that depends on microbial commensalism.";
RL Nucleic Acids Res. 32:4937-4944 (2004).
CC -!- CATALYTIC ACTIVITY: ATP + L-citrulline + L-aspartate = AMP +
CC -!- diphosphate + (N(omega)-L-arginino)succinate.
CC -!- PATHWAY: Arginine biosynthesis; seventh step.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the argininosuccinate synthase family. Type
1 subfamily.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; AP006840; BAD1857.1; -; Genomic_DNA.
DR HAMAP; MF_00005; -; 1.
DR InterPro; IPR001518; Arginosuc_synth.
DR FANTHER; FTHR11587; Arginosuc_synth; 1.
DR Pfam; PF00764; Arginosuc_synth; 1.
DR TIGRFAMs; TIGR00032; argG; 1.
DR PROSITE; PS00564; ARGININOSUCCIN SYN_1; 1.
DR PROSITE; PS00565; ARGININOSUCCIN SYN_2; 1.
KW Amino-acid biosynthesis; Arginine biosynthesis; ATP-binding;
SQ Complete proteome; Ligase; Nucleotide-binding.
SQ SEQUENCE 401 AA; 44594 MW; F8B6C472B9981D64 CRC64;

Query Match 48.5%; Score 50; DB 1; Length 401;
Best Local Similarity 57.1%; Pred. No. 11e+02;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGW 14
Db |||||:|
192 EDPWAEAPEAEFW 205

RESULT 30

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Q9AA10 CAUCR
ID Q9AA10 CAUCR PRELIMINARY; PRT; 442 AA.
AC Q9AA10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mannanase, putative.
GN OrderedLocusNames=CC0801;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.P., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Uterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).
DR EMBL; AE005756; AAK22786.1; -; Genomic_DNA.
DR PIR; F87348; F87348.
DR TIGR; CC0801; -.
KW Complete proteome.
SQ SEQUENCE 442 AA; 48582 MW; 45277F0542736FD1 CRC64;

Query Match 48.5%; Score 50; DB 2; Length 442;
Best Local Similarity 35.3%; Pred. No. 1.2e+02;
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGW 17
Db |||||:|
156 DGPWFQGDPRYPWPQY 172

RESULT 31
Q9DUC7_9VIRU
ID Q9DUC7_9VIRU PRELIMINARY; PRT; 732 AA.
AC Q9DUC7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ORF1.
GN Name=ORF1;
OS Torque teno virus.
OC Viruses; ssDNA viruses; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20534983; PubMed=11080484; DOI=10.1006/viro.2000.0588;
RA Okamoto H., Nishizawa T., Tawara A., Peng Y., Takahashi M.,
RA Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.;
RT "Species-specific TT viruses in humans and nonhuman primates and their
phylogenetic relatedness.";
RL Virology 277:368-378 (2000).
DR EMBL; AB041958; BAB19310.1; -; Genomic_DNA.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT ORF1; 1.
SQ SEQUENCE 732 AA; 86905 MW; C284D108508EEA2 CRC64;

Query Match 48.5%; Score 50; DB 2; Length 732;
Best Local Similarity 53.8%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 GPWLEEEERAYGW 14
Db |||||:|
538 GPWMPRDEARSW 550

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RESULT 32
Q7M4T4_9PEZI
ID Q7M4T4_9PEZI PRELIMINARY; PRT; 229 AA.
AC Q7M4T4_9PEZI
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Cellulase (EC 3.2.1.4).
OS Scopulariopsis brevicaulis (arsenic fungus).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Microascales; mitosporic Microascales;
OC Scopulariopsis.
OX NCBI_TaxID=40375;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20378318; PubMed=10923796; DOI=10.1271/bbb.64.1238;
RA Nakatani P., Kawaguchi T., Takada G., Sumitani J., Moriyama Y.,
RA Arai M.;
RT "Cloning and sequencing of an endoglucanase gene from Scopulariopsis
RT brevicaulis TOP-1212, and its expression in Saccharomyces
RT cerevisiae.";
RL Biosci. Biotechnol. Biochem. 64:1238-1246(2000).
DR PIR; JC7308; JC7308.
DR HSP; P43316; LHD5.
DR GO; GO:0008810; F:cellulase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0030245; P:cellulose catabolism; IEA.
DR GO; GO:000272; P:polysaccharide catabolism; IEA.
DR InterPro; IPR000334; Glyco_hydro_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL HYDROL F45; 1.
SQ SEQUENCE 229 AA; 24332 MW; P88PD68CB7A15C1 CRC64;

Query Match 47.6%; Score 49; DB 2; Length 229;
Best Local Similarity 58.3%; Pred. No. 84;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PWTLEEEAYGW 14
DB 85 PWAVDDELAYGW 96
||:|||||
||:|||||

RESULT 33
ASNO BACSU
ID ASNO BACSU STANDARD; PRT; 614 AA.
AC O05272;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Asparagine synthetase [glutamine-hydrolyzing] 3 (EC 6.3.5.4).
GN Name=asno; OrderedLocuNames=BSU10790;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STPAIn=168;
RA Oudega B., Koningsstein G., Dueterhoeft A.;
RT "Bacillus subtilis genome project, DNA sequence from yuCA to yuch.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP STPAIn=168; PubMed=9353931;
RA Medina N., Vannier F., Roche B., Autret S., Levine A., Seror S.J.;
RT "Sequencing of regions downstream of addA (98 degrees) and citG (289
RL degrees) in Bacillus subtilis.";
RN Microbiology 143:3305-3308(1997).
[3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

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RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunec F., Ogasawara N., Mosser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brulliet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Deniot P., Devine K.M., Dueterhoeft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,
RA Ghim S.-Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haeich J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinis S., Lauber J.,
RA Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Maue C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitsengger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
[4]
RN CHARACTERIZATION.
RX MEDLINE=99429856; PubMed=10498721;
RA Yoshida K.-I., Fujita Y., Ehrlich S.D.;
RT "Three asparagine synthetase genes of Bacillus subtilis.";
RL J. Bacteriol. 181:6081-6091(1999).
CC -1- FUNCTION: Asparagine synthetase involved in sporulation.
CC -1- CATALYTIC ACTIVITY: ATP + L-aspartate + L-glutamine = AMP +
CC diphosphate + L-asparagine + L-glutamate.
CC -1- PATHWAY: Asparagine biosynthesis.
CC -1- SIMILARITY: Belongs to the asparagine synthetase family.
CC -1- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; Z33940; CAB07965.1; -; Genomic DNA.
DR EMBL; Y09476; CA070643.1; ALT_INIT; Genomic_DNA.
DR EMBL; Z99109; CAB12919.2; -; Genomic_DNA.
DR HSP; P22106; ICT9.
DR Subtilist; BG12240; asno.
DR InterPro; IPR006426; Asn_synth_AEB.
DR InterPro; IPR001962; Asn_synthase.
DR InterPro; IPR000583; GATase_2.
DR Pfam; PF00733; Asn_synthase; 1.
DR Pfam; PF00310; GATase_2; 1.
DR TIGRfams; TIGR01536; asn_synth_AEB; 1.
KW Amino-acid biosynthesis; Asparagine biosynthesis; Complete proteome;
KW Glutamine amidotransferase; Ligase; Sporulation.
FT ACT_SITE 2 2
SQ SEQUENCE 614 AA; 70714 MW; D621D9A4557A8AC1 CRC64;

Query Match 47.6%; Score 49; DB 1; Length 614;
Best Local Similarity 53.8%; Pred. No. 2.4e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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QY 1 EGPWLEEEYAYG 13  
 :|||:|: |||:  
 Db 313 DGPWIEKMTAFG 325

RESULT 34  
 Q5Y0Q6 9ALPH  
 ID Q5Y0Q6 9ALPH PRELIMINARY; PRT; 680 AA.  
 AC Q5Y0Q6;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Tegument phosphoprotein VP11/12.  
 GN Name=UL46;  
 OS Cercopithecine herpesvirus 2.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OX NCBI\_TaxID=10317;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC PubMed=15629785; DOI=10.1016/j.virol.2004.09.042;  
 RA Tyler S.D., Peters G.A., Severini A.;  
 RT "Complete genome sequence of cercopithecine herpesvirus 2 (SA8) and  
 RT comparison with other simplexviruses";  
 RL Virology 331:429-440(2005).  
 DR EMBL; AF714813; AAU88112.1; -; Genomic DNA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001719; AP endonuclease2.  
 DR InterPro; IPR005051; Helices UL46.  
 DR Pfam; PF03387; Herpes UL46; 1.  
 DR PROSITE; PS00729; AP\_NUCLEASE\_F2\_1; UNKNOWN 1.  
 SQ SEQUENCE 680 AA; 72787 MW; 3339B3F4D5ADFE2B CRC64;

Query Match 47.6%; Score 49; DB 2; Length 680;  
 Best Local Similarity 53.8%; Pred. No. 2.7e+02;  
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 WLEEEYAYGWMD 16  
 :|||:|: |||:  
 Db 613 WVEEDNPYWGMD 625

RESULT 35  
 Q560Q5 CRYNE  
 ID Q560Q5 CRYNE PRELIMINARY; PRT; 751 AA.  
 AC Q560Q5;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=CNBA1850;  
 OS Cryptococcus neoformans var. neoformans B-3501A.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
 OX NCBI\_TaxID=283643;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=B-3501A;  
 RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,  
 RA Wickes B.L., Fu J., Davis R.W.;  
 RT "Cryptococcus neoformans serotype D sequencing";  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AA0100003; EAL23538.1; -; Genomic DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 751 AA; 88116 MW; EE7307142C85E722 CRC64;

Query Match 47.6%; Score 49; DB 2; Length 751;  
 Best Local Similarity 72.7%; Pred. No. 3e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 EEEYAYGWMD 16  
 :|||:|: |||:  
 Db 306 EEEEGWGWAD 316

RESULT 36  
 Q5KPQ4 CRYNE  
 ID Q5KPQ4 CRYNE PRELIMINARY; PRT; 751 AA.  
 AC Q5KPQ4;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Cactin, putative.  
 GN ORFNames=CNAA01920;  
 OS Cryptococcus neoformans var. neoformans JEC21.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
 OX NCBI\_TaxID=214684;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=JEC21;  
 RA Vamathevan J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,  
 RA Loftus B.J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,  
 RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,  
 RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,  
 RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,  
 RA Lenggeler K.B., Maiti R., Marra M.A., Marra R.E., Mathewson C.A.,  
 RA Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L., Shvartsbeyn A.,  
 RA Schein J.E., Shin H., Specht C.A., Suh B., Tenney A., Utterback T.,  
 RA Wickes B.L., Wye N.H., Kronstad J., Lodge J.K., Heitman J.,  
 RA Davis R.W., Fraser C.M., Hyman R.W.;  
 RT "The genome and transcriptome of Cryptococcus neoformans, a  
 RT basidiomycete fungal pathogen of humans";  
 RL Science 0:0-0(2005).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=JEC21;  
 RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,  
 RA Van Aken S., Fraser C.;  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=JEC21;  
 RX PubMed=15653466; DOI=10.1126/science.1103773;  
 RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,  
 RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,  
 RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,  
 RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,  
 RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,  
 RA Kwon-Chung K.J., Lenggeler K.B., Maiti R., Marra M.A., Marra R.E.,  
 RA Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,  
 RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,  
 RA Suh B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,  
 RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,  
 RA Fraser C.M., Hyman R.W.;  
 RT "The genome of the basidiomycetous yeast and human pathogen  
 RT Cryptococcus neoformans";  
 RL Science 307:1321-1324(2005).  
 DR EMBL; AE017341; AA040750.1; -; Genomic DNA.  
 KW Complete proteome.  
 SQ SEQUENCE 751 AA; 88145 MW; 0739726FF8859AAB CRC64;

Query Match 47.6%; Score 49; DB 2; Length 751;  
 Best Local Similarity 72.7%; Pred. No. 3e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 EEEYAYGWMD 16  
 :|||:|: |||:  
 Db 306 EEEEGWGWAD 316

RESULT 37  
 Q6LU36\_PROPR

ID Q6LJ36\_PROPR PRELIMINARY; PRT; 931 AA.  
AC Q6LJ36;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
DE Hypothetical protein.  
DE Hypothetical protein.  
GN OrderedLocNames=PBPA0776;  
OC Photobacterium profundum (Photobacterium sp. (strain S99)).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Photobacterium.  
OX NCBI\_TaxID=74109;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX PubMed=15746425; DOI=10.1126/science.1103341;  
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N.,  
RA Lauro F.M., Cestaro A., Malacrida G., Simonati B., Cannata N.,  
RA Romualdi C., Bartlett D.H., Valle G.,  
RT "Life at depth: Photobacterium profundum genome sequence and  
RT expression analysis.";  
RL Science 307:1459-1461(2005).  
RL EMBL; CR378665; CAG19189.1; -; Genomic\_DNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004871; P:signal transducer activity; IEA.  
DR GO; GO:0006935; P:chemotaxis; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR004089; C:chemotaxis trans.  
DR InterPro; IPR003660; H:kin HAM.  
DR InterPro; IPR004090; M:Chemotaxis.  
DR Pfam; PF00672; HAM; 1.  
DR Pfam; PF00015; MCPsignal; 1.  
DR PRINTS; PR00260; MCPsignal; 1.  
DR SMART; SM00304; HAM; 1.  
DR SMART; SM00283; HAM; 1.  
DR PROSITE; PS01111; CHEMOTAXIS\_TRANSDUC\_2; 1.  
DR PROSITE; PS00885; HAM; 1.  
DR PROSITE; PS00885; HAM; 1.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 931 AA; 100660 MW; 040A6D16951E97FC CRC64;

Query Match 47.6%; Score 49; DB 2; Length 931;  
Best Local Similarity 53.8%; Pred. No. 3.8e+02;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GPWLEEEBAYGWD 16  
Db 150 GPWLSRYKHYGYD 164

RESULT 38  
QSK800\_CRYNE PRELIMINARY; PRT; 1029 AA.  
AC QSK800;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein.  
DE Hypothetical protein.  
GN ORFNames=CNM00690;  
OS Cryptococcus neoformans var. neoformans JEC21.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
OX NCBI\_TaxID=214684;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX STRAIN=JEC21;  
RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,  
RA Van Aken S., Fraser C.,  
RL Submitted (MAY-2004) to the ENBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=JEC21;  
RX PubMed=15653466; DOI=10.1126/science.1103773;  
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,  
RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,  
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,

RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,  
RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,  
RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,  
RA Mathewson C.A., Mitchell T.G., Pertea M., Riggs P.R., Salzberg S.L.,  
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,  
RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,  
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,  
RA Fraser C.M., Hyman R.W.,  
RT "The genome of the basidiomycetous yeast and human pathogen  
RT Cryptococcus neoformans.";  
RL Science 307:1321-1324(2005).  
RL EMBL; AS017353; AAW46820.1; -; Genomic\_DNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR InterPro; IPR003864; DUF221.  
DR Pfam; PF02714; DUF221; 1.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 1029 AA; 115147 MW; 5353DFD0DDDE07D CRC64;

Query Match 47.6%; Score 49; DB 2; Length 1029;  
Best Local Similarity 53.8%; Pred. No. 4.3e+02;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EGPWLEEEBAYG 13  
Db 941 QDPWLNEDDNAYG 953

RESULT 39  
Q6CJC3\_KLJLA PRELIMINARY; PRT; 1133 AA.  
AC Q6CJC3;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Similar to sg|S0002535 Saccharomycetes cerevisiae YDR128w.  
GN OrderedLocNames=KLJA0P19734g;  
OS Kluyveromyces lactis (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
OX NCBI\_TaxID=28985;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;  
RX PubMed=15229592; DOI=10.1038/nature02579;  
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
RA Boistrasse A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Nicaud J.-M., Nikolski M., Ostas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Potier S., Richard G.-P., Straub M.-L., Suleau A.,  
RA Swennen D., Tekala P., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.-L.,  
RT "Genome evolution in yeasts.";  
RL Nature 430:35-44(2004).  
DR EMBL; CR382126; CAG98674.1; -; Genomic\_DNA.  
DR InterPro; IPR006575; RWD.  
DR Pfam; PF00400; WD40; 4.  
DR PRINTS; PR00320; GPROTEINRPT.  
DR ProDom; PD000018; WD40; 1.  
DR SMART; SM00591; RWD; 1.  
DR SMART; SM00320; WD40; 5.  
DR PROSITE; PS00908; RWD; 1.  
DR PROSITE; PS00678; WD\_REPEATS\_1; UNKNOWN\_1.  
DR PROSITE; PS00082; WD\_REPEATS\_2; 2.  
DR PROSITE; PS0294; WD\_REPEATS\_REGION; 1.  
KW Complete proteome; Repeat; WD repeat.

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SQ SEQUENCE 1133 AA; 129160 MW; EB5B55B5D7B5C1CC CRC64;
Query Match 47.6%; Score 49; DB 2; Length 1133;
Best Local Similarity 57.1%; Pred. NO. 4.7e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 GPWLSEEEAYGWM 15
Db 467 GPWVEEDPEKYTFM 480

RESULT 40
Q9HXG2_PSEAE PRELIMINARY; PRT; 203 AA.
AC Q9HXG2;
DT 01-WAR-2001 (TREMBLrel. 16, Created)
DT 01-WAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PA3844;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saiter M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964 (2000).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL; AE004801; AAG07231.1; -; Genomic_DNA.
DR PIR; E83166; E83166.
DR HSSP; Q92V03; 1E6B.
DR InterPro; IPR004045; GST_Nterm.
DR InterPro; IPR012336; Thioredoxin-like.
DR InterPro; IPR012335; Thioredoxin_fold.
DR Pfam; PF02798; GST_N; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 203 AA; 22795 MW; 2A12E16100BB118E CRC64;

Query Match 46.6%; Score 48; DB 2; Length 203;
Best Local Similarity 47.4%; Pred. NO. 1e+02;
Matches 9; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

QY 2 GPWLSEEE---EAYGWM 16
Db 122 GPWLVEGQLLAAYDWLE 140

RESULT 41
Q6DJG8_XENLA PRELIMINARY; PRT; 225 AA.
AC Q6DJG8;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE MGC84287 protein.
GN Name=MGC84287;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC075211; AAH75211.1; -; mRNA.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF00030; Crystallin_2.
DR PRINTS; PR01367; BGCYSTALLIN.
DR SMART; SM00247; XTALbg; 2.
DR PROSITE; PS50915; CRYSTALLIN_BETAGAMMA; 4.
SQ SEQUENCE 225 AA; 25707 MW; 27EB2A019067A8B6 CRC64;

Query Match 46.6%; Score 48; DB 2; Length 225;
Best Local Similarity 50.0%; Pred. NO. 1.1e+02;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GPWLSEEEAYGWMDF 17
Db 64 GPWLSEERQSYGGEQF 79

RESULT 42
Q642R0_XENLA PRELIMINARY; PRT; 227 AA.
AC Q642R0;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE MGC84109 protein.
GN Name=MGC84109;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;

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"Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus* Initiative.";  
 RT Dev. Dyn. 225:384-391 (2002).  
 RN [2]  
 RC NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klapper S.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).  
 RN [3]  
 RC NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Brain;  
 RA Klein S., Gerhard D.S.;  
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC081142; AAH81142.1; -; mRNA.  
 DR InterPro; IPR001064; Crystallin.  
 DR Pfam; PF003030; Crystallin; 2.  
 DR PRINTS; PR01367; BGCYSTALLIN.  
 DR SMART; SM00247; XTALB9; 2.  
 DR PROSITE; PS00915; CRYSTALLIN BETA-GAMMA; 4.  
 SQ SEQUENCE 227 AA; 25940 MW; 3C63A25979455442 CRC64;  
 Query Match 46.6%; Score 48; DB 2; Length 227;  
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 2 GPWLEEEERAYGWMDF 17  
 ||| | : : : |  
 DB 64 GPWLSPERQSGGEQF 79  
 RESULT 43  
 Q4LT50\_9BURK  
 ID Q4LT50\_9BURK PRELIMINARY; PRT; 749 AA.  
 AC Q4LT50;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Twin-arginine translocation pathway signal (EC 3.1.4.3).  
 GN ORFNames=Bcen2424DRAFT\_4306;  
 OS Burkholderia cenocepacia HI2424.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.  
 CC NCBI\_TaxID=331272;  
 CC [1]  
 CC NUCLEOTIDE SEQUENCE.  
 RP STRAIN=HI2424;  
 RC US DOE Joint Genome Institute (JGI-PGF);  
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,  
 RA Hammon N., Irani S., Pitluck S., Richardson P.;  
 RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia  
 HI2424.";  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=HI2424;  
 RG US DOE Joint Genome Institute (JGI-ORNL);  
 RA Larimer F., Land M.;  
 RT "Annotation of the draft genome assembly of Burkholderia cenocepacia  
 HI2424.";  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AAHL01000018; BAM19252.1; -; Genomic\_DNA.  
 KW Hydrolase.  
 SQ SEQUENCE 749 AA; 82016 MW; D1CFFBE7E76C7281 CRC64;  
 Query Match 46.6%; Score 48; DB 2; Length 749;  
 Best Local Similarity 50.0%; Pred. No. 4.2e+02;  
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 2 GPWLEEEERAYGWMDF 17  
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 DB 230 GPVLGNEEKGYWTYY 245  
 RESULT 44  
 Q4WJ47\_ASPFU  
 ID Q4WJ47\_ASPFU PRELIMINARY; PRT; 762 AA.  
 AC Q4WJ47;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE SPX domain protein.  
 GN ORFNames=Afu1907250;  
 OS Aspergillus fumigatus Af293.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 OX NCBI\_TaxID=330879;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Af293;  
 RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,  
 RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,  
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,  
 RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,  
 RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,  
 RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,  
 RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,  
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,  
 RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,  
 RA Majors W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,  
 RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,  
 RA Penava M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,  
 RA Rabinowitz E., Rawlings N., Rajandream M.-A., Reischardt U.,  
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,  
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,  
 RA Sanchez-Peterson J.C., Saunders D., Seeger K., Squares R., Squares S.,  
 RA Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J.,  
 RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,  
 RA Machida M., Hall N., Barrell B., Denning D.W.;  
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus  
 Aspergillus fumigatus.";  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AAH01000007; EAL88435.1; -; Genomic DNA.  
 SQ SEQUENCE 762 AA; 87054 MW; 43F498F2700951B9 CRC64;  
 Query Match 46.6%; Score 48; DB 2; Length 762;  
 Best Local Similarity 58.3%; Pred. No. 4.3e+02;  
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEERAY 12  
 ||| | : : : |  
 DB 43 ESPWTEQDEEAP 54

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RESULT 45
Q6ZQA9 ORYA
ID Q6ZQA9_ORYA PRELIMINARY; PRT; 971 AA.
AC Q6ZQA9;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Putative S-locus protein 4.
GN Name=P0020810.24;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_TaxID=39947;
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP004656; BAD03324.1; -; Genomic_DNA.
DR Gramene; Q6ZQA9; -.
DR InterPro; IPR006569; RPR.
DR InterPro; IPR007087; Znf_C2H2.
DR SMART; SM00582; RPR; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN 1.
SQ SEQUENCE 971 AA; 106749 MW; 385DE9DBEEF2D8D1 CRC64;

Query Match 46.6%; Score 48; DB 2; Length 971;
Best Local Similarity 61.5%; Pred. No. 5.6e+02;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 WLEEEERAYGMD 16
Db 411 WLTSBEETWED 423

RESULT 46
Q7ULE2 RHOB
ID Q7ULE2_RHOB PRELIMINARY; PRT; 1016 AA.
AC Q7ULE2;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RB9557;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]_TaxID=117;
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
DR EMBL; BX294149; CAD76335.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1016 AA; 113586 MW; E3CD67DC7E6F90CA CRC64;

Query Match 46.6%; Score 48; DB 2; Length 1016;
Best Local Similarity 46.7%; Pred. No. 5.8e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 GPWLEEEERAYGMD 16
Db 467 GPWIDDEVNADQWD 481

RESULT 47
ASSY SYNEL STANDARD; PRT; 401 AA.
ID ASSY SYNEL STANDARD; PRT; 401 AA.
AC Q8DKY7;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Argininosuccinate synthase (EC 6.3.4.5) (Citruilline--aspartate
DE ligase).
GN Name=argG; OrderedLocusNames=tlr0712;
OS Synecococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=32046;
RN [1]_TaxID=32046;
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=BP-1;
RX MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1."
RL DNA Res. 9:123-130 (2002).
CC -!- CATALYTIC ACTIVITY: ATP + L-citrulline + L-aspartate = AMP +
CC diphosphate + (N(omega)-L-arginino)succinate.
CC -!- PATHWAY: Arginine biosynthesis; seventh step.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the argininosuccinate synthase family. Type
CC 1 subfamily.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; BA000039; BAC08263.1; -; Genomic_DNA.
DR HSP; P22767; 1KP2; 1.
DR HAMAP; MF_00005; 1.
DR InterPro; IPR001518; Arginosuc_synth.
DR PANTHER; PTHR11587; Arginosuc_synth; 1.
DR Pfam; PF00764; Arginosuc_synth; 1.
DR TIGRfam; TIGR00032; argG; 1.
DR PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
DR PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
KW Amino-acid biosynthesis; Arginine biosynthesis; ATP-binding;
KW Complete proteome; Ligase; Nucleotide-binding.
SQ SEQUENCE 401 AA; 44422 MW; B7495A302A1C8695 CRC64;

Query Match 46.1%; Score 47.5; DB 1; Length 401;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 EGPWLEEEERAYGWM 15
Db 193 EDPWMEPLEEYV-WM 206

RESULT 48
Q6LLMO PHOPR
ID Q6LLMO_PHOPR PRELIMINARY; PRT; 51 AA.
AC Q6LLMO;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical ferredoxin.
GN Name=VV3178; OrderedLocusNames=PBPA3537;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;

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RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed=15746425; DOI=10.1126/science.1103341;
RX Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N.,
RA Lauro F.M., Cestaro A., Malacrida G., Simionati B., Cannata N.,
RA Romaldi C., Bartlett D.H., Valle G.;
RT "Life at depth: Photobacterium profundum genome sequence and
RT expression analysis.";
RL Science 307:1459-1461(2005).
DR ENBL; CR378674; CAG21808.1; -; Genomic DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR01041; Ferredoxin.
KW Complete proteome.
SQ SEQUENCE 51 AA; 5749 MW; 68CF047A40C14524 CRC64;

Query Match 45.6%; Score 47; DB 2; Length 51;
Best Local Similarity 61.5%; Pred. No. 32;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PWLEEEEEAYGWM 15
DB 23 PMLTEKEAQGWM 35

RESULT 49
Q5QC16_9CAUD
ID Q5QC16_9CAUD PRELIMINARY; PRT; 84 AA.
AC Q5QC16;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE RB69 orf092c-like.
OS Enterobacteria phage JS98.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OC NCBI_TaxID=293178;
RN [1]
RX NUCLEOTIDE SEQUENCE.
RP PubMed=15576776; DOI=10.1128/JB.186.24.8276-8286.2004;
RA Chibani-Chemoufi S., Canchaya C., Bruttin A., Brussow H.;
RT "Comparative genomics of the T4-like Escherichia coli phage JS98:
RT implications for the evolution of T4 phages.";
RL J. Bacteriol. 186:8276-8286(2004).
DR ENBL; AY746496; AAU29267.1; -; Genomic DNA.
SQ SEQUENCE 84 AA; 9829 MW; C5FD5FC857833856 CRC64;

Query Match 45.6%; Score 47; DB 2; Length 84;
Best Local Similarity 53.8%; Pred. No. 55;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 WLSEEEEEAYGWM 16
DB 58 WLKEATEWGWTD 70

RESULT 50
Q92AF3_LISIN
ID Q92AF3_LISIN PRELIMINARY; PRT; 274 AA.
AC Q92AF3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lin1969 protein.
GN OrderedLocustNames=lin1969;
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CLIP 11262 / Serovar 6a;

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RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangeul L., Buchrieser C., Ruanlok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Eutlian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefz J., Kuhn M., Kunst F., Kurapkak G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordieik G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR ENBL; AL596170; CAC97199.1; -; Genomic DNA.
DR FIR; AG1678; AG1678.
DR MEROPS; M15.010; -.
DR ListList; LIN1969; -.
DR GO; GO:0008233; P:peptidase activity; IEA.
DR GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR003709; Pept_M15B_M15C.
DR Pfam; PF02557; Vany; 1.
KW Complete proteome.
SQ SEQUENCE 274 AA; 31191 MW; D92265111782A3EC CRC64;

Query Match 45.6%; Score 47; DB 2; Length 274;
Best Local Similarity 53.3%; Pred. No. 2e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEAYGWM 15
DB 204 EKWLEENAHNYGFI 218

Search completed: January 3, 2006, 09:49:25
Job time : 219.048 secs

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104	42	40.8	822	2	A47485	ABR protein 1 - hu	177	40	38.8	460	2	A31897	muscarinic acetyl
105	42	40.8	952	2	T48510	MYB like histone d	178	40	38.8	460	2	I51837	muscarinic recepto
106	42	40.8	1095	2	T13964	probable histone d	179	40	38.8	460	2	S09508	muscarinic acetyl
107	42	40.8	1277	2	T15109	hypothetical prote	180	40	38.8	460	2	A24325	muscarinic acetyl
108	42	40.8	2174	2	E95965	hypothetical glyci	181	40	38.8	460	2	A29514	muscarinic acetyl
109	41.5	40.3	427	2	C83591	N-carbamoyl-beta-a	182	40	38.8	463	2	A46172	glucagon-like pept
110	41.5	40.3	448	2	A27631	cellulase (EC 3.2	183	40	38.8	472	1	B53236	transcription fact
111	41.5	40.3	579	2	E75275	hypothetical prote	184	40	38.8	473	2	H71044	hypothetical prote
112	41.5	40.3	720	2	E72074	1,4-alpha-glucan b	185	40	38.8	477	2	B75170	hypothetical prote
113	41.5	40.3	720	2	G86549	glucan branching e	186	40	38.8	488	2	T47273	hypothetical prote
114	41	39.8	66	2	A90838	hypothetical prote	187	40	38.8	529	2	T48253	myb-like protein -
115	41	39.8	69	2	T36721	hypothetical prote	188	40	38.8	560	2	T17263	hypothetical prote
116	41	39.8	89	2	H82338	ferredoxin VC0311	189	40	38.8	567	2	AE0382	conserved hypotet
117	41	39.8	159	2	T30745	hypothetical prote	190	40	38.8	580	2	JH0224	site-specific meth
118	41	39.8	226	2	A69904	hypothetical prote	191	40	38.8	614	2	T09902	hypothetical prote
119	41	39.8	248	2	C91080	hypothetical prote	192	40	38.8	621	2	S28365	gene 1 protein - m
120	41	39.8	248	2	D85925	hypothetical prote	193	40	38.8	645	2	G01205	tyl protein - huma
121	41	39.8	273	1	JQ2390	MYB transcription	194	40	38.8	753	2	G02173	senaphorin III fam
122	41	39.8	293	2	T09758	myb-related protei	195	40	38.8	798	2	D96563	probable bZIP prot
123	41	39.8	293	2	T49947	hypothetical prote	196	40	38.8	834	2	S66498	M-sema F protein p
124	41	39.8	305	2	B69548	molybdopterin oxid	197	40	38.8	894	2	T26149	hypothetical prote
125	41	39.8	325	2	AF1947	hypothetical prote	198	40	38.8	899	2	A35895	androgen receptor
126	41	39.8	368	2	C90558	lipoprotein [impor	199	40	38.8	902	2	B40494	androgen receptor
127	41	39.8	381	2	G89009	protein R08F11.5 [	200	40	38.8	910	2	A48403	alpha-actinin - Ca
128	41	39.8	403	2	E84063	multidrug resistan	201	40	38.8	912	2	T01769	hypothetical prote
129	41	39.8	498	2	G87567	monooxygenase, fla	202	40	38.8	920	2	T26147	hypothetical prote
130	41	39.8	499	2	S74396	hypothetical prote	203	40	38.8	922	2	D70066	SNF2 helicase homo
131	41	39.8	526	2	AF3570	nickel-binding per	204	40	38.8	1115	2	A70990	carbamoyl-phosphat
132	41	39.8	566	2	T49333	hypothetical prote	205	40	38.8	1148	2	D82091	exodeoxyribonuclea
133	41	39.8	614	2	D34106	protein kinase (EC	206	40	38.8	1224	2	D86940	probable transcrip
134	41	39.8	625	2	S65829	hypothetical prote	207	40	38.8	1556	2	S76781	glutamate synthase
135	41	39.8	628	2	T04252	probable phosphati	208	40	38.8	3388	1	GNWVDP	genome polyprotein
136	41	39.8	633	2	B82990	hypothetical prote	209	40	38.8	3391	1	GNWV16	genome polyprotein
137	41	39.8	662	2	AG2420	hypothetical prote	210	40	38.8	3391	1	GNWV26	genome polyprotein
138	41	39.8	729	2	D86422	glycyl-cRNA synthe	211	40	38.8	3391	1	GNWVJA	genome polyprotein
139	41	39.8	817	2	T49642	hypothetical prote	212	40	38.8	3391	2	J50219	polyprotein - deng
140	41	39.8	818	2	T19120	hypothetical prote	213	40	38.8	4006	2	T09070	probable tenascin
141	41	39.8	934	2	T08418	protein kinase (EC	214	40	38.8	5126	2	S40450	ryanodine receptor
142	41	39.8	1019	2	C96519	probable disease r	215	39.5	38.3	199	2	B90047	conserved hypotet
143	41	39.8	1129	2	H86975	probable carbamoyl	216	39.5	38.3	204	2	C35878	class I major hist
144	41	39.8	1266	2	AG2695	conserved hypotet	217	39.5	38.3	325	2	H86670	hypothetical prote
145	41	39.8	1266	2	G97477	hypothetical prote	218	39.5	38.3	372	2	T00243	sopa protein - Esc
146	41	39.8	2128	2	I52577	beta-spectrin - mo	219	39.5	38.3	377	2	A49885	MHC class I histoc
147	41	39.8	2137	1	SJHUB	spectrin beta chai	220	39.5	38.3	379	2	E35878	class I major hist
148	40.5	39.3	273	2	S64054	hypothetical prote	221	39.5	38.3	383	2	S61195	hypothetical prote
149	40.5	39.3	297	2	T47857	myb protein-like -	222	39.5	38.3	388	1	BVECAF	sopa protein - Esc
150	40.5	39.3	340	2	S11143	class I histocompa	223	39.5	38.3	406	2	B55878	class I major hist
151	40.5	39.3	379	2	A35878	hypothetical prote	224	39.5	38.3	410	2	T47586	hypothetical prote
152	40.5	39.3	400	2	F72350	hypothetical prote	225	39.5	38.3	699	2	A12686	proteinase II [imp
153	40.5	39.3	464	2	B71123	hypothetical prote	226	39.5	38.3	699	2	S97468	dipeptidyl aminope
154	40.5	39.3	1073	1	T08228	plasmid replicatio	227	39.5	38.3	710	2	S40934	hypothetical prote
155	40	38.8	110	2	S20350	napin n1a - rape	228	39.5	38.3	715	2	T04452	transforming prote
156	40	38.8	145	2	S38235	hypothetical prote	229	39.5	38.3	776	2	E85384	probable myb-prote
157	40	38.8	148	2	H83054	suppressor protein	230	39.5	38.3	805	2	T49385	hypothetical prote
158	40	38.8	230	2	D70400	probable 2-oxoacid	231	39.5	38.3	907	2	A24938	hypothetical T2 pr
159	40	38.8	253	2	S76489	hypothetical prote	232	39.5	38.3	925	2	S27920	nuclear antigen BB
160	40	38.8	259	2	E64174	hypothetical prote	233	39.5	38.3	964	2	D59404	plectin isoform pl
161	40	38.8	264	2	S52102	thioether S-methyl	234	39.5	38.3	1121	2	C87973	plectin Y43F8C.12
162	40	38.8	269	2	JC7536	chitinase (EC 3.2	235	39.5	38.3	1153	2	T26883	hypothetical prote
163	40	38.8	274	2	E69423	branched-chain ami	236	39.5	38.3	2677	2	A38194	desmoplakin I - hu
164	40	38.8	278	2	T03850	myb-related protei	237	39.5	38.3	4574	2	G02520	plectin - human
165	40	38.8	299	2	T47917	meiosis inhibitor	238	39.5	38.3	4684	2	A59404	plectin [imported]
166	40	38.8	300	2	A41517	hypothetical prote	239	39.5	38.3	4687	1	A39638	plectin - rat
167	40	38.8	323	2	E87298	hypothetical prote	240	39.5	38.3	7576	2	T17428	FK506 polyketide s
168	40	38.8	325	2	T51509	probable transcrip	241	39	37.9	58	2	B82565	hypothetical prote
169	40	38.8	368	2	T03828	myb protein - rice	242	39	37.9	98	1	FERW2E	ferredoxin [2Fe-2S
170	40	38.8	375	2	S05390	fibromodulin precu	243	39	37.9	114	2	T31192	hypothetical prote
171	40	38.8	377	2	JC7535	chitinase (EC 3.2	244	39	37.9	115	2	C83187	conserved hypotet
172	40	38.8	382	2	C86230	hypothetical prote	245	39	37.9	132	2	AC0371	conserved hypotet
173	40	38.8	405	2	C83204	argininosuccinate	246	39	37.9	132	2	AF3329	hypothetical prote
174	40	38.8	421	1	EFHST	translation elonga	247	39	37.9	152	2	G81175	dAMP pyrophospho
175	40	38.8	432	2	C87581	integrase/recombin	248	39	37.9	152	2	H81930	probable nucleosid

249	39	37.9	176	2	T24670	hypothetical prote	322	39	37.9	1002	2	AF1909	two-component hybr
250	39	37.9	182	2	AB0698	probable pathogeni	323	39	37.9	1064	2	A41542	adenylate cyclase
251	39	37.9	204	2	S20587	DNA-directed RNA p	324	39	37.9	1118	2	T27865	hypothetical prote
252	39	37.9	233	2	H69130	conserved hypothet	325	39	37.9	1157	2	G89863	hypothetical prote
253	39	37.9	248	2	H84008	hypothetical prote	326	39	37.9	1193	2	JC2489	peptidyl-dipectida
254	39	37.9	250	2	T13459	hypothetical prote	327	39	37.9	1234	2	G70622	probable transcrip
255	39	37.9	250	2	S41513	Bm-3c protein - m	328	39	37.9	1502	2	T14278	myosin-like protei
256	39	37.9	254	2	F70891	hypothetical prote	329	39	37.9	1549	2	T11974	glutamate synthase
257	39	37.9	261	2	G47116	trifoliotoxin resis	330	39	37.9	1607	2	T02837	long chain fatty a
258	39	37.9	275	2	T02988	myb-related protei	331	39	37.9	1683	2	S56811	probable membrane
259	39	37.9	283	2	I45962	phenylethanolamine	332	39	37.9	1750	2	E86151	hypothetical prote
260	39	37.9	284	1	A24313	phenylethanolamine	333	39	37.9	1750	2	G88493	protein F5789.2 [i
261	39	37.9	284	2	T21722	hypothetical prote	334	39	37.9	3119	2	I49729	HD protein - mouse
262	39	37.9	289	2	E90906	probable transposa	335	39	37.9	3390	1	GNWV33	genome polyprotein
263	39	37.9	291	2	S10867	early B4 34K prote	336	38.5	37.4	295	2	C84830	probable protein x
264	39	37.9	293	2	D85711	probable transposa	337	38.5	37.4	321	1	T27049	phosphoprotein pho
265	39	37.9	300	2	T33392	hypothetical prote	338	38.5	37.4	364	2	I46604	MHC PD14a transpla
266	39	37.9	303	2	AP2852	coproporphyrinogen	339	38.5	37.4	366	2	I46603	MHC PD14a transpla
267	39	37.9	303	2	D97829	coproporphyrinogen	340	38.5	37.4	400	2	A89924	hypothetical prote
268	39	37.9	304	2	AB0390	conserved hypothet	341	38.5	37.4	1197	2	T28628	hypothetical prote
269	39	37.9	305	1	S71284	myb-related protei	342	38.5	37.4	1355	2	T00961	hypothetical prote
270	39	37.9	307	2	G75088	probable sulfatase	343	38.5	37.4	1514	2	T52080	multi resistance p
271	39	37.9	316	2	H75421	acetyl-CoA carboxy	344	38.5	37.4	2201	2	AH0095	transcription regu
272	39	37.9	322	2	AF0726	protein-Npi-phosph	345	38	36.9	68	2	F82158	deleted in split h
273	39	37.9	322	2	AD3044	hypothetical prote	346	38	36.9	70	2	G02284	hypothetical prote
274	39	37.9	322	2	H98241	ABC transporter su	347	38	36.9	85	2	D90732	T-cell receptor al
275	39	37.9	323	1	WQECM3	phosphotransferase	348	38	36.9	95	2	F30603	ferredoxin 2[4Fe-4
276	39	37.9	323	2	B85793	PTS enzyme IIAb, m	349	38	36.9	96	2	I49890	hypothetical prote
277	39	37.9	323	2	G90944	mannose-specific p	350	38	36.9	96	2	F69516	hypothetical prote
278	39	37.9	325	2	C75280	phenylacetic acid	351	38	36.9	116	2	S26309	Ig heavy chain v r
279	39	37.9	325	2	A87443	GTP-binding protei	352	38	36.9	120	2	P85582	unknown protein en
280	39	37.9	335	2	JE0115	zinc-finger protei	353	38	36.9	168	2	C85715	unknown protein en
281	39	37.9	338	2	B49642	POU-domain protei	354	38	36.9	176	2	I84638	pituitary adenylat
282	39	37.9	343	2	AG2465	hypothetical prote	355	38	36.9	203	2	I68521	hypothetical prote
283	39	37.9	348	2	S11198	transforming prote	356	38	36.9	204	2	S20585	DNA-directed RNA p
284	39	37.9	359	2	E89784	hypothetical prote	357	38	36.9	205	2	T34773	probable lipoprote
285	39	37.9	366	1	XNBVUG	UDPglucose-hexose	358	38	36.9	213	2	B27898	beta-crystallin B3
286	39	37.9	367	2	E83676	pyruvate dehydroge	359	38	36.9	221	2	D71145	hypothetical prote
287	39	37.9	376	2	T47761	hypothetical prote	360	38	36.9	225	2	B88712	protein ClH12.10
288	39	37.9	378	2	D82158	N-acetylglucosamin	361	38	36.9	227	2	E90420	DNA endonuclease I
289	39	37.9	379	2	T03608	chilling-induced p	362	38	36.9	234	2	T51666	myb-related transc
290	39	37.9	426	2	B71408	probable acylanino	363	38	36.9	234	2	T26560	hypothetical prote
291	39	37.9	441	2	A48455	acidic phosphoprot	364	38	36.9	237	2	H70554	hypothetical prote
292	39	37.9	460	2	A96555	unknown protein [i	365	38	36.9	240	2	B64063	nasd protein homol
293	39	37.9	476	1	T05701	carboxypeptidase D	366	38	36.9	241	2	C81971	hypothetical prote
294	39	37.9	488	2	B82967	probable glucose-6	367	38	36.9	241	2	H81026	conserved hypothet
295	39	37.9	498	2	S11246	LAG-3 protein prec	368	38	36.9	248	2	B64926	probable ABC-type
296	39	37.9	510	2	I56242	lymphoid cell acti	369	38	36.9	248	2	E90927	hypothetical prote
297	39	37.9	529	2	F70550	probable acdcl pro	370	38	36.9	248	2	AI0702	hypothetical prote
298	39	37.9	542	2	H84509	hypothetical prote	371	38	36.9	248	2	A85776	probable ATP-depen
299	39	37.9	554	2	T15992	hypothetical prote	372	38	36.9	248	2	AC0293	myb-related protei
300	39	37.9	554	2	S50309	hypothetical prote	373	38	36.9	249	1	S68688	hypothetical protei
301	39	37.9	624	1	I51591	transforming prote	374	38	36.9	251	2	F96008	hypothetical prote
302	39	37.9	636	1	TVMSNB	transforming prote	375	38	36.9	256	2	T49254	Myb DNA binding pr
303	39	37.9	640	1	A55073	transforming prote	376	38	36.9	262	2	E70172	carboxypeptidase h
304	39	37.9	655	2	T30044	hypothetical prote	377	38	36.9	263	2	S77321	hypothetical prote
305	39	37.9	686	1	S28050	transforming prote	378	38	36.9	272	2	H69300	hypothetical prote
306	39	37.9	700	1	S01991	transforming prote	379	38	36.9	278	2	T36647	probable hydrolase
307	39	37.9	704	1	S33704	transforming prote	380	38	36.9	297	2	S66102	protein secretion
308	39	37.9	714	2	G86844	hypothetical prote	381	38	36.9	308	1	A34082	branched-chain-ami
309	39	37.9	714	2	AP2458	hypothetical prote	382	38	36.9	308	2	AI0474	branched-chain-ami
310	39	37.9	715	4	TVMSNY	transforming prote	383	38	36.9	309	1	XNECV	branched-chain-ami
311	39	37.9	728	1	S36095	transforming prote	384	38	36.9	309	2	AD0924	branched-chain ami
312	39	37.9	739	2	A55314	glycine-tRNA ligas	385	38	36.9	309	2	A86063	branched-chain ami
313	39	37.9	751	1	I49497	transforming prote	386	38	36.9	309	2	H91216	branched-chain ami
314	39	37.9	752	1	S03423	transforming prote	387	38	36.9	313	2	T39974	hypothetical prote
315	39	37.9	757	1	I50667	transforming prote	388	38	36.9	317	2	B83760	hypothetical prote
316	39	37.9	758	2	C96749	transforming prote	389	38	36.9	325	2	T47229	arginase (EC 3.5.3
317	39	37.9	761	1	TVCHM	transforming prote	390	38	36.9	340	2	E95964	probable iron upta
318	39	37.9	761	1	TVHUMB	transforming prote	391	38	36.9	352	1	S58293	myb-related protei
319	39	37.9	764	2	JC8016	acylaminoacyl-pept	392	38	36.9	358	2	T47228	arginase (EC 3.5.3
320	39	37.9	960	2	T00808	hypothetical prote	393	38	36.9	359	2	D83103	probable phospholi
321	39	37.9	970	2	S77202	sensory transducti	394	38	36.9	365	2	D84532	hypothetical prote

395	38	36.9	370	2	C75268	carboxypeptidase G	468	38	36.9	1148	2	S51855	hypothetical prote
396	38	36.9	379	2	F83496	probable acyl-CoA	469	38	36.9	1193	2	T50729	magnesium-protopor
397	38	36.9	387	2	S32934	aminotransferase p	470	38	36.9	1201	2	A83007	hypothetical prote
398	38	36.9	387	2	H64182	xylose operon regl	471	38	36.9	1239	2	S74355	hypothetical prote
399	38	36.9	393	1	S22520	myb-related protei	472	38	36.9	1260	2	A72603	probable nitrate r
400	38	36.9	396	2	T51387	UVB-resistance pro	473	38	36.9	1301	2	D84384	hypothetical prote
401	38	36.9	399	2	T19115	hypothetical prote	474	38	36.9	1343	2	T20718	hypothetical prote
402	38	36.9	401	2	B70398	argininosuccinate	475	38	36.9	1363	2	I58375	protein-tyrosine k
403	38	36.9	402	2	A10323	transposase, IS285	476	38	36.9	1825	2	S13507	microtubule-associ
404	38	36.9	402	2	AB0193	transposase, IS285	477	38	36.9	1828	2	A40115	microtubule-associ
405	38	36.9	402	2	T14710	probable transposa	478	38	36.9	1830	2	A37981	microtubule-associ
406	38	36.9	402	2	AE0267	transposase, IS285	479	38	36.9	2288	2	T30568	acetyl-CoA carboxy
407	38	36.9	402	2	AI0256	transposase, IS285	480	38	36.9	2958	2	S64921	probable membrane
408	38	36.9	402	2	AH0298	transposase, IS285	481	38	36.9	4152	2	T31102	filamentous hemagg
409	38	36.9	402	2	AB0264	transposase, IS285	482	38	36.9	4644	1	A38905	dynein heavy chain
410	38	36.9	402	2	AB0472	transposase, IS285	483	37.5	36.4	87	2	S52290	HLA-A30 variant ex
411	38	36.9	402	2	AH0197	transposase, IS285	484	37.5	36.4	116	2	B75550	hypothetical prote
412	38	36.9	402	2	AE0190	transposase, IS285	485	37.5	36.4	125	2	D70732	hypothetical prote
413	38	36.9	402	2	AG0210	transposase, IS285	486	37.5	36.4	126	2	A82519	hypothetical prote
414	38	36.9	402	2	AG0339	transposase, IS285	487	37.5	36.4	133	2	H81191	hypothetical prote
415	38	36.9	402	2	AB0358	transposase, IS285	488	37.5	36.4	136	1	C69411	conserved hypother
416	38	36.9	402	2	AI0181	transposase, [impor	489	37.5	36.4	165	2	G82322	dihydrofolate redu
417	38	36.9	402	2	AH0193	transposase, IS285	490	37.5	36.4	206	2	UJ0059	H-2 class I histoc
418	38	36.9	402	2	AE0242	transposase, IS285	491	37.5	36.4	206	2	UJ0058	H-2 class I histoc
419	38	36.9	402	2	AG0260	transposase, IS285	492	37.5	36.4	229	2	S66577	ribosomal protein
420	38	36.9	402	2	AC0341	transposase, IS285	493	37.5	36.4	246	2	F83734	hypothetical prote
421	38	36.9	402	2	AD0002	transposase, IS285	494	37.5	36.4	252	2	C85708	probable colonizat
422	38	36.9	402	2	AI0313	transposase, IS285	495	37.5	36.4	252	2	D90850	probable colonizat
423	38	36.9	402	2	AF0348	transposase, IS285	496	37.5	36.4	274	2	T39289	probable RNA bindi
424	38	36.9	421	2	C96806	unknown protein T5	497	37.5	36.4	286	2	T38768	probable sec14 cyt
425	38	36.9	421	2	G96730	hypothetical prote	498	37.5	36.4	295	2	AC2357	DNA-methyltransfer
426	38	36.9	427	2	F83984	acetylornithine de	499	37.5	36.4	297	1	H64783	carbamate kinase (
427	38	36.9	429	2	F86240	hypothetical prote	500	37.5	36.4	297	2	G90701	probable carbamate
428	38	36.9	430	1	A27655	adenosylhomocyste	501	37.5	36.4	297	2	B85552	carbamate kinase (
429	38	36.9	450	2	F70681	probable trpE - My	502	37.5	36.4	298	2	B83293	tetratricopeptide
430	38	36.9	467	2	CJ7923	microtubule-associ	503	37.5	36.4	317	2	G83033	vanillate O-demeth
431	38	36.9	468	1	TVMSE2	transcription fact	504	37.5	36.4	323	2	S72473	type II site-speci
432	38	36.9	469	1	TVHUE2	transcription fact	505	37.5	36.4	335	2	A40038	MHC class I histoc
433	38	36.9	500	2	A99999	probable portal pr	506	37.5	36.4	335	2	T51489	hypothetical prote
434	38	36.9	500	2	H85818	hypothetical prote	507	37.5	36.4	340	2	AE3310	coroporphyrinogen
435	38	36.9	512	2	T35115	zinc metalloprotei	508	37.5	36.4	362	1	HLMSLD	MHC class I histoc
436	38	36.9	538	2	A54391	translation initia	509	37.5	36.4	362	2	C60854	MHC class I histoc
437	38	36.9	544	2	T40058	probable chromatin	510	37.5	36.4	362	2	B60854	MHC class I histoc
438	38	36.9	564	2	AH2066	hypothetical prote	511	37.5	36.4	365	2	I72170	MHC class I histoc
439	38	36.9	567	2	AE1044	thiol disulfide in	512	37.5	36.4	365	2	I37476	MHC class I histoc
440	38	36.9	569	2	E95309	probable calcium b	513	37.5	36.4	365	2	I56039	HLA-A30.3 precurs
441	38	36.9	570	1	A34354	sulfite reductase	514	37.5	36.4	365	2	I38519	MHC class I histoc
442	38	36.9	570	1	RDECSH	sulfite reductase	515	37.5	36.4	366	2	A60369	MHC class I histoc
443	38	36.9	570	2	AF0858	sulfite reductase	516	37.5	36.4	390	1	ACBPMG	maturation protein
444	38	36.9	570	2	B91081	sulfite reductase	517	37.5	36.4	419	2	JC7863	ICS3 protein - hum
445	38	36.9	570	2	C85926	sulfite reductase,	518	37.5	36.4	450	2	T35873	zinc proteinase -
446	38	36.9	581	2	R83729	sulfite reductase,	519	37.5	36.4	503	2	F65027	probable GTPase/GT
447	38	36.9	589	2	D84530	adenine deaminase,	520	37.5	36.4	503	2	A85895	probable GTP-bindi
448	38	36.9	599	2	G86204	probable Tail-like	521	37.5	36.4	536	2	E91050	probable GTP-bindi
449	38	36.9	605	2	S06398	hypothetical prote	522	37.5	36.4	536	2	A10063	probable OmpA-fam
450	38	36.9	609	2	S55957	alpha-globulin typ	523	37.5	36.4	538	2	D83891	medium-chain fatty
451	38	36.9	644	2	G96748	hypothetical prote	524	37.5	36.4	562	2	C72278	hypothetical prote
452	38	36.9	646	2	D70939	hypothetical prote	525	37.5	36.4	1825	2	T42725	actin binding prot
453	38	36.9	654	2	H85717	hypothetical prote	526	37.5	36.4	1885	2	T30847	actin binding prot
454	38	36.9	667	2	JCS889	OS-9 protein precu	527	37.5	36.4	2033	2	T30849	actin binding prot
455	38	36.9	673	2	AE0692	probable NADH redu	528	37.5	36.4	2311	1	TVCHSR	kinase-related pro
456	38	36.9	686	2	A75126	hypothetical prote	529	37.5	36.4	2515	2	S47008	tenascin-like prot
457	38	36.9	692	2	H82246	DNA polymerase III	530	37.5	36.4	2554	1	TVFF7L	kinase-related pro
458	38	36.9	706	2	H82764	O-antigen acetyl	531	37.5	36.4	2594	2	A35774	kinase-related pro
459	38	36.9	721	2	E64397	kIba homolog - Met	532	37	35.9	9	2	A61357	phyllocaeerulein -
460	38	36.9	770	2	T09026	hypothetical prote	533	37	35.9	75	2	T06013	hypothetical prote
461	38	36.9	772	2	C69920	transcription regu	534	37	35.9	97	2	S28198	ferredoxin [2Fe-2S
462	38	36.9	795	2	T34468	hypothetical prote	535	37	35.9	106	2	S26636	napin nib - rape
463	38	36.9	813	2	T12506	hypothetical prote	536	37	35.9	106	2	C70033	hypothetical prote
464	38	36.9	819	2	G81698	leucyl-tRNA synth	537	37	35.9	112	1	ASLJCK	vpu protein - huma
465	38	36.9	853	2	T08162	amylopullulanase (	538	37	35.9	114	2	A13284	hypothetical prote
466	38	36.9	880	2	C72521	hypothetical prote	539	37	35.9	144	2	T07175	ferredoxin [2Fe-2S
467	38	36.9	894	2	C86756	prophage p12 prote	540	37	35.9	152	2	B65043	yfjX protein - Esc

541	37	35.9	152	2	H64749	yafX protein - Esc	614	37	35.9	471	2	C71439	hypothetical prote
542	37	35.9	158	2	G82332	bacterioferritin V	615	37	35.9	477	2	D83724	beta-glucosidase g
543	37	35.9	165	2	S74730	hypothetical prote	616	37	35.9	480	2	D75050	hypothetical prote
544	37	35.9	158	2	T31043	hypothetical prote	617	37	35.9	482	2	G96616	hypothetical prote
545	37	35.9	169	2	D23364	procaerulein precu	618	37	35.9	484	2	T51070	hypothetical prote
546	37	35.9	185	1	A69169	hypothetical prote	619	37	35.9	484	2	E84765	hypothetical prote
547	37	35.9	188	2	A23364	caerulein precursu	620	37	35.9	489	2	JC4787	shaw protein - Cal
548	37	35.9	212	2	T51640	myb-related transc	621	37	35.9	491	1	D64947	glucose-6-phosphat
549	37	35.9	222	2	F69335	conserved hypotet	622	37	35.9	491	2	AB0742	glucose-6-phosphat
550	37	35.9	231	2	D96718	hypothetical prote	623	37	35.9	491	2	S37053	glucose-6-phosphat
551	37	35.9	233	1	SCXL	caerulein precursu	624	37	35.9	491	2	F85797	glucose-6-phosphat
552	37	35.9	234	2	A23043	caerulein precursu	625	37	35.9	491	2	B90949	phenylcarbamate hy
553	37	35.9	234	2	A24968	caerulein precursu	626	37	35.9	493	2	A45737	glucose-6-phosphat
554	37	35.9	234	2	T36740	probable transcrip	627	37	35.9	494	2	AB0252	potassium channel
555	37	35.9	235	2	S70219	sipA protein - Sal	628	37	35.9	498	2	A41359	hypothetical prote
556	37	35.9	237	2	S51889	ras suppressor SHR	629	37	35.9	499	2	E86206	zinc finger protei
557	37	35.9	262	2	G95327	TRM3 transposase f	630	37	35.9	507	2	G01614	calcium-dependent
558	37	35.9	263	2	E81243	pyrroline-5-carbox	631	37	35.9	514	2	T10938	3-oxosteroid 1-deh
559	37	35.9	272	1	LPEC28	lipoprotein-28 pre	632	37	35.9	515	2	S61889	hypothetical prote
560	37	35.9	274	2	F75328	conserved hypotet	633	37	35.9	520	2	T08399	hypothetical prote
561	37	35.9	275	2	B72484	hypothetical prote	634	37	35.9	520	2	T48988	hypothetical prote
562	37	35.9	276	2	B96996	hypothetical prote	635	37	35.9	524	2	C69297	acetyl-CoA decarbo
563	37	35.9	279	2	T03830	probable myb facto	636	37	35.9	529	2	S52976	hypothetical prote
564	37	35.9	280	1	S26604	myb-related protei	637	37	35.9	530	2	JN0597	calnexin-like prot
565	37	35.9	282	2	B85327	probable transcrip	638	37	35.9	532	2	T49873	calnexin homolog -
566	37	35.9	288	2	D69480	conserved hypotet	639	37	35.9	533	2	A84512	hypothetical prote
567	37	35.9	292	1	A70047	RNA polymerase hom	640	37	35.9	535	2	E95929	probable methylo
568	37	35.9	295	2	B74715	kinase, GHMP fami	641	37	35.9	535	2	T52098	probable nuclear t
569	37	35.9	296	2	T35345	chitinase - Strept	642	37	35.9	537	2	T20525	hypothetical prote
570	37	35.9	301	1	A37766	SEC14 protein - ye	643	37	35.9	540	2	T10892	probable calnexin
571	37	35.9	312	2	T47345	hypothetical prote	644	37	35.9	540	2	T46386	hypothetical prote
572	37	35.9	324	2	B85064	MYB-like protein [	645	37	35.9	546	2	T06415	calnexin - soybean
573	37	35.9	326	2	T49966	myb-related protei	646	37	35.9	549	2	B83149	probable acyl-CoA
574	37	35.9	328	2	T20344	hypothetical prote	647	37	35.9	561	2	AG2336	potassium-dependen
575	37	35.9	334	2	T50816	probable transcrip	648	37	35.9	566	2	T34842	probable transfera
576	37	35.9	343	2	T36590	hypothetical prote	649	37	35.9	579	2	I40371	methyltransferase
577	37	35.9	343	2	H84000	spore photoproduct	650	37	35.9	586	1	C64988	probable sulfatase
578	37	35.9	348	2	A85535	probable NAGC-like	651	37	35.9	586	2	B85858	probable sulfatase
579	37	35.9	348	2	E90684	probable NAGC-like	652	37	35.9	586	2	H91013	signal peptide pep
580	37	35.9	348	2	B64768	yaif protein - Esc	653	37	35.9	594	2	C87364	hypothetical prote
581	37	35.9	361	2	T29437	probable transcrip	654	37	35.9	614	2	T43477	hypothetical prote
582	37	35.9	362	2	AP0159	probable membrane	655	37	35.9	615	2	H96732	hypothetical prote
583	37	35.9	365	2	D86470	F2iH2.9 protein -	656	37	35.9	617	2	T37732	conserved hypotet
584	37	35.9	372	2	T47763	hypothetical prote	657	37	35.9	634	2	E86293	T24D18.1 protein -
585	37	35.9	373	2	B95871	probable CDP-tyel	658	37	35.9	637	2	A82301	beta-N-acetylhexos
586	37	35.9	374	2	F86632	pyruvate dehydroge	659	37	35.9	639	2	T46577	arylsulfatase (EC
587	37	35.9	382	2	S40987	hypothetical prote	660	37	35.9	647	2	D95098	topoisomerase IV,
588	37	35.9	383	2	T15698	hypothetical prote	661	37	35.9	647	2	D97966	topoisomerase IV c
589	37	35.9	387	2	G87537	acyl-CoA dehydroge	662	37	35.9	662	2	T01533	topoisomerase IV c
590	37	35.9	398	2	A75128	probable transamin	663	37	35.9	666	2	E82619	transketolase I XF
591	37	35.9	399	2	F69034	argininosuccinate	664	37	35.9	670	2	S77387	nitrate transport
592	37	35.9	400	2	S24759	probable transposa	665	37	35.9	676	2	C97775	acylamino-acid-rel
593	37	35.9	400	2	A42727	probable transposa	666	37	35.9	685	2	T40162	transketolase - fi
594	37	35.9	400	2	C95306	TRM3 transposase [	667	37	35.9	685	2	AF0850	hypothetical prote
595	37	35.9	400	2	E95287	TRM3 transposase [	668	37	35.9	691	2	JE0150	acetylcholinestera
596	37	35.9	400	2	F95291	TRM3 transposase [	669	37	35.9	702	2	C86268	F31B4.2 protein -
597	37	35.9	400	2	T37132	probable hydrolase	670	37	35.9	719	2	S51739	transcription repr
598	37	35.9	401	2	T31132	K06H7.2 protein -	671	37	35.9	737	2	S18207	adducin alpha chai
599	37	35.9	406	2	S44842	hypothetical prote	672	37	35.9	769	1	ISBYT1	DNA topoisomerase
600	37	35.9	414	2	H95843	probable two compo	673	37	35.9	770	2	A54444	DNA-binding protei
601	37	35.9	420	1	S95966	myb-related protei	674	37	35.9	770	2	I49508	ISGF3 p91-related
602	37	35.9	421	1	S26605	myb-related protei	675	37	35.9	773	2	D86268	F31B4.3 protein -
603	37	35.9	421	1	S24244	hypothetical prote	676	37	35.9	776	2	T20896	hypothetical prote
604	37	35.9	422	2	T33186	hypothetical prote	677	37	35.9	810	2	B71639	virB4 protein prec
605	37	35.9	426	2	G83320	seryl-tRNA synthet	678	37	35.9	812	1	ISZPT1	DNA topoisomerase
606	37	35.9	428	2	B81531	conserved hypotet	679	37	35.9	814	2	T50327	probable disease r
607	37	35.9	432	2	D72008	CR850 hypothetical	680	37	35.9	835	2	T05259	probable trichalose
608	37	35.9	432	2	E86616	CR850 hypothetical	681	37	35.9	862	2	E84567	p97 protein - Toxo
609	37	35.9	442	2	I39174	seven trans-membra	682	37	35.9	877	2	T03098	probable alpha-act
610	37	35.9	444	2	B95065	conserved hypotet	683	37	35.9	895	2	T13414	probable alpha-act
611	37	35.9	462	2	A57120	small nuclear ribo	684	37	35.9	910	2	A34721	androgen receptor
612	37	35.9	464	2	C86422	probable glycyl-tr	685	37	35.9	911	2	B34721	androgen receptor
613	37	35.9	468	2	S75389	probable phenylala	686	37	35.9	919	2	A39248	androgen receptor

687	37	35.9	922	2	D75615	excinuclease ABC c	760	36	35.0	263	2	AD2992	phosphoprotein pho
688	37	35.9	924	2	T13413	probable alpha-act	761	36	35.0	263	2	C97225	hypothetical prote
689	37	35.9	986	2	T10770	cis-Golgi matrix p	762	36	35.0	263	2	F84770	hypothetical prote
690	37	35.9	1041	2	C83548	hypothetical prote	763	36	35.0	274	2	T07393	myb-related transc
691	37	35.9	1095	2	AC2059	hypothetical prote	764	36	35.0	274	2	C75255	iron ABC transport
692	37	35.9	1106	2	T31742	hypothetical prote	765	36	35.0	277	2	A72640	probable dimethyla
693	37	35.9	1140	1	I38908	UV-damaged DNA-bin	766	36	35.0	280	2	AF1773	conserved dimethyl
694	37	35.9	1140	1	S38777	UV-damaged DNA-bin	767	36	35.0	284	2	G81144	hypothetical prote
695	37	35.9	1140	1	JC7152	UV-damaged DNA-bin	768	36	35.0	285	2	A96548	hypothetical prote
696	37	35.9	1164	2	S71792	phosphatidylinosit	769	36	35.0	289	2	T31057	hypothetical prote
697	37	35.9	1186	2	T23327	adenomatous polypo	770	36	35.0	294	2	I84606	translation elonga
698	37	35.9	1188	2	T05324	hypothetical prote	771	36	35.0	297	2	B70685	hypothetical prote
699	37	35.9	1188	2	T23330	hypothetical prote	772	36	35.0	302	2	T21257	hypothetical prote
700	37	35.9	1214	2	JC2069	zinc-finger protei	773	36	35.0	306	2	I49139	lymphotoxin-beta -
701	37	35.9	1477	2	T00957	myosin heavy chain	774	36	35.0	309	2	T00503	probable MYB fami
702	37	35.9	1611	2	A84743	probable myosin he	775	36	35.0	311	2	C70463	branched-chain ami
703	37	35.9	1677	2	T18344	P-glycoprotein E -	776	36	35.0	315	2	B69751	conserved hypothet
704	37	35.9	1940	2	A58287	myosin heavy chain	777	36	35.0	316	2	S58719	probable membrane
705	37	35.9	2599	2	A96616	unknown protein F1	778	36	35.0	317	2	B95113	competence protein
706	36.5	35.4	204	2	F84184	hypothetical prote	779	36	35.0	317	2	A37982	competence protein
707	36.5	35.4	255	2	AE0537	hypothetical prote	780	36	35.0	318	2	C71173	hypothetical prote
708	36.5	35.4	277	2	G75520	hypothetical prote	781	36	35.0	319	2	G82374	branched-chain ami
709	36.5	35.4	279	2	T43601	hypothetical prote	782	36	35.0	320	2	S29310	phosphoprotein pho
710	36.5	35.4	343	2	E70674	hypothetical prote	783	36	35.0	320	2	T31130	hypothetical prote
711	36.5	35.4	348	2	I68745	MHC class I lympho	784	36	35.0	320	2	C85440	myb-related protei
712	36.5	35.4	356	2	A27797	class I histocompa	785	36	35.0	321	2	S50540	hypothetical prote
713	36.5	35.4	358	2	A28834	MHC class I histoc	786	36	35.0	321	2	C64977	hypothetical prote
714	36.5	35.4	376	2	D87700	iron-sulfur-bindin	787	36	35.0	320	2	F69057	branched-chain ami
715	36.5	35.4	392	2	T05422	hypothetical prote	788	36	35.0	330	2	T08351	hypothetical prote
716	36.5	35.4	438	2	D90994	metadate metaboli	789	36	35.0	332	2	E36717	probable transact
717	36.5	35.4	460	2	JC5137	beta-glucosidase (	790	36	35.0	336	2	S09532	int protein - phag
718	36.5	35.4	501	2	H69119	hypothetical prote	791	36	35.0	339	2	E37261	hypothetical prote
719	36.5	35.4	575	1	JC5432	glycoprotein 6-alp	792	36	35.0	368	1	BGHUN	biglycan precursor
720	36.5	35.4	669	2	AB2028	hypothetical prote	793	36	35.0	370	1	S68187	choline-phosphate
721	36.5	35.4	705	2	B75371	ABC transporter, A	794	36	35.0	370	2	B70310	conserved hypothet
722	36.5	35.4	708	2	T02005	hypothetical prote	795	36	35.0	370	2	D71080	hypothetical prote
723	36.5	35.4	779	2	T47756	phosphatidylinosit	796	36	35.0	372	2	AB3466	mandelate racemase
724	36.5	35.4	859	2	S69700	hypothetical prote	797	36	35.0	380	2	S49116	hypothetical prote
725	36.5	35.4	958	2	T02741	probable ligand-ga	798	36	35.0	381	2	A83514	conserved hypothet
726	36.5	35.4	1066	2	T30903	arachidonate 8-lip	799	36	35.0	387	2	AH1050	conserved hypothet
727	36.5	35.4	1148	2	T09073	splicing factor Si	800	36	35.0	387	2	H86445	probable G-Box bin
728	36.5	35.4	1321	2	AI1592	phage protein homo	801	36	35.0	389	2	JS0671	sarcosine oxidase
729	36.5	35.4	6420	2	T30283	polyketide synthas	802	36	35.0	393	2	F64161	hypothetical prote
730	36	35.0	10	2	A61337	caerulein - frog (	803	36	35.0	397	1	AJMXRV	argininosuccinate
731	36	35.0	62	2	I36967	gene MHC DQ-alpha	804	36	35.0	398	2	H72660	probable N-Acylami
732	36	35.0	63	2	B34513	MHC class II histo	805	36	35.0	404	2	S75792	hypothetical prote
733	36	35.0	87	2	C30575	MHC class II histo	806	36	35.0	408	2	F86729	30S ribosomal prot
734	36	35.0	97	1	F87A	ferredoxin [2Fe-2S	807	36	35.0	408	2	B84518	hypothetical prote
735	36	35.0	99	2	B87374	transcription regu	808	36	35.0	411	2	T04987	hypothetical prote
736	36	35.0	100	2	C72655	hypothetical prote	809	36	35.0	414	2	B86230	hypothetical prote
737	36	35.0	109	2	AI3379	glutathione transf	810	36	35.0	423	2	T23223	hypothetical prote
738	36	35.0	122	1	S58294	myb-related protei	811	36	35.0	431	2	AB2949	MPS permease (mono
739	36	35.0	130	2	H71415	hypothetical prote	812	36	35.0	433	2	H58333	hypothetical prote
740	36	35.0	173	2	JC2356	gamma-crystallin M	813	36	35.0	438	2	H75477	chorismate synthas
741	36	35.0	172	2	D98083	conserved hypothet	814	36	35.0	445	2	A97321	6-phospho-alpha-gl
742	36	35.0	193	2	B82063	conserved hypothet	815	36	35.0	453	2	AB2122	hypothetical prote
743	36	35.0	202	2	D72573	hypothetical prote	816	36	35.0	455	1	T21089	acid phosphatase (
744	36	35.0	211	1	CYRTB3	beta-crystallin B3	817	36	35.0	455	1	A69753	glucarate dehydrat
745	36	35.0	213	2	D84565	probable protein k	818	36	35.0	463	2	F69778	transcription regu
746	36	35.0	222	2	F98291	orf, similar to se	819	36	35.0	467	2	AF1983	3-isopropylmalate
747	36	35.0	226	2	A70436	hypothetical prote	820	36	35.0	469	2	H83591	S-adenosyl-L-homoc
748	36	35.0	230	2	B70732	hypothetical prote	821	36	35.0	469	2	A87467	glycosyl hydrolase
749	36	35.0	233	1	R3YM3C	ribosomal protein	822	36	35.0	472	1	A53236	transcription fact
750	36	35.0	242	2	C95139	probable phosphopr	823	36	35.0	472	2	A83738	uronate isomerase
751	36	35.0	249	2	E84717	probable MYB fami	824	36	35.0	475	2	T27811	hypothetical prote
752	36	35.0	249	2	A92222	conserved hypothet	825	36	35.0	477	2	T01828	hypothetical prote
753	36	35.0	249	2	B87309	hypothetical prote	826	36	35.0	485	2	E70363	4-alpha-glucanotra
754	36	35.0	253	2	E84289	hypothetical prote	827	36	35.0	489	2	S47608	actin homolog YJL0
755	36	35.0	257	2	T03825	myb protein homolo	828	36	35.0	494	2	G82356	ketol-acid reducto
756	36	35.0	257	2	T12092	G-box-binding prot	829	36	35.0	499	1	B29042	nitrogenase (BC 1
757	36	35.0	258	2	T48247	expansin-like prot	830	36	35.0	500	2	T52642	transcription init
758	36	35.0	262	2	S51830	alpha-amylase inhi	831	36	35.0	500	2	B41853	hexose phosphate t
759	36	35.0	262	2	S51830		832	36	35.0	502	2	H96671	RNA polymerase sig

833	36	35.0	507	2	T08337	hypothetical prote	906	35.5	34.5	137	2	I80175	class I histocompa
834	36	35.0	529	2	A86428	probable lipase [i	907	35.5	34.5	137	2	I80173	class I histocompa
835	36	35.0	549	2	S04845	lg heavy chain pre	908	35.5	34.5	137	2	I80176	class I histocompa
836	36	35.0	554	2	H82255	asparagine synthas	909	35.5	34.5	137	2	I80174	class I histocompa
837	36	35.0	561	2	T46845	K+-transporting AR	910	35.5	34.5	137	2	I38875	MHC class I antige
838	36	35.0	563	2	D82846	asparagine synthas	911	35.5	34.5	137	2	I38860	MHC class I antige
839	36	35.0	566	2	T16375	hypothetical prote	912	35.5	34.5	137	2	I38874	MHC class I antige
840	36	35.0	574	2	G83794	hypothetical prote	913	35.5	34.5	137	2	I38876	MHC class I antige
841	36	35.0	579	2	A81855	hypothetical prote	914	35.5	34.5	153	2	A12636	conserved hypothet
842	36	35.0	586	2	A27763	succinate dehydrog	915	35.5	34.5	167	2	H97418	hypothetical prote
843	36	35.0	588	1	FWCNAB	alpha-globulin B p	916	35.5	34.5	174	2	T41733	cytochrome c oxida
844	36	35.0	589	2	D84036	succinate dehydrog	917	35.5	34.5	177	2	S54778	NR-13 protein - qu
845	36	35.0	598	2	T38241	probable U3 small	918	35.5	34.5	181	2	I59188	MHC cell surface g
846	36	35.0	599	2	JC8009	choline dehydrogen	919	35.5	34.5	255	2	I54307	MHC HLA-A30J3 heav
847	36	35.0	610	2	T06280	probable starch sy	920	35.5	34.5	267	2	C97690	exodeoxyribonuclea
848	36	35.0	612	2	T36880	hypothetical prote	921	35.5	34.5	267	2	AH2915	exodeoxyribonuclea
849	36	35.0	613	2	I39295	X-linked PRGT-cont	922	35.5	34.5	270	1	HLHU28	MHC class I histoc
850	36	35.0	627	2	E95107	choline binding pr	923	35.5	34.5	273	1	HLHU40	MHC class I histoc
851	36	35.0	646	2	T01079	sulfate transport	924	35.5	34.5	273	1	HLHU69	MHC class I histoc
852	36	35.0	655	2	S64749	probable membrane	925	35.5	34.5	273	2	I38509	MHC class I histoc
853	36	35.0	680	2	D86925	probable acyl-CoA	926	35.5	34.5	274	1	HLHU32	MHC class I histoc
854	36	35.0	682	2	C56591	E75 B steroid rece	927	35.5	34.5	274	1	I68774	MHC HLA-B39 chain
855	36	35.0	705	2	T34313	hypothetical prote	928	35.5	34.5	274	2	I54463	MHC HLA-B38 chain
856	36	35.0	723	2	E83971	penicillin-binding	929	35.5	34.5	274	2	S24439	class I histocompa
857	36	35.0	731	2	T08855	nephrocystin - hum	930	35.5	34.5	277	2	T06760	hypothetical prote
858	36	35.0	757	2	T16349	hypothetical prote	931	35.5	34.5	285	2	A95846	probable EGF-sigma
859	36	35.0	757	2	E97230	trehalose/maltose	932	35.5	34.5	292	2	T05317	hypothetical prote
860	36	35.0	759	2	G86506	hypothetical prote	933	35.5	34.5	305	2	S07115	class I histocompa
861	36	35.0	759	2	G72115	hypothetical prote	934	35.5	34.5	308	2	I36956	MHC class I histoc
862	36	35.0	765	2	H70763	probable glycy prot	935	35.5	34.5	318	2	A13090	MHC class I histoc
863	36	35.0	779	2	E81287	hypothetical prote	936	35.5	34.5	320	2	A96196	hypothetical prote
864	36	35.0	812	2	A83379	glycogen phosphory	937	35.5	34.5	322	2	A21125	MHC class I histoc
865	36	35.0	819	2	F75196	pyruvate, water di	938	35.5	34.5	325	2	S20045	MHC class I histoc
866	36	35.0	821	2	B71229	pyruvate, water di	939	35.5	34.5	326	2	A32273	MHC class I histoc
867	36	35.0	834	1	WMVXPJ	rRNA replicase 2 (E	940	35.5	34.5	332	2	S06424	MHC class I histoc
868	36	35.0	839	2	A56337	glycoprotein phosp	941	35.5	34.5	333	2	D64979	molt 3 protein - E
869	36	35.0	848	2	E86443	probable G-protein	942	35.5	34.5	338	2	I56116	MHC class I histoc
870	36	35.0	865	2	D72206	valine-tRNA ligase	943	35.5	34.5	339	2	A37028	MHC class I histoc
871	36	35.0	866	2	S57936	CotC protein precu	944	35.5	34.5	342	2	S33355	class I histocompa
872	36	35.0	868	2	G72085	2-oxoglutarate deh	945	35.5	34.5	350	2	I54308	MHC class I lympho
873	36	35.0	908	2	H86537	oxoglutarate dehyd	946	35.5	34.5	350	2	I68747	MHC class I histoc
874	36	35.0	908	2	T50695	secA protein limpo	947	35.5	34.5	354	2	S24433	class I histocompa
875	36	35.0	909	2	AG3419	phage host specif	948	35.5	34.5	354	2	I59308	class I histocompa
876	36	35.0	955	2	S44622	C50C3.3 protein -	949	35.5	34.5	354	2	I80166	class I histocompa
877	36	35.0	1003	2	A38234	oxoglutarate dehyd	950	35.5	34.5	354	2	I80167	class I histocompa
878	36	35.0	1023	2	B59430	KIAA0189 protein (	951	35.5	34.5	354	2	I80165	class I histocompa
879	36	35.0	1042	2	S43904	hyaluronidase - Cl	952	35.5	34.5	354	2	I80170	class I histocompa
880	36	35.0	1051	2	C95367	conserved hypotet	953	35.5	34.5	354	2	I80168	class I histocompa
881	36	35.0	1077	2	S66842	hypothetical prote	954	35.5	34.5	354	2	S24438	class I histocompa
882	36	35.0	1112	2	S70522	cyclic nucleotide	955	35.5	34.5	354	2	S24436	class I histocompa
883	36	35.0	1306	1	A31759	peptidyl-di-peptida	956	35.5	34.5	354	2	S24440	class I histocompa
884	36	35.0	1309	1	S35484	peptidyl-di-peptida	957	35.5	34.5	354	2	S24437	class I histocompa
885	36	35.0	1312	1	A34171	peptidyl-di-peptida	958	35.5	34.5	355	2	I80171	class I histocompa
886	36	35.0	1313	1	JC2038	peptidyl-di-peptida	959	35.5	34.5	355	2	I80169	class I histocompa
887	36	35.0	1387	2	A96771	hypothetical prote	960	35.5	34.5	355	2	I37516	HLA-B alpha-chain
888	36	35.0	1415	2	T08945	hypothetical prote	961	35.5	34.5	356	2	A21198	H-2 class I histoc
889	36	35.0	1462	1	S32437	pol polyprotein -	962	35.5	34.5	357	2	S11136	class I histocompa
890	36	35.0	1502	2	D84587	probable myosin he	963	35.5	34.5	357	2	S11137	class I histocompa
891	36	35.0	1515	2	S51824	myosin heavy chain	964	35.5	34.5	357	2	S11133	class I histocompa
892	36	35.0	1643	2	T07961	myosin heavy chain	965	35.5	34.5	357	2	S11140	class I histocompa
893	36	35.0	1674	2	T01265	scarch synthase DU	966	35.5	34.5	357	2	I36966	MHC class I protei
894	36	35.0	1805	2	A34736	nestin - rat	967	35.5	34.5	357	2	I36965	MHC class I protei
895	36	35.0	2186	2	T13169	tiggrin - fruit fl	968	35.5	34.5	358	2	S03538	class I histocompa
896	36	35.0	2606	2	T03159	large tegument pro	969	35.5	34.5	358	1	HLHUB4	MHC class I histoc
897	36	35.0	2869	2	T18518	apolipoprotein(a)	970	35.5	34.5	359	2	I67483	MHC class I heavy
898	36	35.0	3519	2	S43048	polyketide synthas	971	35.5	34.5	361	2	I54418	MHC class I histoc
899	36	35.0	4367	1	B54802	dynein heavy chain	972	35.5	34.5	361	2	B27638	MHC class I histoc
900	36	35.0	4613	2	T17409	polyketide synthas	973	35.5	34.5	361	2	I46030	MHC class I antige
901	36	35.0	13055	2	T16580	hypothetical prote	974	35.5	34.5	361	2	I48160	MHC class I protei
902	35.5	34.5	47	2	A47204	feline class I maj	975	35.5	34.5	362	1	HLHUB8	MHC class I histoc
903	35.5	34.5	65	2	S51099	MHC class I histoc	976	35.5	34.5	362	1	HLHU40	MHC class I histoc
904	35.5	34.5	115	2	AE1417	hypothetical prote	977	35.5	34.5	362	1	HLHUB2	MHC class I histoc
905	35.5	34.5	137	2	I80172	class I histocompa	978	35.5	34.5	362	1	HLHUB7	MHC class I histoc

979 35.5 34.5 362 1 HLMSDB  
 980 35.5 34.5 362 2 JH0541  
 981 35.5 34.5 362 2 JH0539  
 982 35.5 34.5 362 2 JH0540  
 983 35.5 34.5 362 2 J35962  
 984 35.5 34.5 362 2 I8486  
 985 35.5 34.5 362 2 I62042  
 986 35.5 34.5 362 2 I37492  
 987 35.5 34.5 362 2 I37120  
 988 35.5 34.5 362 2 S52486  
 989 35.5 34.5 362 2 B30345  
 990 35.5 34.5 362 2 A45834  
 991 35.5 34.5 362 2 I61907  
 992 35.5 34.5 362 2 I38421  
 993 35.5 34.5 362 2 I37515  
 994 35.5 34.5 362 2 C35997  
 995 35.5 34.5 362 2 I61861  
 996 35.5 34.5 362 2 I56149  
 997 35.5 34.5 362 2 A45850  
 998 35.5 34.5 362 2 I81233  
 999 35.5 34.5 362 2 I61864  
 1000 35.5 34.5 362 2 I72755

MHC class I histoc  
 class I histocompa  
 class I histocompa  
 class I histocompa  
 MHC class I protei  
 transmembrane glyco  
 MHC HLA-B cell sur  
 HLA-B alpha-chain  
 MHC class I histoc  
 HLA-B protein alph  
 MHC class I histoc  
 MHC class I histoc  
 MHC class I histoc  
 gene HLA B-1519 pr  
 MHC class I histoc  
 MHC class I histoc  
 MHC class I histoc  
 MHC HLA-B44.2 chai  
 lymphocyte antigen  
 MHC class I histoc  
 lymphocyte antigen  
 MHC HLA-Bw41 chain  
 HLA-B\*5602 - human

## ALIGNMENTS

RESULT 1  
 GWHUB  
 Gastrin precursor [validated] - human  
 N:Contains: big gastrin; cryptagastrin; gastrin; gastrin-17  
 C:Species: Homo sapiens (man)  
 C>Date: 24-Apr-1984 #sequence revision 30-Jun-1987 #text change 09-Jul-2004  
 C:Accession: A93997; A93497; A94473; A93152; A91628; A18854; A40869; A32487; B32487; C32487  
 R:Ito, R.; Sato, K.; Helmer, T.; Jay, G.; Agarwal, K.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 4662-4666, 1984  
 A>Title: Structural analysis of the gene encoding human gastrin: the large intron contains a 17-residue repeat  
 A:Reference number: A93997; MUID:84272693; PMID:6087340  
 A:Accession: A93997  
 A:Molecule type: DNA  
 A:Residues: 1-101 <TO>  
 A:Cross-references: UNIPROT:P01350; UNIPARC:UPI000012B0F4; GB:K01254; GB:J00147; NID:g18  
 R:Kato, K.; Hayashizaki, Y.; Takahashi, Y.; Himeno, S.; Matsubara, K.  
 Nucleic Acids Res. 11, 8197-8203, 1983  
 A>Title: Molecular cloning of the human gastrin gene.  
 A:Reference number: A93497, MUID:84169471; PMID:6324077  
 A:Accession: A93497  
 A:Molecule type: DNA  
 A:Residues: 1-101 <XAT>  
 A:Cross-references: UNIPARC:UPI000012B0F4; GB:X00183; NID:g31648; PIDN:CAA25005.1; PID:g  
 R:Harris, J.I.; Kenner, E.W.  
 unpublished results, cited by Gregory, R.A., and Tracy, H.J., in Gastrointestinal Hormon  
 A:Reference number: A94473  
 A:Accession: A94473  
 A:Molecule type: protein  
 A:Residues: 59-64, 'H', '66', 'S', '68-92 <HAR>  
 A:Cross-references: UNIPARC:UPI0000173595  
 A:Experimental source: Gastrinoma tissue  
 R:Bentley, P.H.; Kenner, G.W.; Sheppard, R.C.  
 Nature 209, 583-585, 1966  
 A>Title: Human gastrin isolation, structure and synthesis.  
 A:Reference number: A93152; MUID:67021327; PMID:5921183  
 A:Accession: A93152  
 A:Molecule type: protein  
 A:Residues: 76-92 <BEN>  
 A:Cross-references: UNIPARC:UPI000014A9F1  
 A>Note: Gastrin comprises the carboxyl-terminal 17 residues of big gastrin  
 R:Gregory, R.A.; Tracy, H.J.; Agarwal, K.L.; Grossman, M.I.  
 Gut 10, 603-608, 1969  
 A>Title: Aminoacid constitution of two gastrins isolated from Zollinger-Ellison tumour b  
 A:Reference number: A91628; MUID:69298172; PMID:5822140  
 A:Accession: A91628  
 A:Molecule type: protein

A:Residues: 76-92 <GRE>  
 A:Cross-references: UNIPARC:UPI000014A9F1  
 A>Note: the gastrin was isolated from human Zollinger-Ellison pancreatic tumor  
 R:Wiborg, O.; Berglund, L.; Boel, E.; Norris, F.; Rehfeld, J.F.; Marcker, K.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 1067-1069, 1984  
 A>Title: Structure of a human gastrin gene. PMID:6322186  
 A:Reference number: A18854; MUID:84144842; PMID:6322186  
 A:Accession: A18854  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-101 <WTB>  
 A:Cross-references: UNIPARC:UPI000012B0F4; GB:K01254; GB:J00147; NID:g182987; PIDN:AA859  
 R:Huebner, V.D.; Jiang, R.; Lee, T.D.; Legesse, K.; Walsh, J.H.; Shively, J.E.; Chew, P.  
 J. Biol. Chem. 266, 12223-12227, 1991  
 A>Title: Purification and structural characterization of progastrin-derived peptides fro  
 A:Reference number: A40869; MUID:91286236; PMID:2061307  
 A:Accession: A40869  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 22-51 <HUB>  
 A:Cross-references: UNIPARC:UPI0000173596  
 R:Higashimoto, Y.; Himeno, S.; Shinomura, Y.; Nagao, K.; Tamura, T.; Tarui, S.  
 Biochem. Biophys. Res. Commun. 160, 1364-1370, 1989  
 A>Title: Purification and structural determination of urinary NH-2-terminal big gastrin  
 A:Reference number: A32487; MUID:89273602; PMID:2730647  
 A:Accession: A32487  
 A:Molecule type: protein  
 A:Residues: 59-67 <HI2>  
 A:Cross-references: UNIPARC:UPI000014A9EF  
 A:Experimental source: urine  
 A>Note: this urinary fragment of big gastrin was designated peak Ia  
 A:Accession: B32487  
 A:Molecule type: protein  
 A:Residues: 59-66 <HI3>  
 A:Cross-references: UNIPARC:UPI0000173597  
 A:Experimental source: urine  
 A>Note: this urinary fragment of big gastrin was designated peak Ib  
 A:Accession: C32487  
 A:Molecule type: protein  
 A:Residues: 59-68 <HI4>  
 A:Cross-references: UNIPARC:UPI0000173598  
 A:Experimental source: urine  
 A>Note: this urinary fragment of big gastrin was designated peak II  
 R:Higashimoto, Y.; Shinomura, Y.; Nagao, K.; Yasunaga, Y.; Tamura, T.; Tarui, S.  
 Biochem. Biophys. Res. Commun. 172, 1392-1399, 1990  
 A>Title: Purification of N-terminal hexapeptide of big gastrin from human urine.  
 A:Reference number: A36249; MUID:91058586; PMID:2244919  
 A:Accession: A36249  
 A:Molecule type: protein  
 A:Residues: 59-64 <HIG>  
 A:Cross-references: UNIPARC:UPI0000173599  
 A>Note: this urinary fragment of big gastrin was designated peak III  
 R:Boel, E.; Vuust, J.; Norris, F.; Norris, K.; Wind, A.; Rehfeld, J.F.; Marcker, K.A.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 2866-2869, 1983  
 A>Title: Molecular cloning of human gastrin cDNA: evidence for evolution of gastrin by g  
 A:Reference number: 137408; MUID:83221503; PMID:6574456  
 A:Accession: 137408  
 A:Molecule type: mRNA  
 A:Residues: 1-101 <RES>  
 A:Cross-references: UNIPARC:UPI000012B0F4; EMBL:V00511; NID:g31654; PIDN:CAA23769.1; PII  
 R:Rehfeld, J.F.; Johnsen, A.H.  
 Eur. J. Biochem. 223, 765-773, 1994  
 A>Title: Identification of gastrin component I as gastrin-71. The largest possible bioac  
 A:Reference number: S48183; MUID:94333379; PMID:8055952  
 A:Accession: S48183  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 22-40 <REH>  
 A:Cross-references: UNIPARC:UPI000017359A  
 R:Kariya, Y.; Kato, K.; Hayashizaki, Y.; Himeno, S.; Tarui, S.; Matsubara, K.  
 Gene 50, 345-352, 1986  
 A>Title: Expression of human gastrin gene in normal and gastrinoma tissues.  
 A:Reference number: 154006; MUID:87219893; PMID:3034736

A;Accession: I54006  
 A;Status: translated from GB/EMBL/DBDJ  
 A;Molecule type: DNA  
 A;Residues: 1-101 <KAR>  
 A;Cross-references: UNIPARC:UPI000012B0F4; GB:M15958; NID:g182990; PIDN:AAAS2520.1; PID:EMBO J. 14, 389-396, 1995  
 R;Bahfeld, J.F.; Hansen, C.P.; Johnsen, A.H.  
 A;Title: Post-poly(Glu) cleavage and degradation modified by O-sulfated tyrosine: a novel  
 A;Reference number: S54350; MUID:95137019; PMID:7530658  
 A;Accession: S54350  
 A;Molecule type: protein  
 A;Residues: 76-92 <REW>  
 A;Cross-references: UNIPARC:UPI000014A9F1  
 A;Note: Gastrin-6 isolated from gastric mucosa and blood is fully active; sulfation of it  
 C;Genetics:  
 A;Gene: GDB:GAS  
 A;Cross-references: GDB:119261; OMIM:137250  
 A;Map position: 17q-17q  
 A;Introns: 71/1  
 C;Superfamily: Gastrin  
 C;Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein  
 F;1-21/Domain: signal sequence #status predicted <SIG>  
 F;22-56/Product: cryptogastrin (amino-terminal propeptide) #status experimental <PRO>  
 F;59-92/Product: big gastrin #status experimental <BGN>  
 F;76-92/Product: gastrin #status experimental <SGN>  
 F;78-92/Product: gastrin-6 #status experimental <GN6>  
 F;79/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #link BGN #status  
 F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #link SGN #status  
 F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
 F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 97.1%; Score 100; DB 1; Length 101;  
 Best Local Similarity 94.1%; Pred. No. 1.6e-07;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDF 17  
 :|||||  
 Db 76 QGPWLEEEERAYGWMDF 92

RESULT 2  
 GMPGB  
 Gastrin precursor [validated] - pig  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 17-Dec-1982 #sequence revision 17-Dec-1982 #text change 09-Jul-2004  
 C;Accession: A93903; B94473; A93148; I46622; A60070; A01618  
 R;Yoo, O.J.; Powell, C.T.; Agarwal, K.L.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 1049-1053, 1982  
 A;Title: Molecular cloning and nucleotide sequence of full-length cDNA coding for porcine  
 A;Reference number: A93903; MUID:82174533; PMID:6951161  
 A;Accession: A93903  
 A;Molecule type: mRNA  
 A;Residues: 1-104 <YOO>  
 A;Cross-references: UNIPROT:P01351; UNIPARC:UPI000012B0F6; GB:V01303; GB:J00651; NID:g18  
 R;Harris, J.I.; Kenner, E.W.  
 unpublished results, cited by Gregory, R.A., and Tracy, H.J., in Gastrointestinal Hormon  
 A;Reference number: A94473  
 A;Accession: B94473  
 A;Molecule type: protein  
 A;Residues: 59-64, HPP, 68-92 <HAR>  
 A;Cross-references: UNIPARC:UPI000017359B  
 A;Note: Tyr-87 is sulfated in two-thirds of the molecules  
 A;Note: this peptide was extracted from the antral mucosa  
 R;Gregory, H.; Hardy, P.M.; Jones, D.S.; Kenner, G.W.; Sheppard, R.C.  
 Nature 204, 931-933, 1964  
 A;Title: The antral hormone gastrin.  
 A;Reference number: A93148  
 A;Accession: A93148  
 A;Molecule type: protein  
 A;Residues: 76-92 <GRB>  
 A;Cross-references: UNIPARC:UPI000017359C  
 R;Anderson, J.C.; Barton, M.A.; Gregory, R.A.; Hardy, P.M.; Kenner, G.W.; MacLeod, J.K.;  
 Nature 204, 933-934, 1964

A;Reference number: A93149  
 A;Contents: annotation; synthesis  
 R;Agarwal, K.L.; Noyes, B.E.  
 Ann. N. Y. Acad. Sci. 343, 433-442, 1980  
 A;Title: Studies on gastrin mRNA structure using an oligonucleotide probe.  
 A;Reference number: I46622; MUID:80240380; PMID:6930858  
 A;Accession: I46622  
 A;Status: translated from GB/EMBL/DBDJ  
 A;Molecule type: mRNA  
 A;Residues: 56-82 <AGA>  
 A;Cross-references: UNIPARC:UPI000016C6EA; GB:M25036; NID:g164626; PIDN:AAA31111.1; PID:R;Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.  
 Regul. Pept. 25, 223-233, 1989  
 A;Title: The constitution and properties of phosphorylated and unphosphorylated C-term  
 A;Reference number: A60070; MUID:89331947; PMID:2756156  
 A;Accession: A60070  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 97-104 <DES>  
 A;Cross-references: UNIPARC:UPI000017359D  
 C;Superfamily: gastrin  
 C;Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein  
 F;1-21/Domain: signal sequence #status predicted <SIG>  
 F;22-56/Domain: amino-terminal propeptide #status predicted <PRO>  
 F;59-92/Product: big gastrin #status experimental <BGN>  
 F;76-92/Product: gastrin #status experimental <SGN>  
 F;79/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experime  
 F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experime  
 F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
 F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gl  
 F;96/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 95.1%; Score 98; DB 1; Length 104;  
 Best Local Similarity 88.2%; Pred. No. 3.2e-07;  
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDF 17  
 :|||||  
 Db 76 QGPWLEEEERAYGWMDF 92

RESULT 3  
 GMPCT  
 Gastrin precursor [validated] - cat  
 N;Contains: big gastrin (gastrin-34); Gastrin  
 C;Species: Felis silvestris catus (domestic cat)  
 C;Date: 13-Jun-1983 #sequence revision 02-Jun-1994 #text change 09-Jul-2004  
 C;Accession: S14401; A01621; A61074  
 R;Kim, S.J.; Uhm, K.N.; Kang, Y.K.; Yoo, O.J.  
 DNA Seq. 1, 181-187, 1991  
 A;Title: Bovine and feline gastrin cDNA sequences and the amino acid and nucleotide seq  
 A;Reference number: S14400; MUID:92127058; PMID:1773057  
 A;Accession: S14401  
 A;Molecule type: mRNA  
 A;Residues: 1-104 <KIM>  
 A;Cross-references: UNIPROT:P01354; UNIPARC:UPI000012B0F2; EMBL:X16582; NID:g1099; PIDN:R;Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.  
 J. Am. Chem. Soc. 91, 3096-3097, 1969  
 A;Title: Feline gastrin. An example of peptide sequence analysis by mass spectrometry.  
 A;Reference number: A01621; MUID:69206035; PMID:5784957  
 A;Accession: A01621  
 A;Molecule type: protein  
 A;Residues: 76-92 <AGA>  
 A;Cross-references: UNIPARC:UPI00001735A3  
 R;Eng, J.; Du, B.H.; Johnson, G.F.; Kanakamedala, S.; Samuel, S.; Raufman, J.P.; Straus  
 Regul. Pept. 37, 9-13, 1992  
 A;Title: Cat gastrinoma and the sequence of cat gastrins.  
 A;Reference number: A61074; MUID:92262853; PMID:1585019  
 A;Accession: A61074  
 A;Molecule type: protein  
 A;Residues: 59-92 <ENG>  
 A;Cross-references: UNIPARC:UPI00001735A4  
 C;Superfamily: Gastrin

C:Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:59-92/Product: big gastrin #status experimental <BNAT>  
 F:76-92/Product: gastrin #status experimental <MAT>  
 F:76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental  
 F:87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
 F:92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 91.3%; Score 94; DB 1; Length 104;  
 Best Local Similarity 88.2%; Pred. No. 1.2e-06;  
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMD 17  
 DB 76 QGPWLEEEEAAYGWMD 92

RESULT 4  
 A60071  
 Gastrin - rhesus macaque  
 C:Species: Macaca mulatta (rhesus macaque)  
 C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 09-Jul-2004  
 C:Accession: A60071  
 R:Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.  
 Regul. Pept. 32, 39-45, 1991  
 A:Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences.  
 A:Reference number: A60071; MUID:91164506; PMID:2003150  
 A:Accession: A60071  
 A:Molecule type: protein  
 A:Residues: 1-17 <Y>  
 A:Cross-references: UNIPROT:P33714; UNIPARC:UPI000012B0F5  
 C:Superfamily: Gastrin  
 C:Keywords: amidated carboxyl end; hormone; intestine; pyroglutamic acid; sulfoprotein  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:12/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
 F:17/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 89.3%; Score 92; DB 2; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 3.1e-07;  
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMD 17  
 DB 1 QGPWLEEEEAAYGWMD 17

RESULT 5  
 GMDG  
 Gastrin precursor [validated] - dog  
 N:Contains: big gastrin; gastrin  
 C:Species: Canis lupus familiaris (dog)  
 C:Date: 13-Jun-1983 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
 C:Accession: B61053; A61053; J50425; A01620; B60070  
 R:Gantz, I.; Takeuchi, T.; Yamada, T.  
 Digestion 46, 99-104, 1990  
 A:Title: Cloning of canine gastrin cDNA's encoding variant amino acid sequences.  
 A:Reference number: A61053; MUID:91085716; PMID:2262079  
 A:Accession: B61053  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-104 <GAN>  
 A:Cross-references: UNIPROT:P01353; UNIPARC:UPI000012B0ED  
 A:Accession: A61053  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-84, 'T', '86-104 <GA2>  
 A:Cross-references: UNIPARC:UPI000017359E  
 A:Note: it is unclear whether the sequence difference results from polymorphism, multiple  
 R:Bonato, C.; Eng, J.; Hulmes, J.D.; Miedel, M.; Pan, Y.C.E.; Yalow, R.S.  
 Peptides 7, 689-693, 1986  
 A:Title: Sequences of gastrins purified from a single antrum of dog and of goat.  
 A:Reference number: J50425; MUID:87016557; PMID:3763441  
 A:Accession: J50425

A:Molecule type: protein  
 A:Residues: 59-92 <BON>  
 A:Cross-references: UNIPARC:UPI000017359F  
 A:Experimental source: antral mucosa  
 A:Note: about 10% of gastrin is sulfated  
 R:Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.  
 Experientia 25, 346-348, 1969  
 A:Title: Structure and synthesis of canine gastrin.  
 A:Reference number: A01620; MUID:69253357; PMID:5799207  
 A:Accession: A01620  
 A:Molecule type: protein  
 A:Residues: 76-82, 'A', '84', 'E', '86-92 <AGA>  
 A:Cross-references: UNIPARC:UPI00001735A0  
 R:Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.  
 Regul. Pept. 25, 223-233, 1989  
 A:Title: The constitution and properties of phosphorylated and unphosphorylated C-terminin  
 A:Reference number: A60070; MUID:89331947; PMID:2756156  
 A:Accession: B60070  
 A:Molecule type: protein  
 A:Residues: 96-104 <DES>  
 A:Cross-references: UNIPARC:UPI00001735A1  
 C:Comment: Big gastrin constitutes only about 5% of antral gastrin.  
 C:Superfamily: Gastrin  
 C:Keywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic acid;  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:59-92/Product: big gastrin #status experimental <MAT>  
 F:76-92/Product: gastrin #status experimental <MAT>  
 F:59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental  
 F:76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental  
 F:87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
 F:92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly  
 F:96/Binding site: phosphate (Ser) (covalent) (partial) #status experimental

Query Match 89.3%; Score 92; DB 1; Length 104;  
 Best Local Similarity 82.4%; Pred. No. 2.4e-06;  
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMD 17  
 DB 76 QGPWLEEEEAAYGWMD 92

RESULT 6  
 GMSH  
 Gastrin - sheep  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 13-Jun-1983 #sequence\_revision 13-Jun-1983 #text\_change 20-Mar-1998  
 C:Accession: A01619  
 R:Agarwal, K.L.; Beacham, J.; Bentley, P.H.; Gregory, R.A.; Kenner, G.W.; Sheppard, R.C.  
 Nature 219, 614-615, 1968  
 A:Title: Isolation, structure and synthesis of ovine and bovine gastrins.  
 A:Reference number: A01619; MUID:68357500; PMID:5665711  
 A:Accession: A01619  
 A:Molecule type: protein  
 A:Residues: 1-17 <AGA>  
 A:Cross-references: UNIPARC:UPI00001735A2  
 C:Superfamily: Gastrin  
 C:Keywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic acid;  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:12/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
 F:17/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 88.3%; Score 91; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 4.3e-07;  
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMD 17  
 DB 1 QGPWLEEEEAAYGWMD 17

RESULT 7  
 JS0426

big gastrin - goat  
N/Contains: gastrin  
C/Species: Capra aegagrus hircus (domestic goat)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C/Accession: J50426  
R/Bonato, C.; Eng, J.; Hulmes, J.D.; Miedel, M.; Pan, Y.C.E.; Yalow, R.S.  
Peptides 7, 689-693, 1986  
A/Title: Sequences of gastrins purified from a single antrum of dog and of goat.  
A/Reference number: J50425; MUID:87016557; PMID:3763441  
A/Molecule type: protein  
A/Accession: J50426  
A/Residues: 1-34 <BON>  
A/Cross-references: UNIPROT:P04564; UNIPARC:UPI0000012B0EE  
A/Experimental source: antrum  
A/Note: about 90% of gastrin is sulfated  
C/Superfamily: gastrin  
C/Keywords: amidated carboxyl end; hormone; pancreas; pyroglutamic acid; secretagogue; gastrin  
P/1-34/Product: big gastrin #status experimental <BGS>  
P/18-34/Product: gastrin #status experimental <GSN>  
P/1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
P/18/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experimental  
P/23/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
P/34/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 88.3%; Score 91; DB 2; Length 34;  
Best Local Similarity 82.4%; Pred. No. 9.3e-07; Indels 0; Gaps 0;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYGWMDF 17  
:|||||  
DB 18 QGPWVEEEAYGWMDF 34

RESULT 8  
GMOB  
gastrin precursor [validated] - bovine  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 31-Dec-1991 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
C/Accession: S14400; A41409; B01619; A01619  
R/Kim, S.J.; Uhm, K.N.; Kang, Y.K.; Yoo, O.J.  
DNA Seq. 1, 181-187, 1991  
A/Title: Bovine and feline gastrin cDNA sequences and the amino acid and nucleotide sequences  
A/Reference number: S14400; MUID:92127058; PMID:1773057  
A/Accession: S14400  
A/Molecule type: mRNA  
A/Residues: 1-104 <KIM>  
A/Cross-references: UNIPROT:P01352; UNIPARC:UPI000012B0EC; EMBL:X16581; NID:9648; PIDN:C  
P/Lund, T.; Olsen, J.; Rehfeld, J.F.  
Mol. Endocrinol. 3, 1585-1588, 1989  
A/Title: Cloning and sequencing of the bovine gastrin gene.  
A/Reference number: A41409; MUID:90114160; PMID:2608050  
A/Accession: A41409  
A/Molecule type: DNA  
A/Residues: 1-31, 'L', 33-36, 'R', 38-47, 'T', 49-73, 'N', 75-80, 'G', 82-95, 'M', 97-98, 'G', 100-104  
A/Cross-references: UNIPARC:UPI000016C311; GB:M1657; NID:9163079; PIDN:AAA30537.1; PID:  
A/Note: the authors translated the codon CTG for residue 32 as Ala, AAT for residue 39 as  
P/Agarwal, K.L.; Beacham, J.; Bentley, P.H.; Gregory, R.A.; Kenner, G.W.; Sheppard, R.C.  
Nature 219, 614-615, 1968  
A/Title: Isolation, structure and synthesis of ovine and bovine gastrins.  
A/Reference number: A01619; MUID:68357500; PMID:5665711  
A/Accession: B01619  
A/Molecule type: protein  
A/Residues: 76-92 <AGA>  
A/Cross-references: UNIPARC:UPI00001735A2  
C/Genetics:  
A/Introns: 71/1  
C/Superfamily: gastrin  
C/Keywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic acid;  
P/1-19/Domain: signal sequence #status predicted <SIG>  
P/59-92/Product: big gastrin #status predicted <BGN>  
P/76-92/Product: gastrin #status experimental <SGN>  
P/59/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status predicted  
P/76/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experimental

P/87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
P/92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 88.3%; Score 91; DB 1; Length 104;  
Best Local Similarity 82.4%; Pred. No. 3.3e-06;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYGWMDF 17  
:|||||  
DB 76 QGPWVEEEAYGWMDF 92

RESULT 9  
A60506  
big gastrin - North American opossum  
N/Contains: gastrin  
C/Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)  
C/Date: 19-Mar-1993 #sequence\_revision 19-Mar-1993 #text\_change 09-Jul-2004  
C/Accession: A60506  
R/Shinomura, Y.; Eng, J.; Rattan, S.C.; Yalow, R.S.  
Comp. Biochem. Physiol. B 96, 239-242, 1990  
A/Title: Opossum (Didelphis virginiana) "little" and "big" gastrins.  
A/Reference number: A60506; MUID:90298616; PMID:2361360  
A/Accession: A60506  
A/Molecule type: protein  
A/Residues: 1-33 <SHI>  
A/Cross-references: UNIPROT:P33713; UNIPARC:UPI000012B0F1  
C/Superfamily: gastrin  
C/Keywords: amidated carboxyl end; hormone; pyroglutamic acid; sulfoprotein  
P/1-33/Product: big gastrin #status experimental <MATB>  
P/18-33/Product: gastrin #status experimental <MATL>  
P/1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
P/28/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
P/33/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 82.0%; Score 84.5; DB 2; Length 33;  
Best Local Similarity 88.2%; Pred. No. 7.8e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EGPWLEEEAYGWMDF 17  
:|||||  
DB 18 QGPWLEEEAYGWMDF 33

RESULT 10  
A29541  
little gastrin - Chinchilla brevicaudata  
C/Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata  
C/Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 09-Jul-2004  
C/Accession: A29541  
R/Shinomura, Y.; Eng, J.; Yalow, R.S.  
Biochem. Biophys. Res. Commun. 143, 7-14, 1987  
A/Title: Chinchilla "big" and "little" gastrins.  
A/Reference number: A90130; MUID:87156784; PMID:3827930  
A/Accession: A29541  
A/Molecule type: protein  
A/Residues: 1-16 <SHI>  
A/Cross-references: UNIPROT:P10034; UNIPARC:UPI0000176683  
C/Superfamily: gastrin

Query Match 74.3%; Score 76.5; DB 2; Length 16;  
Best Local Similarity 82.4%; Pred. No. 4.9e-05;  
Matches 14; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 EGPWLEEEAYGWMDF 17  
:|||||  
DB 1 EGPWLEEEAYGWMDF 16

RESULT 11  
S68861  
gastrin precursor [similarity] - mouse  
C/Species: Mus musculus (house mouse)

A:Molecule type: mRNA  
A:Residues: 56-92 <SCH>  
A:Cross-references: UNIPARC:UPI000017096C; GB:M25459; NID:g204252; PIDN:AAA41195.1; PID:  
C:Superfamily: gastrin  
F:56-92/Product: gastrin-34 #status predicted <GAS>  
F:74-92/Product: gastrin-17 #status predicted <GAT>  
F:92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match  
Best Local Similarity 72.8%; Score 75; DB 2; Length 104;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEEEEEAYGWMDf 17  
|:|||||  
Db 78 PPMEEEEEAYGWMDf 92

RESULT 13  
GMGPB  
big gastrin [validated] - guinea pig  
N:Contains: gastrin  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 30-Sep-1987 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
C:Accession: A26089  
R:Bonato, C.; Eng, J.; Pan, Y.C.E.; Miedel, M.; Hulmes, J.D.; Yalow, R.S.  
Life Sci. 39, 959-964, 1986  
A:Title: Guinea pig 33-amino acid gastrin.  
A:Reference number: A26089; MUID:86309993; PMID:3747718  
A:Accession: A26089  
A:Molecule type: protein  
A:Residues: 1-33 <BON>  
A:Cross-references: UNIPROT:P06885; UNIPARC:UPI000012B0EF  
C:Comment: Big gastrin constitutes only about 5% of antral gastrin.  
C:Superfamily: gastrin  
C:Keywords: amidated carboxyl end; hormone; pyroglutamic acid  
F:1-33/Product: big gastrin #status experimental <BGN>  
F:18-33/Product: gastrin #status experimental <SGN>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:33/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match  
Best Local Similarity 71.4%; Score 73.5; DB 1; Length 33;  
Matches 13; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EGPWLEEEEEEAYGWMDf 17  
|:|||||  
Db 18 QGPW-AEEEAAYGWMDf 33

RESULT 14  
B29541  
big gastrin - Chinchilla brevicaudata  
C:Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata  
C:Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 09-Jul-2004  
C:Accession: B29541  
R:Shinomura, Y.; Eng, J.; Yalow, R.S.  
Biochem. Biophys. Res. Commun. 143, 7-14, 1987  
A:Title: Chinchilla "big" and "little" gastrins.  
A:Reference number: A90130; MUID:87156784; PMID:3827930  
A:Accession: B29541  
A:Molecule type: protein  
A:Residues: 1-33 <SHI>  
A:Cross-references: UNIPROT:P10034; UNIPARC:UPI000012B0F0  
C:Superfamily: gastrin

Query Match  
Best Local Similarity 71.4%; Score 73.5; DB 2; Length 33;  
Matches 13; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EGPWLEEEEEEAYGWMDf 17  
|:|||||  
Db 18 QGPW-AEEEAAYGWMDf 33

A:Accession: JCT308  
A:Molecule type: DNA  
A:Residues: 1-229 <NAK>  
A:Cross-references: UNIPROT:Q7M4T4; UNIPARC:UPI000017CA62  
A:Experimental source: strain TOP-1212  
A:Accession: PC7087  
A:Molecule type: protein  
A:Residues: 21-37;149-164 <NA2>  
A:Cross-references: UNIPARC:UPI000017CA63; UNIPARC:UPI000017CA64  
C:Genetics:  
A:Gene: eg1  
A:Introns: 147/3  
C:Keywords: glycosidase; hydrolase

Query Match 47.6%; Score 49; DB 2; Length 229;  
Best Local Similarity 58.3%; Pred. No. 9;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PMLSEEEAYGW 14  
|| :|||  
DB 85 PMAVDDEAYGW 96

RESULT 18  
F69837  
asparagine synthase homolog ylsO - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000  
C:Accession: F69837  
R:Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte  
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F  
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecell  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Sero  
teuchi, M.; Tanakaoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tozato, V.; Uchiyama  
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: F69837  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-591 <KUN>  
A:Cross-references: UNIPARC:UPI00000601C9; GB:Z99109; GB:AL009126; NID:G2633260; PIDN:C  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: ylsO  
C:Superfamily: asparagine synthase (glutamine-hydrolyzing)

Query Match 47.6%; Score 49; DB 2; Length 591;  
Best Local Similarity 53.8%; Pred. No. 26;  
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYG 13  
:||||: |||  
DB 290 DGPWLEEEAYG 302

RESULT 19  
E83166  
hypotheical protein PA3844 [imported] - Pseudomonas aeruginosa (strain PAO1)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: E83166  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Li  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin  
A:Reference number: JCT308

A:Accession: JCT308  
A:Molecule type: DNA  
A:Residues: 1-229 <NAK>  
A:Cross-references: UNIPROT:Q7M4T4; UNIPARC:UPI000017CA62  
A:Experimental source: strain TOP-1212  
A:Accession: PC7087  
A:Molecule type: protein  
A:Residues: 21-37;149-164 <NA2>  
A:Cross-references: UNIPARC:UPI000017CA63; UNIPARC:UPI000017CA64  
C:Genetics:  
A:Gene: eg1  
A:Introns: 147/3  
C:Keywords: glycosidase; hydrolase

Query Match 48.5%; Score 50; DB 2; Length 238;  
Best Local Similarity 88.9%; Pred. No. 6.8;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPWLSEEE 10  
|||||:  
DB 12 GPWLSEEE 20

RESULT 16  
F87348  
mannanase, probable [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: F87348  
R:Nierman, W.C.; Feidblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: F87348  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-442 <STO>  
A:Cross-references: UNIPROT:Q9AA10; UNIPARC:UPI00000C718D; GB:A8005673; NID:G13422046; F  
C:Genetics:  
A:Gene: CC0801

Query Match 48.5%; Score 50; DB 2; Length 442;  
Best Local Similarity 35.3%; Pred. No. 14;  
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYGWDP 17  
:||||: |||  
DB 156 DGPWFQGGPAYPQY 172

RESULT 17  
JCT308  
cellulase (SC 3.2.1.4) - Scopulariopsis brevicaulis  
N:Alternate names: endoglucanase I  
C:Species: Scopulariopsis brevicaulis  
C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: JCT308; PC7087  
R:Nakagami, F.; Kawaguchi, T.; Takada, G.; Sumitani, J.; Moriyama, Y.; Arai, M.  
Biochim. Biophys. Acta 1238, 1238-1246, 2000  
A:Title: Cloning and sequencing of an endoglucanase gene from Scopulariopsis brevicaulis  
A:Reference number: JCT308

Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: E83166  
A>Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-203 <STO>  
A:Cross-references: UNIPROT:Q9HXG2; UNIPARC:UPI00000C5B39; GB:AE004081; GB:AE004091; NID  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA3844

Query Match 46.6%; Score 48; DB 2; Length 203;  
Best Local Similarity 47.4%; Pred. No. 11;  
Matches 9; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

QY 2 GPWLEEE-----ENYGWMD 16  
|||||:|:|:|:|:  
Db 122 GPWLERVEGQLLAAYDWLE 140

RESULT 20  
AG1678  
D-alanyl-D-alanine carboxypeptidases homolog lin1969 [imported] - *Listeria innocua* (strain  
C:Species: *Listeria innocua*  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
A:Accession: AG1678  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, H.;  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schluter, T.; Simoes, N.; Tixeret, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
A:Title: Comparative genomics of *Listeria* species  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AG1678  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-274 <GLA>  
A:Cross-references: UNIPROT:Q92AF3; UNIPARC:UPI00000CC6F9; GB:AL592022; PIDN:CAC97199.1;  
A:Experimental source: strain C1p11262  
C:Genetics:  
A:Gene: lin1969

Query Match 45.6%; Score 47; DB 2; Length 274;  
Best Local Similarity 53.3%; Pred. No. 21;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWM 15  
|||:|:|:|:|:  
Db 204 EGKWLSEAHNYGFI 218

RESULT 21  
C75119  
deoxyhypusine synthase (EC 2.5.1.46) dyl1 PAB0511 [similarity] - *Pyrococcus abyssi* (stra  
C:Species: *Pyrococcus abyssi*  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
A:Accession: C75119  
R:Anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A:Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome stru  
A:Reference number: A75001  
A:Accession: C75119  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-335 <XAW>  
A:Cross-references: UNIPROT:Q9V0N5; UNIPARC:UPI00001293BA; GB:AJ248285; GB:AL096836; NID  
A:Experimental source: strain Orey  
C:Genetics:  
A:Gene: dyl1; PAB0511  
C:Superfamily: yeast deoxyhypusine synthase  
C:Keywords: hypusine biosynthesis; oxidoreductase; transferase

Query Match 45.6%; Score 47; DB 2; Length 335;  
Best Local Similarity 47.1%; Pred. No. 27;  
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWMDF 17  
|||||:|:|:|:|:  
Db 20 EGPWLDEVESLEGVVISY 36

RESULT 22  
AH2052  
hypotheical protein all1974 [imported] - *Nostoc* sp. (strain PCC 7120)  
C:Species: *Nostoc* sp. PCC 7120  
A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
A:Accession: AH2052  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing *Cyanobacterium* Ana  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AH2052  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1209 <KUR>  
A:Cross-references: UNIPROT:Q8YVK3; UNIPARC:UPI00000CE28E; GB:BA000019; PIDN:BA073673.1;  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: all1974

Query Match 45.6%; Score 47; DB 2; Length 1209;  
Best Local Similarity 44.4%; Pred. No. 1.1e+02;  
Matches 8; Conservative 3; Mismatches 3; Indels 4; Gaps 1;

QY 1 EGPWLEEEEA-----YGW 14  
:|:|:|:|:|:|:  
Db 217 DAAMIDEREALTRYGW 234

RESULT 23  
G69355  
MJ0653 homolog AF0847 - *Archaeoglobus fulgidus*  
N:Alternate names: inosine-monophosphate dehydrogenase (guaB-1) homolog [mismomer]  
C:Species: *Archaeoglobus fulgidus*  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
A:Accession: G69355  
R:Kienk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
A:Reference number: A69250; MUID:98049343; PMID:9389475  
A:Accession: G69355  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-189 <KLE>  
A:Cross-references: UNIPROT:Q29411; UNIPARC:UPI0000056F4F; GB:AE001045; GB:AE000782; NID  
C:Superfamily: conserved hypothetical protein MJ0653; CBS homology  
C:Keywords: duplication  
F,79-127/Domain: CBS homology <CBS>

Query Match 44.7%; Score 46; DB 1; Length 189;  
Best Local Similarity 62.5%; Pred. No. 20;  
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWM 16  
|||:|:|:|:|:  
Db 148 EGPVIEEEIGGICD 163

## RESULT 24

AD3486  
hypothetical protein BMEI1874 [imported] - Brucella melitensis (strain 16M)  
C/Species: Brucella melitensis  
C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C/Accession: AD3486  
R/DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,  
; Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A/Reference number: AD3252; PMID:11756688  
A/Accession: AD3486  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-276 <KUR>  
A/Cross-references: UNIPROT:Q8YK4; UNIPARC:UPI000059235; GB:AB08917; PIDN:AAU53055.1;  
A/Experimental source: strain 16M  
C/Genetics:  
A/Gene: BMEI1874  
A/Map position: 1

Query Match 44.7%; Score 46; DB 2; Length 276;

Best Local Similarity 57.1%; Pred. No. 30;

Matches 8; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

## QY

4 WLEEEEA--YGM 15

|||||

90 WLEESAAQYGM 103

## RESULT 25

A28171  
phenylethanolamine N-methyltransferase (EC 2.1.1.28) - human  
C/Species: Homo sapiens (man)  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: A28171; S10894; A28210  
R/Kaneda, N.; Ichinose, H.; Kobayashi, K.; Oka, K.; Kishi, F.; Nakazawa, A.; Kurosawa, Y  
J. Biol. Chem. 263, 7672-7677, 1988  
A/Title: Molecular cloning of cDNA and chromosomal assignment of the gene for human phen  
A/Reference number: A28171; MUID:88227966; PMID:3372503  
A/Accession: A28171  
A/Molecule type: mRNA  
A/Residues: 1-282 <KAN>  
A/Cross-references: UNIPROT:P11086; UNIPARC:UPI0000111BE4; GB:J03727; NID:gi90141; PIDN:  
R/Sasaoka, T.; Kaneda, N.; Kurosawa, Y.; Fujita, K.; Nagatsu, T.  
Neurochem. Int. 15, 555-565, 1989  
A/Title: Structure of human phenylethanolamine N-methyltransferase gene: existence of tw  
A/Reference number: S10894  
A/Accession: S10894  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-282 <SAS>  
A/Cross-references: UNIPARC:UPI0000111BE4; EMBL:X52730; NID:g35560; PIDN:CAA36944.1; PID  
R/Baetge, E.E.; Behringer, R.R.; Messing, A.; Brinster, R.L.; Palminter, R.D.  
Proc. Natl. Acad. Sci. U.S.A. 85, 3648-3652, 1988  
A/Title: Transgenic mice express the human phenylethanolamine N-methyltransferase gene i  
A/Reference number: A28210; MUID:88217959; PMID:2835776  
A/Accession: A28210  
A/Molecule type: mRNA  
A/Residues: 1-168, 'AQ', 171-282 <BAE>  
A/Cross-references: UNIPARC:UPI000016AED9; GB:J03280; NID:gi90143; PIDN:AAA60131.1; PID:  
C/Genetics:  
A/Gene: GDB:PNNMT; PENT  
A/Cross-references: GDB:120271; OMIM:171190  
A/Map position: 17pter-17qter  
A/Introns: 68/1; 137/2  
C/Superfamily: phenylethanolamine N-methyltransferase  
C/Keywords: methyltransferase; S-adenosylmethionine

Query Match

Best Local Similarity 53.8%; Score 46; DB 1; Length 282;

Matches 7; Conservative 2; Mismatches 4; Indels 4; Gaps 0;

## QY

2 GFWLEEEEA YGM 14

|||||

111 GRWLOEEPCGFNM 123

## RESULT 26

T01017  
Probable MYB family transcription factor [imported] - Arabidopsis thaliana  
N/Alternate names: hypothetical protein T517.18  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 09-Jul-2004  
C/Accession: T01017; E84822  
R/Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau  
submitted to the EMBL Data Library, November 1997  
A/Description: Arabidopsis thaliana chromosome II BAC T517 genomic sequence.  
A/Reference number: Z14162  
A/Accession: T01017  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-367 <ROU>  
A/Cross-references: UNIPROT:004192; UNIPARC:UPI00000A34F9; EMBL:AC003000; NID:g2642152;  
A/Experimental source: cultivar Columbia  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nucleic Acids Res. 26, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: E84822  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-367 <STO>  
A/Cross-references: UNIPARC:UPI00000A34F9; GB:AE002093; NID:g2088641; PIDN:AAB95273.1;  
C/Genetics:  
A/Gene: T517.18; At2g39880  
A/Map position: 2  
A/Introns: 107/1  
C/Superfamily: Arabidopsis myb-related protein 1; myb DNA-binding repeat homology  
F; 97-147/Domain: myb DNA-binding repeat homology <MYB>

Query Match

Best Local Similarity 63.6%; Score 46; DB 2; Length 367;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

## QY

1 EGPWLEEEEA 11

|||||

50 KGPWLPEQDEA 60

## RESULT 27

T02021  
hypothetical protein T9E19.2 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 26-Feb-1999 #sequence\_revision 26-Feb-1999 #text\_change 09-Jul-2004  
C/Accession: T02021  
R/Strowmatt, C.; Johnson, D.; Le, T.  
submitted to the EMBL Data Library, November 1998  
A/Description: The sequence of A. thaliana T9E19.  
A/Reference number: Z14496  
A/Accession: T02021  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-374 <STR>  
A/Cross-references: UNIPROT:Q9ZSH6; UNIPARC:UPI00000A530C; EMBL:AF104920; NID:g3859610;  
A/Experimental source: cultivar Columbia  
C/Genetics:  
A/Map position: 4  
A/Introns: 279/3  
A/Note: T9E19.2

Query Match

Best Local Similarity 63.6%; Score 46; DB 2; Length 374;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WLEEEERAYGW 14  
 ||:||||  
 Db 133 WLQEEESMEGW 143

RESULT 28  
 S19483  
 Probable membrane protein YCR068w - Yeast (Saccharomyces cerevisiae)  
 C:Species: Saccharomyces cerevisiae  
 C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
 C:Accession: S19483  
 R:Contreras, R.; Demolder, J.; Fiers, W.; Molemans, P.  
 Submitted to the Protein Sequence Database, March 1992  
 A:Reference number: S19482  
 A:Accession: S19483  
 A:Molecule type: DNA  
 A:Residues: 1-429 <CON>  
 A:Cross-references: UNIPROT:P25641; UNIPARC:UPI000013A72A; EMBL:X59720; NID:G1907116; PI  
 C:Genetics:  
 A:Gene: SGD:CVT17; MIPS:YCR068w  
 A:Map position: 3R  
 A:Superfamily: Saccharomyces cerevisiae probable membrane protein YCR068w  
 C:Keywords: transmembrane protein  
 F:11-37/Domain: transmembrane #status predicted <TM1>  
 F:265-281/Domain: transmembrane #status predicted <TM2>

Query Match 44.7%; Score 46; DB 2; Length 429;  
 Best Local Similarity 58.3%; Pred. No. 50;  
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 PWLEEEERAYGW 14  
 ||:||||:|  
 Db 206 PWNTEPEDFGW 217

RESULT 29  
 E91268  
 thiol disulfide interchange protein [imported] - Escherichia coli (strain O157:H7, subst  
 C:Species: Escherichia coli  
 C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
 C:Accession: E91268  
 R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ighil, K.; Yokoyama, K.; Han, C.G.  
 Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.  
 DNA Res. 8, 11-22, 2001  
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc  
 A:Reference number: A99629; MUID:21156231; PMID:11258796  
 A:Accession: E91268  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-565 <HAY>  
 A:Cross-references: UNIPROT:P58162; UNIPARC:UPI00001298D6; GB:BA000007; PIDN:BA838540.1;  
 A:Experimental source: strain O157:H7, substrain RIMD 0509952  
 C:Genetics:  
 A:Gene: ECs5117

Query Match 44.7%; Score 46; DB 2; Length 565;  
 Best Local Similarity 42.9%; Pred. No. 68;  
 Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 GPWLEEEERAYGWM 15  
 ||:||||:|  
 Db 355 GPWMEQVKTAFGFV 368

RESULT 30  
 C86109  
 thiol disulfide interchange protein [imported] - Escherichia coli (strain O157:H7, subst  
 C:Species: Escherichia coli  
 C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
 C:Accession: C86109  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: C86109  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-565 <STO>  
 A:Cross-references: UNIPROT:P58162; UNIPARC:UPI00001298D6; GB:AE005174; NID:G13519115; P  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: dsbD

Query Match 44.7%; Score 46; DB 2; Length 565;  
 Best Local Similarity 42.9%; Pred. No. 68;  
 Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 GPWLEEEERAYGWM 15  
 ||:||||:|  
 Db 355 GPWMEQVKTAFGFV 368

RESULT 31  
 S56364  
 inner membrane copper tolerance protein cyc2 - Escherichia coli (strain K-12)  
 N:Alternate names: thiol:disulfide interchange protein dsbD  
 C:Species: Escherichia coli  
 C>Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
 C:Accession: S56364; I41028; I41037; S42064; F65223; S57220; S47295  
 R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.  
 Nucleic Acids Res. 23, 2105-2119, 1995  
 A:Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92  
 A:Reference number: S56314; MUID:95334362; PMID:7610040  
 A:Accession: S56364  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-565 <BUR>  
 A:Cross-references: UNIPROT:P36655; UNIPARC:UPI00001298D7; EMBL:U14003; NID:G1263172; PI  
 R:Fong, S.T.; Camakaris, J.; Lee, B.T.  
 Mol. Microbiol. 15, 1127-1137, 1995  
 A:Title: Molecular genetics of a chromosomal locus involved in copper tolerance in Esche  
 A:Reference number: I41027; MUID:95349397; PMID:7623666  
 A:Accession: I41028  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 'M', 78-565 <RES>  
 A:Cross-references: UNIPARC:UPI00001587BA; EMBL:Z36905; NID:G535290; PIDN:CAA85375.1; PI  
 A:Note: in this report, the codon GTG for Val-77 was interpreted as a start codon  
 R:Crooke, H.; Cole, J.  
 Mol. Microbiol. 15, 1139-1150, 1995  
 A:Title: The biogenesis of c-type cytochromes in Escherichia coli requires a membrane-bc  
 A:Reference number: I41036; MUID:95349398; PMID:7623667  
 A:Accession: I41037  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 'M', 78-565 <RE2>  
 A:Cross-references: UNIPARC:UPI00001587BA; EMBL:X77707; NID:G871027; PIDN:CAA54781.1; PI  
 A:Note: in this report, the codon GTG for Val-77 was interpreted as a start codon  
 R:Crooke, H.R.; Cole, J.A.  
 Submitted to the EMBL Data Library, February 1994  
 A:Description: The biogenesis of C-type cytochromes in Escherichia coli requires an inte  
 A:Reference number: S42063  
 A:Accession: S42064  
 A:Molecule type: DNA  
 A:Residues: 1-328, 'V', 330-565 <CRO>  
 A:Cross-references: UNIPARC:UPI0000170C87; EMBL:X77707  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
 A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; MUID:97426617; PMID:9278503  
 A:Accession: F65223

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-565 <BLAT>

A;Cross-references: UNIPARC:UPI00001298D7; GB:AE000486; GB:U00096; NID:g1790574; PIDN:AP

A;Experimental source: strain K-12, substrain MG1655

R;Misslakaas, D.; Schwager, P.; Raina, S.

EMBO J. 14, 3415-3424, 1995

A;Title: Identification and characterization of a new disulfide isomerase-like protein

A;Reference number: S57220; MUID:95354659; PMID:7628442

A;Accession: S57220

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 462-540 <MIS>

A;Cross-references: UNIPARC:UPI000017CC88

C;Genetics:

A;Gene: ddbD; cycZ; CutA2; dipZ

C;Keywords: inner membrane; redox-active disulfide; transmembrane protein

Query Match 44.7%; Score 46; DB 2; Length 565;

Best Local Similarity 42.9%; Pred. No. 68;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GPMLEEEERAYGWM 15

||||:|:|:|:|:

Db 355 GPMWEQVKTAFGV 368

RESULT 32

D86393

hypothetical protein T1K7.1 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C;Accession: D86393

R;Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.P.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: D86393

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-867 <STO>

A;Cross-references: UNIPROT:Q9PZE6; UNIPARC:UPI00000A5E14; GB:AE005172; NID:g9797740; P

C;Genetics:

A;Map position: 1

Query Match 44.7%; Score 46; DB 2; Length 867;

Best Local Similarity 46.7%; Pred. No. 1.1e+02;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWM 15

:|:|:|:|:

Db 210 QGWLKRNRTQNGWM 224

RESULT 33

T47381

hypothetical protein T5C2.90 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004

C;Accession: T47381

R;Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Lemcke, K.; M

submitted to the Protein Sequence Database, March 2000

A;Reference number: 224463

A;Accession: T47381

A;Status: preliminary

A;Molecule type: DNA

Query Match 44.7%; Score 46; DB 2; Length 1198;

Best Local Similarity 63.6%; Pred. No. 1.5e+02;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

A;Residues: 1-1113 <OBE>

A;Cross-references: UNIPROT:QSM180; UNIPARC:UPI00000A5EDF; EMBL:AL138664

A;Experimental source: cultivar Columbia; BAC clone T5C2

C;Genetics:

A;Map position: 3

A;Introns: 42/1; 351/3; 418/1; 617/3; 659/3; 690/3; 732/3; 767/3; 801/3; 816/3; 845/3;

A;Note: T5C2.90

Query Match 44.7%; Score 46; DB 2; Length 1113;

Best Local Similarity 63.6%; Pred. No. 1.5e+02;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 WLEEEERAYGW 14

||||:|:|:|:

Db 205 WLQEEESMEGW 215

RESULT 34

D85089

hypothetical protein AT4G08880 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C;Accession: D85089

R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spr

Nature 402, 769-777, 1999

A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A;Reference number: A85001; MUID:20083488; PMID:10617198

A;Accession: D85089

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1175 <STO>

A;Cross-references: UNIPROT:Q9ZPF3; UNIPARC:UPI000009F708; GB:NC\_001268; NID:g7267530;

C;Genetics:

A;Gene: AT4G08880

A;Map position: 4

Query Match 44.7%; Score 46; DB 2; Length 1175;

Best Local Similarity 63.8%; Pred. No. 1.5e+02;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 WLEEEERAYGW 14

||||:|:|:|:

Db 69 WLQEEESMEGW 79

RESULT 35

E86402

hypothetical protein F28L5.2 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C;Accession: E86402

R;Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.P.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: E86402

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1198 <STO>

A;Cross-references: UNIPROT:Q9C6N9; UNIPARC:UPI00000A5394; GB:AE005172; NID:g10998930;

C;Genetics:

A;Map position: 1

Query Match 44.7%; Score 46; DB 2; Length 1198;

Best Local Similarity 63.6%; Pred. No. 1.5e+02;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WLEEEERAYGW 14  
 ||:||||  
 Db 205 WLQEESEMEGW 215

RESULT 36  
 F86386  
 hypothetical protein F14G11.4 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C:Accession: F86386

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.  
 ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F86386  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1201 <STO>  
 A:Cross-references: UNIPROT:Q9C607; UNIPARC:UPI00000A1C16; GB:AE005172; NID:gl1560181; F  
 C:Genetics:  
 A:Map position: 1

Query Match 44.7%; Score 46; DB 2; Length 1201;  
 Best Local Similarity 63.6%; Pred. No. 1.6e+02;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WLEEEERAYGW 14  
 ||:||||  
 Db 205 WLQEESEMEGW 215

RESULT 37  
 H85041  
 hypothetical protein AT4g03300 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
 C:Accession: H85041

R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
 Nature 402, 769-777, 1999

A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
 A:Reference number: A85001; MUID:20083488; PMID:10617198

A:Accession: H85041  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1285 <STO>  
 A:Cross-references: UNIPROT:Q9ZR01; UNIPARC:UPI00000A72B2; GB:NC\_001268; NID:g2720200; F  
 C:Genetics:  
 A:Gene: AT4g03300  
 A:Map position: 4

Query Match 44.7%; Score 46; DB 2; Length 1285;  
 Best Local Similarity 63.6%; Pred. No. 1.7e+02;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WLEEEERAYGW 14  
 ||:||||  
 Db 357 WLQEESEMEGW 367

RESULT 38  
 H96559  
 hypothetical protein F5F19.8 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C:Accession: H96559  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.  
 ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: H96559  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1305 <STO>  
 A:Cross-references: UNIPROT:Q9ZU21; UNIPARC:UPI00000A0A103; GB:AE005173; NID:g4220449; P1  
 C:Genetics:  
 A:Gene: F5F19.8  
 A:Map position: 1

Query Match 44.7%; Score 46; DB 2; Length 1305;  
 Best Local Similarity 63.6%; Pred. No. 1.7e+02;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WLEEEERAYGW 14  
 ||:||||  
 Db 205 WLQEESEMEGW 215

RESULT 39  
 T47331  
 hypothetical protein F7P3.20 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
 C:Accession: T47331

R:Vitale, D.; Liguori, R.; Flores, M.; Argiriou, A.; De Simone, V.; Mewes, H.W.; Rudd, S.  
 submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24461  
 A:Accession: T47331  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1314 <VIT>  
 A:Cross-references: UNIPROT:Q9M194; UNIPARC:UPI00000A4A0F; EMBL:AL138663  
 A:Experimental source: cultivar Columbia; BAC clone F7P3  
 C:Genetics:  
 A:Map position: 3  
 A:Introns: 42/1; 351/3; 416/1; 615/3; 657/3; 712/3; 754/3; 789/3; 819/3; 839/3; 873/3; 9  
 A>Note: F7P3.20

Query Match 44.7%; Score 46; DB 2; Length 1314;  
 Best Local Similarity 63.6%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WLEEEERAYGW 14  
 ||:||||  
 Db 205 WLQEESEMEGW 215

RESULT 40  
 T02599  
 hypothetical protein At2g14770 [imported] - Arabidopsis thaliana  
 N:Alternate names: hypothetical protein F26C24.9  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C>Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004  
 C:Accession: T02599; C84521

R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,  
 submitted to the EMBL Data Library, June 1998

A>Description: Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence.  
 A:Reference number: Z14680  
 A:Accession: T02599  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA

A;Residues: 1-1756 <ROU>  
A;Cross-references: UNIPROT:O80975; UNIPARC:UPI00000AA9BA; EMBL:AC004705; NID:G3252804;  
A;Experimental source: cultivar Columbia  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
Eisen, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: C84521  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1756 <STO>  
A;Cross-references: UNIPARC:UPI00000AA9BA; GB:AE002093; NID:G3252818; PIDN:AAC24188.1; C  
C;Genetics:  
A;Gene: At2g14770; F26C24.9  
A;Map position: 2  
A;Introns: 42/1, 351/3; 418/1; 617/3; 659/3; 725/1; 758/3; 778/3; 812/3; 902/2; 9  
Query Match 44.7%; Score 46; DB 2; Length 1756;  
Best Local Similarity 63.6%; Pred. No. 2.4e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 4 WLEBEEBAYGWM 14  
|||:|||||  
DB 205 WLOEBSMEGW 215  
|||:|||||  
RESULT 41  
A83609  
probable periplasmic polyamine binding protein PA0295 [imported] - Pseudomonas aeruginosa  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 05-Oct-2004  
C;Accession: A83609  
R;Stover, C.K.; Erwin, A.L.; Mizioch, S.D.; Warren, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: A83609  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-353 <STO>  
A;Cross-references: UNIPROT:Q916J6; UNIPARC:UPI00000C4FEA; GB:AE004467; GB:AE004091; NID  
C;Genetics:  
A;Gene: PA0295  
C;Superfamily: spermidine/putrescine-binding protein  
Query Match 44.2%; Score 45.5; DB 2; Length 353;  
Best Local Similarity 44.4%; Pred. No. 47;  
Matches 8; Conservative 2; Mismatches 5; Indels 3; Gaps 1;  
QY 3 PWLEBEEB---AYGWMDF 17  
|||:|||||  
DB 14 PFLAQAEETLRVYNWNY 31  
|||:|||||  
RESULT 42  
JQ0904  
bombyxin A-2 homolog precursor - aianthus silkmoth  
C;Species: Samia cynthia (aianthus silkmoth)  
C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
C;Accession: JQ0904  
R;Iwami, M.  
submitted to JIPID, March 1991  
A;Reference number: JQ0902  
A;Accession: JQ0904  
A;Molecule type: DNA  
A;Residues: 1-100 <IWA>  
A;Cross-references: UNIPROT:P33719; UNIPARC:UPI0000125865  
A;Note: the authors translated the codon CCG for residue 47 as Thr

A;Note: the source is designated as Samia cynthia ricini  
C;Genetics:  
A;Gene: sbx2  
C;Superfamily: insulin  
C;Keywords: hormone  
Query Match 43.7%; Score 45; DB 2; Length 100;  
Best Local Similarity 50.0%; Pred. No. 13;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 3 PWLEBEEBAYGWM 14  
|||:|||||  
DB 48 PYISSENEGWM 59  
|||:|||||  
RESULT 43  
S75616  
hypothetical protein slr1957 - Synechocystis sp. (strain PCC 6803)  
C;Species: Synechocystis sp.  
A;Variety: PCC 6803  
C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: S75616  
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.  
o. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud  
DNA Res. 3, 109-136, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis:  
S.  
A;Reference number: S74322; MUID:97061201; PMID:8905231  
A;Accession: S75616  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-106 <KAN>  
A;Cross-references: UNIPROT:P74093; UNIPARC:UPI00000C0FF5; EMBL:D09012; GB:AB001339; NID  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C;Superfamily: Synechocystis hypothetical protein slr1957  
Query Match 43.7%; Score 45; DB 2; Length 106;  
Best Local Similarity 61.5%; Pred. No. 14;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 4 WLEBEEBAYGWM 16  
|||:|||||  
DB 8 WIEEWCEANGWTD 20  
|||:|||||  
RESULT 44  
JC7669  
acylglycerol lipase (EC 3.1.1.23) - Bacillus sp.  
N;Alternate names: monoacylglycerol lipase  
C;Species: Bacillus sp.  
C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: JC7669; PC7167  
R;Kitaura, S.; Suzuki, K.; Inamura, S.  
J. Biochem. 129, 397-402, 2001  
A;Title: Monoacylglycerol lipase from moderately thermophilic Bacillus sp. strain H-257  
A;Reference number: JC7669; MUID:21125594; PMID:11226879  
A;Accession: JC7669  
A;Molecule type: DNA  
A;Residues: 1-250 <KIT>  
A;Cross-references: UNIPROT:Q7M0R0; UNIPARC:UPI000015690F; GB:E05047  
A;Experimental source: strain H-257  
A;Accession: PC7167  
A;Molecule type: protein  
A;Residues: 2-17;57-85;86-120;217-247 <KI2>  
A;Cross-references: UNIPARC:UPI00000BEE44; UNIPARC:UPI00001798F3; UNIPARC:UPI00001798F4  
C;Comment: This enzyme, a thermostable enzyme, up to 60 degree, hydrolyzes monoacylglyc  
C;Genetics:  
A;Gene: mgip  
C;Superfamily: esterase/lipase  
C;Keywords: carboxylic ester hydrolase  
P;95-99/Region: consensus pentapeptide (-Gly-Leu-Ser-Met-Gly) #status predicted  
Query Match 43.7%; Score 45; DB 2; Length 250;

Best Local Similarity 50.0%; Pred. No. 38;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 WLEEEEEAYGWM 15  
|: |||:  
Db 73 WVASVEEGYGL 84

RESULT 45  
T51005  
hypothetical protein B7J19.40 [imported] - Neurospora crassa  
C:Species: Neurospora crassa  
C:Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 31-Dec-2004  
C:Accession: T51005  
R:Schulte, U.; Aign, V.; Hohseisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,  
submitted to the Protein Sequence Database, July 2000  
A:Reference number: Z25286  
A:Accession: T51005  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-297 <SCH>  
A:Cross-references: UNIPROT:Q96U05; UNIPARC:UPI0000179F64; EMBL:AL389899; GSPDB:GNO00116;  
A:Experimental source: BAC clone B7J19; strain OR74A  
C:Genetics:  
A:Gene: NCSP:B7J19.40  
A:Map position: 6  
A:Introns: 45/2; 205/1; 225/1; 236/1

Query Match 43.7%; Score 45; DB 2; Length 297;  
Best Local Similarity 70.0%; Pred. No. 46;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 LBEEDAYGW 14  
|: |||:  
Db 171 LDEEDAYGW 180

RESULT 46  
A10042  
thiol, disulfide interchange protein [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: A10042  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: A10042  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-595 <KUR>  
A:Cross-references: UNIPROT:Q8Z1Y9; UNIPARC:UPI00001298E0; GB:AL590842; PIDN:CAC89204.1;  
C:Genetics:  
A:Gene: GdbD

Query Match 43.7%; Score 45; DB 2; Length 595;  
Best Local Similarity 42.9%; Pred. No. 1e+02;  
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 GPWLEEEAYGWM 15  
|||: |||:  
Db 382 GPWQVYKEAFGV 395

RESULT 47  
S41008  
hypothetical protein T05G5.8 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Sep-1997  
C:Accession: S41008  
R:Thomas, K.

submitted to the EMBL Data Library, October 1993  
A:Reference number: S41001  
A:Accession: S41008  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-691 <THO>  
A:Cross-references: UNIPARC:UPI000017A082; EMBL:Z27079; NID:G414641; PID:G414649  
C:Genetics:  
A:Introns: 97/3; 319/2; 442/2; 452/2; 569/3

Query Match 43.7%; Score 45; DB 2; Length 691;  
Best Local Similarity 42.9%; Pred. No. 1.2e+02;  
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYGW 14  
|||: |||:  
Db 144 EGAWLDKVDYRKW 157

RESULT 48  
D88564  
protein T05G5.8 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: D88564  
R:Anonymous, The C. elegans Sequencing Consortium.  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
Science 282, 2012-2018, 1998  
A:Reference number: A75000; MUID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_ele  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: D88564  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-808 <STO>  
A:Cross-references: UNIPROT:P34561; UNIPARC:UPI0000061151; GB:chr\_III; PIDN:CAA81595.1;  
C:Genetics:  
A:Gene: T05G5.8  
A:Map position: 3

Query Match 43.7%; Score 45; DB 2; Length 808;  
Best Local Similarity 42.9%; Pred. No. 1.4e+02;  
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYGW 14  
|||: |||:  
Db 261 EGAWLDKVDYRKW 274

RESULT 49  
A42551  
genome polyprotein - dengue virus type 1 (strain Singapore S275/90)  
N:Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS  
a; nonstructural protein NS4b; nonstructural protein NS5  
C:Species: dengue virus type 1  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 31-Dec-2004  
C:Accession: A42551  
R:Fu, J.; Tan, B.H.; Yap, E.H.; Chan, Y.C.; Tan, Y.H.  
Virology 188, 953-958, 1992  
A:Title: Full-length cDNA sequence of dengue type 1 virus (Singapore strain S275/90).  
A:Reference number: A42551; MUID:92263809; PMID:1585663  
A:Accession: A42551  
A:Molecule type: genomic RNA  
A:Residues: 1-3396 <PUJ>  
A:Cross-references: UNIPROT:P33478; UNIPARC:UPI000002F845; GB:M87512  
C:Superfamily: hepatitis C virus genome polyprotein  
C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;  
F:1-114/Product: capsid protein #status predicted <CAP>  
F:115-281/Product: membrane protein precursor #status predicted <MEP>  
F:115-204/Domain: nonterminal signal sequence #status predicted <SIG>  
F:205-281/Product: membrane protein #status predicted <MEM>  
F:267-279/Domain: transmembrane #status predicted <TM1>  
F:282-774/Product: envelope protein #status predicted <ENV>

F;753-769/Domain: transmembrane #status predicted <TM2>  
F;775-1127/Product: nonstructural protein NS1 #status predicted <NS1>  
F;1128-1344/Product: nonstructural protein NS2a #status predicted <N2A>  
F;1345-1474/Product: nonstructural protein NS2b #status predicted <N2B>  
F;1475-2093/Product: nonstructural protein NS3 #status predicted <NS3>  
F;1668-1675/Region: nucleotide-binding motif A (P-loop)  
F;1755-1760/Region: nucleotide-binding motif B  
F;1759-1762/Region: DEAH motif  
F;2094-2243/Product: nonstructural protein NS4a #status predicted <N4A>  
F;2244-2492/Product: nonstructural protein NS4b #status predicted <N4B>  
F;2493-3396/Product: nonstructural protein NS5 #status predicted <NS5>  
F;183,347,433/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 43.7%; Score 45; DB 1; Length 3396;  
Best Local Similarity 37.5%; Pred. No. 7.2e+02;  
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGMD 16

DB 3311 ENPWMEKTHVSSWED 3326

## RESULT 50

JQ0902

bombyxin A-1 homolog - aillanthus silkmoth

C;Species: Samia cynthia (aillanthus silkmoth)

C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004

C;Accession: JQ0902

R;Iwami, M.

submitted to JIPID, March 1991

A;Reference number: JQ0902

A;Accession: JQ0902

A;Molecule type: DNA

A;Residues: 1-99 &lt;IWA&gt;

A;Cross-references: UNIPROT:P33718; UNIPARC:UPI0000126B62

A;Note: the source is designated as Samia cynthia ricini

C;Genetics:

A;Gene: sbxAl

C;Superfamily: insulin

C;Keywords: hormone

Query Match

42.7%; Score 44; DB 2; Length 99;

Best Local Similarity 50.0%; Pred. No. 18;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 PWLEEEERAYGW 14

DB 49 PYISPENEGYGW 60

Search completed: January 3, 2006, 09:11:19

Job time : 40.8095 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:05 ; Search time 31.1667 Seconds  
(without alignments)  
45.096 Million cell updates/sec

Title: US-10-759-832-1

Perfect score: 103

Sequence: 1 EGFWEEREEAYGWDF 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Databases :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	100.0	17	2	US-09-174-216-4
2	103	100.0	17	2	US-09-623-548A-422
3	103	100.0	17	2	US-09-657-276-422
4	100	97.1	17	1	US-08-446-692-74
5	100	97.1	17	1	US-08-488-351A-74
6	100	97.1	17	2	US-09-079-372-17
7	100	97.1	18	2	US-09-079-372-10
8	100	97.1	18	2	US-09-079-372-15
9	100	97.1	21	2	US-09-079-372-12
10	100	97.1	33	2	US-10-360-101-170
11	100	97.1	34	1	US-08-446-692-69
12	100	97.1	34	1	US-08-488-351A-69
13	100	97.1	34	2	US-09-079-372-9
14	100	97.1	34	2	US-09-079-372-16
15	100	97.1	34	2	US-09-623-548A-423
16	100	97.1	34	2	US-09-657-276-423
17	100	97.1	35	2	US-09-079-372-8
18	100	97.1	52	1	US-08-446-692-99
19	100	97.1	52	1	US-08-488-351A-99
20	100	97.1	69	1	US-08-446-692-95
21	100	97.1	69	1	US-08-488-351A-95
22	100	97.1	74	2	US-09-079-372-7
23	100	97.1	100	2	US-09-079-372-14
24	100	97.1	122	2	US-09-949-016-11739
25	98	95.1	17	2	US-09-174-263-2
26	78	75.7	17	2	US-09-623-548A-424
27	78	75.7	17	2	US-09-657-276-424

28	73.5	71.4	17	1	US-08-127-351-3	Sequence 3, Appli
29	73.5	71.4	17	1	US-08-480-367B-3	Sequence 3, Appli
30	73.5	71.4	17	1	US-08-487-221A-3	Sequence 3, Appli
31	73.5	71.4	17	1	US-08-480-370-3	Sequence 3, Appli
32	71.5	69.4	14	6	5169865-8	Patent No. 5169865
33	69	67.0	12	1	US-08-652-971-10	Sequence 10, Appl
34	69	67.0	12	1	US-08-991-258A-10	Sequence 10, Appl
35	69	67.0	12	1	US-08-769-399-10	Sequence 10, Appl
36	69	67.0	12	2	US-08-991-953A-10	Sequence 10, Appl
37	66	64.1	12	1	US-08-446-692-75	Sequence 75, Appl
38	66	64.1	12	1	US-08-488-351A-75	Sequence 75, Appl
39	66	64.1	47	1	US-08-446-692-100	Sequence 100, App
40	66	64.1	47	1	US-08-488-351A-100	Sequence 100, App
41	54	52.4	9	1	US-08-178-570-69	Sequence 69, Appl
42	54	52.4	9	2	US-08-369-643-69	Sequence 69, Appl
43	54	52.4	9	4	PCT-US95-00147-69	Sequence 69, Appl
44	54	52.4	16	4	US-08-151-219-1	Sequence 1, Appli
45	54	52.4	16	4	PCT-US94-13205-1	Sequence 1, Appli
46	53	51.5	9	1	US-08-151-219-2	Sequence 2, Appli
47	53	51.5	9	4	PCT-US94-13205-2	Sequence 2, Appli
48	53	51.5	15	1	US-08-151-219-4	Sequence 4, Appli
49	53	51.5	15	4	PCT-US94-13205-4	Sequence 4, Appli
50	52	50.5	307	2	US-09-270-767-45243	Sequence 45243, A
51	49	47.6	8	1	US-08-178-570-44	Sequence 44, Appl
52	49	47.6	8	2	US-08-369-643-44	Sequence 44, Appl
53	49	47.6	8	4	PCT-US95-00147-44	Sequence 44, Appl
54	48	46.6	210	2	US-09-252-991A-22805	Sequence 22805, A
55	46	44.7	37	2	US-08-651-136C-64	Sequence 64, Appl
56	46	44.7	37	2	US-09-229-911A-64	Sequence 64, Appl
57	46	44.7	37	2	US-10-007-521-64	Sequence 64, Appl
58	46	44.7	225	2	US-08-651-136C-2	Sequence 2, Appli
59	46	44.7	225	2	US-09-229-911A-2	Sequence 2, Appli
60	46	44.7	225	2	US-09-548-938A-14	Sequence 14, Appl
61	46	44.7	225	2	US-10-007-521-2	Sequence 2, Appli
62	46	44.7	282	2	US-09-845-713A-2	Sequence 2, Appli
63	46	44.7	297	2	US-08-651-136C-4	Sequence 4, Appli
64	46	44.7	297	2	US-09-229-911A-4	Sequence 4, Appli
65	46	44.7	297	2	US-10-007-521-4	Sequence 4, Appli
66	46	44.7	308	2	US-08-651-136C-6	Sequence 6, Appli
67	46	44.7	308	2	US-09-229-911A-6	Sequence 6, Appli
68	46	44.7	308	2	US-10-007-521-6	Sequence 6, Appli
69	46	44.7	489	2	US-09-393-171-7	Sequence 7, Appli
70	45.5	44.2	438	2	US-09-252-991A-27560	Sequence 27560, A
71	45	43.7	8	1	US-08-446-692-76	Sequence 76, Appl
72	45	43.7	8	1	US-08-488-351A-76	Sequence 42702, A
73	44.5	43.2	447	2	US-09-270-767-42702	Sequence 15589, A
74	44.5	43.2	460	2	US-09-902-540-15589	Sequence 13922, A
75	44	42.7	103	2	US-09-902-540-13922	Sequence 8349, Ap
76	44	42.7	344	2	US-09-489-039A-8349	Sequence 5447, Ap
77	44	42.7	400	2	US-09-328-352-5447	Sequence 1260, Ap
78	43.5	42.2	2704	2	US-09-538-092-1260	Sequence 2286, Ap
79	43	41.7	57	2	US-09-640-211A-2286	Sequence 2303, Ap
80	43	41.7	64	2	US-09-640-211A-2303	Sequence 32, Appl
81	43	41.7	75	2	US-08-651-136C-32	Sequence 32, Appl
82	43	41.7	75	2	US-09-229-911A-32	Sequence 32, Appl
83	43	41.7	75	2	US-10-007-521-32	Sequence 32, Appl
84	43	41.7	162	2	US-09-640-211A-2204	Sequence 2204, Ap
85	43	41.7	163	2	US-09-328-352-6165	Sequence 6165, Ap
86	43	41.7	191	2	US-09-640-211A-2177	Sequence 2177, Ap
87	43	41.7	262	2	US-09-902-540-15754	Sequence 15754, A
88	43	41.7	264	2	US-09-886-319A-68	Sequence 68, Appl
89	43	41.7	266	2	US-09-949-016-10512	Sequence 10512, A
90	43	41.7	292	2	US-09-605-703B-368	Sequence 368, App
91	43	41.7	303	1	US-08-286-819A-23	Sequence 23, Appl
92	43	41.7	303	2	US-08-980-357-23	Sequence 23, Appl
93	43	41.7	303	2	US-09-357-375-23	Sequence 23, Appl
94	43	41.7	318	2	US-09-543-681A-4414	Sequence 4414, Ap
95	43	41.7	671	2	US-09-121-321-16	Sequence 16, Appl
96	43	41.7	671	2	US-08-933-803A-16	Sequence 16, Appl
97	43	41.7	731	2	US-09-107-532A-6999	Sequence 6999, Ap
98	43	41.7	1162	2	US-09-134-001C-4008	Sequence 4008, Ap
99	43	41.7	2291	1	US-08-286-819A-29	Sequence 29, Appl
100	43	41.7	2291	2	US-08-980-357-29	Sequence 29, Appl

101	43	41.7	2291	2	US-09-357-375-29	Sequence 29, Appl	174	40	38.8	569	2	US-09-773-426A-5	Sequence 5, Appl
102	42.5	41.3	197	2	US-09-328-352-6786	Sequence 6786, Ap	175	40	38.8	569	2	US-10-314-881-5	Sequence 5, Appl
103	42	40.8	225	2	US-09-902-540-15073	Sequence 15073, A	176	40	38.8	569	2	US-09-495-823-5	Sequence 5, Appl
104	42	40.8	234	2	US-09-252-991A-21695	Sequence 21695, A	177	40	38.8	588	2	US-09-949-016-7290	Sequence 7290, Ap
105	42	40.8	287	2	US-09-252-991A-22628	Sequence 22628, A	178	40	38.8	734	2	US-08-706-216-2	Sequence 2, Appl
106	42	40.8	463	2	US-09-631-603-16	Sequence 16, Appl	179	40	38.8	734	2	US-09-641-741-2	Sequence 2, Appl
107	42	40.8	542	2	US-09-902-540-15521	Sequence 15521, A	180	40	38.8	734	2	US-09-650-284B-2	Sequence 2, Appl
108	42	40.8	580	2	US-09-657-252-2	Sequence 2, Appl	181	40	38.8	797	1	US-08-698-551-18	Sequence 18, Appl
109	41.5	40.3	376	2	US-09-270-767-61043	Sequence 61043, A	182	40	38.8	797	1	US-08-839-032A-18	Sequence 18, Appl
110	41.5	40.3	378	2	US-09-328-352-8178	Sequence 8178, Ap	183	40	38.8	797	2	US-09-185-258C-18	Sequence 18, Appl
111	41.5	40.3	495	2	US-09-252-991A-23393	Sequence 23393, A	184	40	38.8	798	2	US-09-533-029-48	Sequence 48, Appl
112	41.5	40.3	582	2	US-09-270-767-45332	Sequence 45332, A	185	40	38.8	834	2	US-10-188-495-65	Sequence 65, Appl
113	41.5	40.3	722	2	US-09-198-452A-513	Sequence 513, App	186	40	38.8	996	2	US-09-497-822C-21	Sequence 21, Appl
114	41.5	40.3	722	2	US-09-438-185A-477	Sequence 477, App	187	39.5	38.3	160	2	US-09-248-796A-14432	Sequence 14432, A
115	41.5	40.3	785	2	US-09-902-540-9973	Sequence 9973, Ap	188	39.5	38.3	249	2	US-09-010-809-8	Sequence 8, Appl
116	41.5	40.3	930	2	US-09-122-126B-15	Sequence 15, Appl	189	39.5	38.3	389	2	US-10-243-468-11	Sequence 11, Appl
117	41.5	40.3	930	2	US-09-634-286A-15	Sequence 15, Appl	190	38.5	38.3	392	2	US-09-488-039A-11256	Sequence 11256, A
118	41.5	40.3	930	2	US-10-247-685-15	Sequence 15, Appl	191	39.5	38.3	589	2	US-09-328-352-6901	Sequence 6901, Ap
119	41	39.8	7	1	US-08-431-539-9	Sequence 9, Appl	192	39.5	38.3	2871	2	US-09-538-092-936	Sequence 936, Ap
120	41	39.8	66	1	US-09-482-273-147	Sequence 147, App	193	39.5	38.3	6095	2	US-09-144-085-2	Sequence 2, Appl
121	41	39.8	66	1	US-09-482-273-147	Sequence 147, App	194	39	37.9	10	2	US-09-214-614-8	Sequence 8, Appl
122	41	39.8	95	2	US-09-482-273-234	Sequence 234, App	195	39	37.9	10	2	US-09-623-548A-401	Sequence 401, App
123	41	39.8	160	2	US-09-248-796A-14567	Sequence 14567, A	196	39	37.9	10	2	US-09-657-276-401	Sequence 401, App
124	41	39.8	209	2	US-09-130-242-4	Sequence 4, Appl	197	39	37.9	50	2	US-09-156-316-4	Sequence 4, Appl
125	41	39.8	209	2	US-09-583-610D-4	Sequence 4, Appl	198	39	37.9	50	2	US-09-156-316-5	Sequence 5, Appl
126	41	39.8	273	2	US-09-533-029-40	Sequence 40, Appl	199	39	37.9	50	2	US-09-156-316-6	Sequence 6, Appl
127	41	39.8	277	2	US-09-248-796A-26292	Sequence 26292, A	200	39	37.9	50	2	US-09-757-049A-4	Sequence 4, Appl
128	41	39.8	442	2	US-09-252-991A-31503	Sequence 31503, A	201	39	37.9	50	2	US-09-757-049A-5	Sequence 5, Appl
129	41	39.8	659	2	US-09-252-991A-22940	Sequence 22940, A	202	39	37.9	50	2	US-09-757-049A-6	Sequence 6, Appl
130	41	39.8	729	2	US-09-230-196-2	Sequence 2, Appl	203	39	37.9	52	1	US-08-519-103-13	Sequence 13, Appl
131	41	39.8	729	2	US-09-949-016-6532	Sequence 6532, Ap	204	39	37.9	52	1	US-08-519-103-14	Sequence 14, Appl
132	41	39.8	841	2	US-09-949-016-10694	Sequence 10694, A	205	39	37.9	52	2	US-09-018-635-13	Sequence 13, Appl
133	41	39.8	704	2	US-09-949-016-7337	Sequence 7337, Ap	206	39	37.9	52	2	US-09-018-635-14	Sequence 14, Appl
134	41	39.8	1088	2	US-09-130-242-2	Sequence 2, Appl	207	39	37.9	52	2	US-09-912-962-13	Sequence 13, Appl
135	41	39.8	1088	2	US-09-583-610D-2	Sequence 2, Appl	208	39	37.9	52	2	US-09-912-962-14	Sequence 14, Appl
136	41	39.8	1088	2	US-09-949-016-6935	Sequence 6935, Ap	209	39	37.9	58	2	US-09-640-211A-2344	Sequence 2344, Ap
137	41	39.8	1091	2	US-09-949-016-8595	Sequence 8595, Ap	210	39	37.9	59	2	US-08-651-136C-66	Sequence 66, Appl
138	41	39.8	1119	2	US-09-396-651B-2	Sequence 2, Appl	211	39	37.9	59	2	US-09-229-911A-66	Sequence 66, Appl
139	41	39.8	2141	2	US-09-949-016-10918	Sequence 10918, A	212	39	37.9	59	2	US-10-007-521-66	Sequence 66, Appl
140	40.5	39.3	172	2	US-09-489-039A-12866	Sequence 12866, A	213	39	37.9	71	2	US-09-902-540-11699	Sequence 11699, A
141	40.5	39.3	5087	2	US-09-144-085-1	Sequence 1, Appl	214	39	37.9	103	2	US-08-894-173-76	Sequence 76, Appl
142	40	38.8	173	2	US-09-637-746-2	Sequence 2, Appl	215	39	37.9	103	2	US-09-398-193-76	Sequence 76, Appl
143	40	38.8	173	2	US-09-637-746-8	Sequence 8, Appl	216	39	37.9	109	2	US-08-894-173-96	Sequence 96, Appl
144	40	38.8	173	2	US-09-637-746-10	Sequence 10, Appl	217	39	37.9	109	2	US-09-398-193-96	Sequence 96, Appl
145	40	38.8	177	2	US-09-252-991A-26800	Sequence 26800, A	218	39	37.9	121	2	US-09-621-976-7091	Sequence 7091, Ap
146	40	38.8	263	2	US-09-949-016-6757	Sequence 6757, Ap	219	39	37.9	149	2	US-09-252-991A-20746	Sequence 20746, A
147	40	38.8	263	2	US-09-949-016-10472	Sequence 10472, Ap	220	39	37.9	151	2	US-09-489-039A-8828	Sequence 8828, Ap
148	40	38.8	278	1	US-08-722-626B-2	Sequence 2, Appl	221	39	37.9	153	2	US-09-240-639-13	Sequence 13, Appl
149	40	38.8	311	2	US-09-949-016-9126	Sequence 9126, Ap	222	39	37.9	153	2	US-09-908-510A-13	Sequence 13, Appl
150	40	38.8	324	2	US-09-949-016-10414	Sequence 10414, A	223	39	37.9	153	2	US-09-905-744B-13	Sequence 13, Appl
151	40	38.8	370	2	US-10-012-231A-315	Sequence 315, App	224	39	37.9	153	2	US-10-107-660-13	Sequence 13, Appl
152	40	38.8	370	2	US-10-015-389A-315	Sequence 315, App	225	39	37.9	153	2	US-10-107-576-13	Sequence 13, Appl
153	40	38.8	370	2	US-10-006-768A-315	Sequence 315, App	226	39	37.9	153	2	US-09-905-732B-13	Sequence 13, Appl
154	40	38.8	370	2	US-10-015-671A-315	Sequence 315, App	227	39	37.9	153	2	US-09-903-743B-13	Sequence 13, Appl
155	40	38.8	370	2	US-10-015-393A-315	Sequence 315, App	228	39	37.9	153	2	US-09-905-589-13	Sequence 13, Appl
156	40	38.8	370	2	US-10-011-833A-315	Sequence 315, App	229	39	37.9	154	2	US-10-108-171A-13	Sequence 13, Appl
157	40	38.8	370	2	US-10-006-041A-315	Sequence 315, App	230	39	37.9	154	2	US-09-240-639-14	Sequence 14, Appl
158	40	38.8	370	2	US-10-012-064A-315	Sequence 315, App	231	39	37.9	154	2	US-09-908-510A-14	Sequence 14, Appl
159	40	38.8	375	1	US-08-303-238-2	Sequence 2, Appl	232	39	37.9	154	2	US-09-905-744B-14	Sequence 14, Appl
160	40	38.8	375	2	US-08-458-834-2	Sequence 2, Appl	233	39	37.9	154	2	US-10-107-660-14	Sequence 14, Appl
161	40	38.8	393	2	US-09-489-039A-12970	Sequence 12970, A	234	39	37.9	154	2	US-10-107-576-14	Sequence 14, Appl
162	40	38.8	397	2	US-09-540-236-2678	Sequence 2678, Ap	235	39	37.9	154	2	US-09-905-732B-14	Sequence 14, Appl
163	40	38.8	412	2	US-09-252-991A-17613	Sequence 17613, A	236	39	37.9	154	2	US-09-905-743B-14	Sequence 14, Appl
164	40	38.8	422	1	US-08-485-938A-34	Sequence 34, Appl	237	39	37.9	154	2	US-09-905-589-14	Sequence 14, Appl
165	40	38.8	460	2	US-09-826-509-513	Sequence 513, App	238	39	37.9	154	2	US-10-108-171A-14	Sequence 14, Appl
166	40	38.8	462	2	US-09-248-796A-18226	Sequence 18226, A	239	39	37.9	156	2	US-08-928-941D-4	Sequence 4, Appl
167	40	38.8	463	1	US-08-142-439A-2	Sequence 2, Appl	240	39	37.9	156	2	US-09-280-590A-4	Sequence 4, Appl
168	40	38.8	463	1	US-08-869-477-2	Sequence 7, Appl	241	39	37.9	156	2	US-09-280-590A-46	Sequence 46, Appl
169	40	38.8	479	1	US-08-313-553-7	Sequence 7, Appl	242	39	37.9	156	2	US-09-892-398-4	Sequence 4, Appl
170	40	38.8	479	2	US-08-767-993-7	Sequence 7, Appl	243	39	37.9	156	2	US-09-892-398-46	Sequence 46, Appl
171	40	38.8	492	2	US-09-252-991A-20403	Sequence 20403, A	244	39	37.9	170	2	US-09-621-976-7090	Sequence 7090, Ap
172	40	38.8	492	2	US-09-949-016-6256	Sequence 6256, Ap	245	39	37.9	170	2	US-09-252-991A-24327	Sequence 24327, A
173	40	38.8	507	2	US-09-248-796A-15003	Sequence 15003, A	246	39	37.9	173	2		

247	39	37.9	205	2	US-09-640-211A-2248	Sequence 2248, Ap	320	38	36.9	21	1	US-08-383-474B-19	Sequence 19, Appl
248	39	37.9	260	2	US-09-248-796A-16370	Sequence 16370, A	321	38	36.9	21	1	US-08-383-474B-257	Sequence 257, App
249	39	37.9	273	2	US-09-270-767-44062	Sequence 44062, A	322	38	36.9	21	1	US-08-383-474B-273	Sequence 273, App
250	39	37.9	281	2	US-09-134-000C-3380	Sequence 3380, Ap	323	38	36.9	21	1	US-08-465-391A-13	Sequence 13, Appl
251	39	37.9	282	2	US-09-949-016-7977	Sequence 7977, Ap	324	38	36.9	21	1	US-08-465-391A-254	Sequence 254, App
252	39	37.9	293	2	US-09-540-236-2400	Sequence 2400, Ap	325	38	36.9	21	1	US-08-465-391A-369	Sequence 269, App
253	39	37.9	299	2	US-09-540-236-2553	Sequence 2553, Ap	326	38	36.9	21	1	US-08-465-391A-270	Sequence 270, App
254	39	37.9	305	2	US-09-533-029-32	Sequence 32, Appl	327	38	36.9	21	1	US-08-464-538B-13	Sequence 13, Appl
255	39	37.9	316	2	US-09-502-540-10498	Sequence 10498, A	328	38	36.9	21	1	US-08-464-538B-254	Sequence 254, App
256	39	37.9	329	2	US-09-489-039A-14305	Sequence 14305, A	329	38	36.9	21	1	US-08-464-538B-269	Sequence 269, App
257	39	37.9	334	2	US-09-710-794-5	Sequence 5, Appli	330	38	36.9	21	1	US-08-464-538B-270	Sequence 270, App
258	39	37.9	363	2	US-09-792-024-80	Sequence 80, Appl	331	38	36.9	21	1	US-08-463-076B-22	Sequence 22, Appl
259	39	37.9	384	1	US-08-637-759B-375	Sequence 375, App	332	38	36.9	21	1	US-08-463-076B-323	Sequence 323, App
260	39	37.9	384	2	US-08-871-355A-375	Sequence 375, App	333	38	36.9	21	1	US-08-463-076B-324	Sequence 324, App
261	39	37.9	384	2	US-09-201-945-375	Sequence 375, App	334	38	36.9	21	2	US-09-205-258-841	Sequence 841, App
262	39	37.9	384	2	US-09-543-681A-8318	Sequence 8318, Ap	335	38	36.9	21	2	US-09-428-082B-215	Sequence 215, App
263	39	37.9	412	2	US-09-374-586-2	Sequence 2, Appli	336	38	36.9	21	2	US-09-428-082B-856	Sequence 856, App
264	39	37.9	439	2	US-09-248-796A-19538	Sequence 19538, A	337	38	36.9	21	2	US-09-428-082B-888	Sequence 888, App
265	39	37.9	465	2	US-08-416-478A-7	Sequence 7, Appli	338	38	36.9	21	2	US-09-428-082B-889	Sequence 889, App
266	39	37.9	470	1	US-08-474-988B-7	Sequence 7, Appli	339	38	36.9	21	2	US-09-428-082B-902	Sequence 902, App
267	39	37.9	470	1	US-08-394-442B-7	Sequence 7, Appli	340	38	36.9	21	2	US-09-428-082B-920	Sequence 920, App
268	39	37.9	471	1	US-08-416-478A-2	Sequence 2, Appli	341	38	36.9	21	2	US-09-428-082B-959	Sequence 959, App
269	39	37.9	471	1	US-08-474-988B-2	Sequence 2, Appli	342	38	36.9	21	2	US-10-004-860-841	Sequence 841, App
270	39	37.9	471	1	US-08-394-442B-2	Sequence 2, Appli	343	38	36.9	44	2	US-09-640-211A-2298	Sequence 2298, Ap
271	39	37.9	476	1	US-08-737-271-1	Sequence 1, Appli	344	38	36.9	44	2	US-09-640-211A-2131	Sequence 2131, Ap
272	39	37.9	476	2	US-09-058-555-1	Sequence 1, Appli	345	38	36.9	53	2	US-08-651-136C-48	Sequence 48, Appl
273	39	37.9	476	2	US-09-319-014B-11	Sequence 11, Appl	346	38	36.9	53	2	US-09-229-911A-48	Sequence 48, Appl
274	39	37.9	476	5	US-09-931-103-1	Sequence 1, Appli	347	38	36.9	53	2	US-10-007-521-48	Sequence 48, Appl
275	39	37.9	498	1	US-08-416-478A-9	Sequence 9, Appli	348	38	36.9	59	2	US-09-205-258-468	Sequence 468, App
276	39	37.9	498	1	US-08-474-988B-9	Sequence 9, Appli	349	38	36.9	59	2	US-10-004-860-468	Sequence 468, App
277	39	37.9	498	1	US-08-394-442B-9	Sequence 9, Appli	350	38	36.9	60	2	US-08-651-136C-70	Sequence 70, Appl
278	39	37.9	502	2	US-09-543-681A-6427	Sequence 6427, Ap	351	38	36.9	60	2	US-09-229-911A-70	Sequence 70, Appl
279	39	37.9	502	2	US-09-557-800C-55	Sequence 55, Appl	352	38	36.9	60	2	US-10-007-521-70	Sequence 70, Appl
280	39	37.9	538	2	US-09-370-625A-38	Sequence 38, Appl	353	38	36.9	70	2	US-09-886-319A-17	Sequence 17, Appl
281	39	37.9	505	2	US-09-252-991A-18767	Sequence 18767, A	354	38	36.9	70	2	US-09-886-319A-18	Sequence 18, Appl
282	39	37.9	505	2	US-09-543-681A-7151	Sequence 7151, Ap	355	38	36.9	76	2	US-09-640-211A-2123	Sequence 2123, Ap
283	39	37.9	510	2	US-08-930-521-1	Sequence 1, Appli	356	38	36.9	87	2	US-09-949-016-10441	Sequence 10441, A
284	39	37.9	510	2	US-09-781-796C-1	Sequence 1, Appli	357	38	36.9	124	2	US-09-345-236B-140	Sequence 140, App
285	39	37.9	510	2	US-09-374-586-1	Sequence 1, Appli	358	38	36.9	126	2	US-08-772-440-10	Sequence 10, Appl
286	39	37.9	529	2	US-09-949-016-6204	Sequence 6204, Ap	359	38	36.9	128	2	US-09-270-767-48582	Sequence 48582, A
287	39	37.9	539	2	US-09-949-016-8355	Sequence 8355, Ap	360	38	36.9	139	2	US-09-205-258-837	Sequence 837, App
288	39	37.9	564	2	US-09-792-024-68	Sequence 68, Appl	361	38	36.9	139	2	US-10-004-860-837	Sequence 837, App
289	39	37.9	581	2	US-09-499-522-18	Sequence 18, Appl	362	38	36.9	144	2	US-09-205-258-838	Sequence 838, App
290	39	37.9	581	2	US-09-269-939A-12	Sequence 12, Appl	363	38	36.9	144	2	US-10-004-860-838	Sequence 838, App
291	39	37.9	581	2	US-09-499-522-16	Sequence 16, Appl	364	38	36.9	170	2	US-10-004-860-838	Sequence 838, App
292	39	37.9	630	2	US-09-269-939A-10	Sequence 10, Appl	365	38	36.9	174	2	US-09-800-170-12	Sequence 12, Appl
293	39	37.9	634	2	US-09-489-039A-8399	Sequence 8399, Ap	366	38	36.9	176	1	US-07-924-054-8	Sequence 10998, A
294	39	37.9	640	2	US-09-538-092-891	Sequence 891, App	367	38	36.9	176	1	US-08-076-011-2	Sequence 8, Appli
295	39	37.9	645	2	US-09-540-236-2083	Sequence 2083, Ap	368	38	36.9	176	1	US-08-062-472B-20	Sequence 20, Appl
296	39	37.9	649	2	US-09-499-522-14	Sequence 14, Appl	369	38	36.9	176	2	US-08-772-440-8	Sequence 8, Appli
297	39	37.9	649	2	US-09-269-939A-8	Sequence 8, Appli	370	38	36.9	176	2	US-10-279-554-3	Sequence 3, Appli
298	39	37.9	700	2	US-09-976-594-67	Sequence 67, Appl	371	38	36.9	176	6	5198542-4	Patent No. 5198542
299	39	37.9	700	2	US-09-538-092-893	Sequence 893, App	372	38	36.9	180	2	US-08-772-440-31	Sequence 31, Appl
300	39	37.9	745	2	US-09-902-540-10275	Sequence 10275, A	373	38	36.9	199	2	US-08-772-440-13	Sequence 13, Appl
301	39	37.9	751	2	US-09-402-329-2	Sequence 2, Appli	374	38	36.9	203	2	US-09-134-001C-3111	Sequence 3111, Ap
302	39	37.9	752	2	US-09-502-329-6	Sequence 6, Appli	375	38	36.9	205	2	US-09-248-796A-18009	Sequence 18009, A
303	39	37.9	752	2	US-09-538-092-892	Sequence 892, App	376	38	36.9	229	2	US-09-489-039A-8347	Sequence 8347, Ap
304	39	37.9	768	2	US-09-134-000C-6467	Sequence 6467, Ap	377	38	36.9	244	2	US-08-772-440-2	Sequence 2, Appli
305	39	37.9	823	2	US-09-949-016-10470	Sequence 10470, A	378	38	36.9	244	2	US-09-830-230A-462	Sequence 462, App
306	39	37.9	961	2	US-09-914-359-66	Sequence 66, Appl	379	38	36.9	251	2	US-09-489-039A-10403	Sequence 10403, A
307	39	37.9	1064	2	US-08-726-214-8	Sequence 8, Appli	380	38	36.9	262	2	US-09-830-230A-461	Sequence 461, App
308	39	37.9	3118	1	US-08-457-273B-8	Sequence 8, Appli	381	38	36.9	266	2	US-09-325-932A-147	Sequence 147, App
309	39	37.9	3119	1	US-08-246-982A-16	Sequence 16, Appl	382	38	36.9	266	2	US-09-543-681A-4474	Sequence 4474, Ap
310	39	37.9	3119	1	US-08-453-265-16	Sequence 16, Appl	383	38	36.9	286	2	US-09-325-932A-146	Sequence 146, App
311	38.5	37.4	397	2	US-10-243-468-8	Sequence 8, Appli	384	38	36.9	315	2	US-09-489-039A-10235	Sequence 10235, A
312	38.5	37.4	413	2	US-10-243-468-9	Sequence 9, Appli	385	38	36.9	317	2	US-09-816-088-2	Sequence 2, Appli
313	38.5	37.4	419	2	US-09-489-039A-9240	Sequence 9240, Ap	386	38	36.9	317	2	US-09-956-993-2	Sequence 2, Appli
314	38.5	37.4	531	1	US-07-862-588B-7	Sequence 7, Appli	387	38	36.9	325	2	US-09-107-532A-6786	Sequence 6786, Ap
315	38.5	37.4	608	2	US-09-489-039A-13503	Sequence 13503, A	388	38	36.9	336	2	US-09-489-039A-7982	Sequence 7982, App
316	38	36.9	21	1	US-08-190-788A-13	Sequence 13, Appl	389	38	36.9	356	2	US-09-134-000C-6438	Sequence 6438, Ap
317	38	36.9	21	1	US-08-190-788A-254	Sequence 254, App	390	38	36.9	369	2	US-09-816-088-4	Sequence 4, Appli
318	38	36.9	21	1	US-08-190-788A-269	Sequence 269, App	391	38	36.9	369	2	US-09-634-955B-8	Sequence 8, Appli
319	38	36.9	21	1	US-08-190-788A-270	Sequence 270, App	392	38	36.9	369	2	US-09-956-993-4	Sequence 4, Appli

393	38	36.9	369	2	US-09-816-760-8	Sequence 8, Appli	466	37	35.9	34	1	US-08-477-727A-1	Sequence 1, Appli
394	38	36.9	369	2	US-09-838-561-8	Sequence 8, Appli	467	37	35.9	45	2	US-09-640-211A-2353	Sequence 2353, Ap
395	38	36.9	406	2	US-09-252-991A-31269	Sequence 31269, A	468	37	35.9	53	2	US-08-651-136C-54	Sequence 54, Appl
396	38	36.9	407	2	US-10-104-047-3895	Sequence 3895, Ap	469	37	35.9	53	2	US-09-229-911A-54	Sequence 54, Appl
397	38	36.9	468	2	US-09-092-636-9	Sequence 9, Appli	470	37	35.9	53	2	US-10-007-521-54	Sequence 54, Appl
398	38	36.9	470	2	US-09-092-636-4	Sequence 4, Appli	471	37	35.9	59	2	US-08-651-136C-34	Sequence 34, Appl
399	38	36.9	531	2	US-09-902-540-14103	Sequence 14103, A	472	37	35.9	59	2	US-09-229-911A-34	Sequence 34, Appl
400	38	36.9	579	2	US-09-489-039A-9900	Sequence 9900, Ap	473	37	35.9	59	2	US-10-007-521-34	Sequence 34, Appl
401	38	36.9	584	2	US-09-252-991A-24311	Sequence 24311, A	474	37	35.9	60	2	US-09-640-211A-2314	Sequence 2314, Ap
402	38	36.9	667	2	US-09-538-092-1307	Sequence 1307, Ap	475	37	35.9	61	2	US-09-640-211A-2324	Sequence 2324, Ap
403	38	36.9	711	2	US-09-252-991A-29660	Sequence 29660, A	476	37	35.9	62	2	US-09-640-211A-2359	Sequence 2359, Ap
404	38	36.9	717	2	US-10-104-047-3100	Sequence 3100, Ap	477	37	35.9	66	2	US-09-640-211A-2254	Sequence 2254, Ap
405	38	36.9	734	2	US-09-252-991A-33036	Sequence 33036, A	478	37	35.9	78	2	US-09-640-211A-2160	Sequence 2160, Ap
406	38	36.9	941	2	US-09-523-849-34	Sequence 34, Appl	479	37	35.9	85	2	US-09-640-211A-869	Sequence 869, App
407	38	36.9	863	2	US-09-252-991A-19574	Sequence 19574, A	480	37	35.9	88	2	US-09-513-999C-4221	Sequence 4221, Ap
408	38	36.9	941	2	US-09-991-181-353	Sequence 153, App	481	37	35.9	102	2	US-09-640-211A-872	Sequence 872, App
409	38	36.9	941	2	US-09-990-444-353	Sequence 353, App	482	37	35.9	106	2	US-09-894-998A-14	Sequence 14, Appl
410	38	36.9	941	2	US-09-997-333-353	Sequence 353, App	483	37	35.9	106	2	US-10-237-551-14	Sequence 14, Appl
411	38	36.9	941	2	US-09-992-598-353	Sequence 353, App	484	37	35.9	120	2	US-09-902-540-15741	Sequence 15741, A
412	38	36.9	948	2	US-09-620-312D-1105	Sequence 1105, Ap	485	37	35.9	146	2	US-09-640-211A-2110	Sequence 2110, A
413	38	36.9	1088	2	US-08-633-768A-1	Sequence 1, Appli	486	37	35.9	149	2	US-09-902-540-10311	Sequence 10311, A
414	38	36.9	1088	2	US-09-280-197-1	Sequence 1, Appli	487	37	35.9	154	2	US-09-387-418A-8	Sequence 8, Appli
415	38	36.9	1088	2	US-09-423-126-1	Sequence 1, Appli	488	37	35.9	154	2	US-10-090-185-8	Sequence 8, Appli
416	38	36.9	1148	2	US-09-538-092-156	Sequence 156, App	489	37	35.9	159	2	US-09-640-211A-2161	Sequence 2161, Ap
417	38	36.9	1247	1	US-08-472-934-10	Sequence 10, Appl	490	37	35.9	168	2	US-09-148-545-280	Sequence 280, App
418	38	36.9	1247	1	US-08-323-460A-10	Sequence 10, Appl	491	37	35.9	168	2	US-09-621-011-280	Sequence 280, App
419	38	36.9	1247	1	US-08-461-146C-10	Sequence 10, Appl	492	37	35.9	175	2	US-09-640-211A-2223	Sequence 2223, Ap
420	38	36.9	1247	1	US-08-461-145C-10	Sequence 10, Appl	493	37	35.9	184	1	US-08-602-359A-33	Sequence 33, Appl
421	38	36.9	1247	2	US-09-134-000C-4968	Sequence 4968, Ap	494	37	35.9	187	2	US-09-477-962-110	Sequence 110, App
422	38	36.9	1363	2	US-09-375-248-19	Sequence 19, Appl	495	37	35.9	193	2	US-09-894-998A-55	Sequence 55, Appl
423	38	36.9	1597	2	US-09-423-890-13	Sequence 13, Appl	496	37	35.9	193	2	US-10-237-551-55	Sequence 55, Appl
424	38	36.9	2496	2	US-08-628-829-14	Sequence 14, Appl	497	37	35.9	193	2	US-10-237-551-233	Sequence 233, App
425	38	36.9	2496	2	US-09-125-028-2	Sequence 2, Appli	498	37	35.9	194	2	US-09-252-991A-28661	Sequence 28661, A
426	38	36.9	2958	2	US-08-894-344C-2	Sequence 2, Appli	499	37	35.9	209	2	US-09-248-796A-15963	Sequence 15963, A
427	38	36.9	2958	2	US-09-678-023A-2	Sequence 2, Appli	500	37	35.9	213	2	US-09-230-665-8	Sequence 8, Appli
428	37.5	36.4	61	2	US-09-640-211A-2331	Sequence 2331, Ap	501	37	35.9	222	2	US-08-651-136C-14	Sequence 14, Appl
429	37.5	36.4	61	2	US-09-640-211A-2361	Sequence 2361, Ap	502	37	35.9	222	2	US-09-229-911A-14	Sequence 14, Appl
430	37.5	36.4	62	2	US-09-050-010-11	Sequence 11, Appl	503	37	35.9	222	2	US-10-007-521-14	Sequence 14, Appl
431	37.5	36.4	176	2	US-09-640-211A-2238	Sequence 2238, Ap	504	37	35.9	254	2	US-09-252-991A-26526	Sequence 26526, A
432	37.5	36.4	182	1	US-08-127-954-158	Sequence 158, App	505	37	35.9	254	2	US-09-540-236-3796	Sequence 3796, Ap
433	37.5	36.4	182	1	US-08-127-954-159	Sequence 159, App	506	37	35.9	277	2	US-10-237-551-234	Sequence 234, App
434	37.5	36.4	182	1	US-08-127-954-161	Sequence 161, App	507	37	35.9	294	2	US-08-651-136C-24	Sequence 24, Appl
435	37.5	36.4	215	2	US-09-902-540-11802	Sequence 11802, A	508	37	35.9	294	2	US-09-229-911A-24	Sequence 24, Appl
436	37.5	36.4	308	1	US-08-484-905-72	Sequence 72, Appl	509	37	35.9	294	2	US-10-007-521-24	Sequence 24, Appl
437	37.5	36.4	308	2	US-08-481-985B-72	Sequence 72, Appl	510	37	35.9	310	2	US-09-602-777A-328	Sequence 328, App
438	37.5	36.4	308	2	US-08-370-476-72	Sequence 72, Appl	511	37	35.9	313	1	US-08-809-860-2	Sequence 2, Appli
439	37.5	36.4	323	2	US-09-280-197-10	Sequence 10, Appl	512	37	35.9	330	2	US-09-533-427-12	Sequence 12, Appl
440	37.5	36.4	338	2	US-09-710-279-1756	Sequence 1756, Ap	513	37	35.9	335	2	US-09-248-796A-19480	Sequence 19480, A
441	37.5	36.4	364	2	US-08-914-372C-11	Sequence 11, Appl	514	37	35.9	338	2	US-09-807-933B-7	Sequence 7, Appli
442	37.5	36.4	387	2	US-09-270-767-42090	Sequence 42090, A	515	37	35.9	344	2	US-09-489-039A-11932	Sequence 11932, A
443	37.5	36.4	391	2	US-09-640-211A-2259	Sequence 2259, Ap	516	37	35.9	349	2	US-08-651-136C-10	Sequence 10, Appl
444	37.5	36.4	406	2	US-09-134-001C-3202	Sequence 3202, Ap	517	37	35.9	349	2	US-09-229-911A-10	Sequence 10, Appl
445	37.5	36.4	432	2	US-09-902-540-13330	Sequence 13330, A	518	37	35.9	349	2	US-10-007-521-10	Sequence 10, Appl
446	37.5	36.4	470	2	US-09-902-540-9896	Sequence 9896, Ap	519	37	35.9	357	1	US-08-411-777-9	Sequence 9, Appli
447	37.5	36.4	501	2	US-09-687-360-2	Sequence 2, Appli	520	37	35.9	357	1	US-09-057-088-9	Sequence 9, Appli
448	37.5	36.4	503	2	US-09-393-858-14	Sequence 14, Appl	521	37	35.9	362	2	US-09-270-767-41944	Sequence 41944, A
449	37.5	36.4	524	2	US-09-252-991A-27006	Sequence 27006, A	522	37	35.9	365	1	US-08-484-905-104	Sequence 104, App
450	37.5	36.4	704	2	US-09-328-352-5144	Sequence 5144, Ap	523	37	35.9	365	2	US-08-481-985B-104	Sequence 104, App
451	37.5	36.4	1091	2	US-08-633-768A-2	Sequence 2, Appli	524	37	35.9	376	1	US-08-370-476-104	Sequence 4, Appli
452	37.5	36.4	1091	2	US-09-280-197-2	Sequence 2, Appli	525	37	35.9	376	1	US-08-090-013-4	Sequence 4, Appli
453	37.5	36.4	1091	2	US-09-423-126-2	Sequence 2, Appli	526	37	35.9	376	1	US-08-081-328-4	Sequence 4, Appli
454	37.5	36.4	1091	2	US-09-423-126-2	Sequence 2, Appli	527	37	35.9	376	1	US-08-232-249-4	Sequence 4, Appli
455	37	35.9	15	2	US-09-894-998A-29	Sequence 29, Appl	528	37	35.9	376	1	US-08-833-642A-4	Sequence 4, Appli
456	37	35.9	15	2	US-09-894-998A-61	Sequence 61, Appl	529	37	35.9	376	1	US-08-389-423-4	Sequence 4, Appli
457	37	35.9	15	2	US-10-237-551-29	Sequence 29, Appl	530	37	35.9	376	2	US-08-875-972-2	Sequence 2, Appli
458	37	35.9	15	2	US-10-237-551-61	Sequence 61, Appl	531	37	35.9	376	2	US-09-230-665-4	Sequence 4, Appli
459	37	35.9	15	2	US-10-237-551-132	Sequence 132, App	532	37	35.9	376	2	US-09-189-028-4	Sequence 4, Appli
460	37	35.9	21	1	US-08-190-788A-258	Sequence 258, App	533	37	35.9	387	2	US-09-807-933B-9	Sequence 9, Appli
461	37	35.9	21	1	US-08-383-474B-261	Sequence 261, App	534	37	35.9	390	2	US-09-533-427-2	Sequence 2, Appli
462	37	35.9	21	1	US-08-465-391A-258	Sequence 258, App	535	37	35.9	397	2	US-09-902-540-9949	Sequence 9949, Ap
463	37	35.9	21	1	US-08-464-538B-258	Sequence 258, App	536	37	35.9	397	2	US-09-640-211A-2258	Sequence 2258, Ap
464	37	35.9	21	1	US-08-463-076B-312	Sequence 312, App	537	37	35.9	419	2	US-09-011-197-4	Sequence 4, Appli
465	37	35.9	21	2	US-09-428-082B-877	Sequence 877, App	538	37	35.9	440	2	US-09-198-452A-1080	Sequence 1080, Ap

539	37	35.9	440	2	US-09-438-185A-1009	Sequence 1009, Ap	612	37	35.9	1140	2	US-09-651-656-21	Sequence 21, Appl
540	37	35.9	444	2	US-09-583-110-2893	Sequence 2893, Ap	613	37	35.9	1140	2	US-09-650-855-21	Sequence 21, Appl
541	37	35.9	452	2	US-08-764-870-16	Sequence 16, Appl	614	37	35.9	1167	2	US-08-857-078-48	Sequence 48, Appl
542	37	35.9	452	2	US-08-980-115-16	Sequence 115, Appl	615	37	35.9	1167	2	US-09-205-658-48	Sequence 48, Appl
543	37	35.9	463	2	US-09-489-039A-11143	Sequence 11143, A	616	37	35.9	1217	2	US-09-949-016-7454	Sequence 7454, Ap
544	37	35.9	466	2	US-09-107-532A-4022	Sequence 4022, Ap	617	37	35.9	1217	2	US-09-919-891-2	Sequence 2, Appl
545	37	35.9	468	2	US-09-875-076-10	Sequence 10, Appl	618	37	35.9	1255	2	US-09-919-891-2	Sequence 2, Appl
546	37	35.9	468	2	US-09-107-433-3766	Sequence 3766, Ap	619	37	35.9	1375	2	US-09-605-703B-2408	Sequence 2408, Ap
547	37	35.9	485	2	US-09-134-000C-6295	Sequence 6295, Ap	620	36.5	35.4	1375	2	US-09-513-998C-4291	Sequence 4291, Ap
548	37	35.9	490	2	US-09-252-991A-31203	Sequence 31203, A	621	36.5	35.4	175	2	US-09-248-796A-19816	Sequence 19816, A
549	37	35.9	493	1	US-07-615-448A-7	Sequence 7, Appl	622	36.5	35.4	358	2	US-09-949-016-6620	Sequence 6620, Ap
550	37	35.9	493	1	US-08-196-361-7	Sequence 7, Appl	623	36.5	35.4	360	2	US-09-949-016-6620	Sequence 6620, Ap
551	37	35.9	493	1	US-08-446-934-7	Sequence 7, Appl	624	36.5	35.4	440	2	US-09-248-796A-19817	Sequence 19817, A
552	37	35.9	493	1	US-08-448-128-7	Sequence 7, Appl	625	36.5	35.4	440	2	US-08-913-805A-2	Sequence 2, Appl
553	37	35.9	493	2	US-08-948-703-7	Sequence 7, Appl	626	36.5	35.4	575	2	US-08-913-805A-10	Sequence 10, Appl
554	37	35.9	504	2	US-09-489-039A-14253	Sequence 14253, A	627	36.5	35.4	575	2	US-09-442-629-2	Sequence 2, Appl
555	37	35.9	508	2	US-09-489-039A-13548	Sequence 13548, A	628	36.5	35.4	575	2	US-09-442-629-10	Sequence 10, Appl
556	37	35.9	525	2	US-09-543-681A-4542	Sequence 4542, Ap	629	36.5	35.4	575	2	US-09-971-773-24	Sequence 24, Appl
557	37	35.9	550	2	US-09-533-427-14	Sequence 14, Appl	630	36.5	35.4	859	2	US-09-538-092-206	Sequence 206, App
558	37	35.9	576	2	US-09-367-206-1	Sequence 1, Appl	631	36.5	35.4	6396	2	US-09-410-551B-72	Sequence 72, Appl
559	37	35.9	576	2	US-09-367-206-21	Sequence 21, Appl	632	36	35.0	6396	2	US-09-940-316B-72	Sequence 72, Appl
560	37	35.9	576	2	US-09-367-206-22	Sequence 22, Appl	633	36	35.0	9	1	US-08-477-727A-12	Sequence 12, Appl
561	37	35.9	576	2	US-09-367-206-23	Sequence 23, Appl	634	36	35.0	9	1	US-08-477-727A-24	Sequence 24, Appl
562	37	35.9	576	2	US-09-298-404-1	Sequence 1, Appl	635	36	35.0	28	1	US-08-477-727A-37	Sequence 37, Appl
563	37	35.9	576	2	US-09-298-404-21	Sequence 21, Appl	636	36	35.0	28	1	US-08-182-175A-7	Sequence 7, Appl
564	37	35.9	576	2	US-09-298-404-22	Sequence 22, Appl	637	36	35.0	28	4	US-08-182-175A-7	Sequence 7, Appl
565	37	35.9	576	2	US-09-298-404-23	Sequence 23, Appl	638	36	35.0	28	4	PCT-US92-06412-5	Sequence 5, Appl
566	37	35.9	608	2	US-09-134-000C-4810	Sequence 4810, Ap	639	36	35.0	28	4	PCT-US92-06412-7	Sequence 7, Appl
567	37	35.9	610	2	US-09-533-427-3	Sequence 3, Appl	640	36	35.0	33	1	US-08-182-175A-51	Sequence 51, Appl
568	37	35.9	647	2	US-09-583-110-2676	Sequence 2676, Ap	641	36	35.0	33	1	US-08-474-633A-60	Sequence 60, Appl
569	37	35.9	653	2	US-09-107-433-4374	Sequence 4374, Ap	642	36	35.0	33	4	US-08-823-771-60	Sequence 60, Appl
570	37	35.9	654	2	US-10-152-886-49	Sequence 49, Appl	643	36	35.0	33	4	PCT-US92-06412-51	Sequence 51, Appl
571	37	35.9	719	2	US-09-641-741-28	Sequence 28, Appl	644	36	35.0	51	2	US-08-551-136C-46	Sequence 46, Appl
572	37	35.9	722	2	US-09-894-998A-15	Sequence 15, Appl	645	36	35.0	51	2	US-09-229-911A-46	Sequence 46, Appl
573	37	35.9	722	2	US-10-237-551-15	Sequence 15, Appl	646	36	35.0	59	2	US-10-007-521-46	Sequence 46, Appl
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575	37	35.9	722	2	US-10-237-551-235	Sequence 235, App	648	36	35.0	59	2	US-10-004-860-731	Sequence 731, App
576	37	35.9	725	2	US-09-448-796A-20849	Sequence 20849, A	649	36	35.0	65	2	US-09-640-211A-2310	Sequence 2310, Ap
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578	37	35.9	747	2	US-09-252-991A-33003	Sequence 33003, A	651	36	35.0	66	2	US-09-513-999C-4328	Sequence 4328, Ap
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582	37	35.9	770	1	US-08-416-581B-5	Sequence 5, Appl	655	36	35.0	77	4	US-08-823-771-75	Sequence 75, Appl
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586	37	35.9	770	1	US-08-852-091-12	Sequence 12, Appl	659	36	35.0	92	2	US-08-830-894-8	Sequence 8, Appl
587	37	35.9	770	2	US-08-956-652-12	Sequence 12, Appl	660	36	35.0	99	2	US-09-828-648-7	Sequence 7, Appl
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594	37	35.9	770	2	US-08-956-653A-12	Sequence 12, Appl	667	36	35.0	126	2	US-09-209-525-45	Sequence 45, Appl
595	37	35.9	770	2	US-09-526-542-2	Sequence 2, Appl	668	36	35.0	127	2	US-09-377-557-2	Sequence 2, Appl
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843	35.5	34.5	156	2	US-09-513-999C-4289	Sequence 4289, Ap	916	365	1	US-08-484-905-98	Sequence 98, Appl
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847	35.5	34.5	182	1	US-08-127-954-137	Sequence 137, App	920	365	1	US-08-484-905-102	Sequence 102, App
848	35.5	34.5	182	1	US-08-127-954-138	Sequence 138, App	921	365	1	US-08-484-905-103	Sequence 103, App
849	35.5	34.5	182	1	US-08-127-954-139	Sequence 139, App	922	365	2	US-08-481-985B-97	Sequence 97, Appl
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853	35.5	34.5	182	1	US-08-127-954-143	Sequence 143, App	926	365	2	US-08-481-985B-101	Sequence 101, App
854	35.5	34.5	182	1	US-08-127-954-144	Sequence 144, App	927	365	2	US-08-481-985B-102	Sequence 102, App
855	35.5	34.5	182	1	US-08-127-954-145	Sequence 145, App	928	365	2	US-08-481-985B-103	Sequence 103, App
856	35.5	34.5	182	1	US-08-127-954-146	Sequence 146, App	929	365	2	US-08-652-265-23	Sequence 23, Appl
857	35.5	34.5	182	1	US-08-127-954-147	Sequence 147, App	930	365	2	US-08-834-497A-23	Sequence 23, Appl
858	35.5	34.5	182	1	US-08-127-954-148	Sequence 148, App	931	365	2	US-08-370-476-97	Sequence 97, Appl
859	35.5	34.5	182	1	US-08-127-954-149	Sequence 149, App	932	365	2	US-08-370-476-98	Sequence 98, Appl
860	35.5	34.5	182	1	US-08-127-954-150	Sequence 150, App	933	365	2	US-08-370-476-99	Sequence 99, Appl
861	35.5	34.5	182	1	US-08-127-954-151	Sequence 151, App	934	365	2	US-08-370-476-100	Sequence 100, App
862	35.5	34.5	182	1	US-08-127-954-152	Sequence 152, App	935	365	2	US-08-370-476-101	Sequence 101, App
863	35.5	34.5	182	1	US-08-127-954-153	Sequence 153, App	936	365	2	US-08-370-476-102	Sequence 102, App
864	35.5	34.5	182	1	US-08-127-954-154	Sequence 154, App	937	365	2	US-08-370-476-103	Sequence 103, App
865	35.5	34.5	182	1	US-08-127-954-155	Sequence 155, App	938	365	2	US-09-503-444A-23	Sequence 23, Appl
866	35.5	34.5	182	1	US-08-127-954-156	Sequence 156, App	939	380	2	US-09-181-336-17	Sequence 17, Appl
867	35.5	34.5	182	1	US-08-127-954-157	Sequence 157, App	940	380	2	US-09-181-336-19	Sequence 19, Appl
868	35.5	34.5	182	1	US-08-127-954-160	Sequence 160, App	941	410	2	US-09-328-352-4860	Sequence 4860, Ap
869	35.5	34.5	182	1	US-08-127-954-162	Sequence 162, App	942	439	1	US-08-519-103-12	Sequence 12, Appl
870	35.5	34.5	182	1	US-08-127-954-163	Sequence 163, App	943	439	1	US-09-018-635-12	Sequence 12, Appl
871	35.5	34.5	182	1	US-08-127-954-164	Sequence 164, App	944	439	2	US-09-912-962-12	Sequence 12, Appl
872	35.5	34.5	182	1	US-08-127-954-165	Sequence 165, App	945	497	2	US-09-540-236-2136	Sequence 2136, Ap
873	35.5	34.5	182	1	US-08-127-954-166	Sequence 166, App	946	498	2	US-09-489-039A-11588	Sequence 11588, A
874	35.5	34.5	182	1	US-08-127-954-167	Sequence 167, App	947	502	2	US-09-489-039A-13376	Sequence 13376, A
875	35.5	34.5	182	1	US-08-127-954-168	Sequence 168, App	948	527	2	US-09-930-218-16	Sequence 16, Appl
876	35.5	34.5	182	1	US-08-127-954-169	Sequence 169, App	949	530	2	US-09-252-586-2	Sequence 2, Appl1
877	35.5	34.5	182	1	US-08-127-954-170	Sequence 170, App	950	532	2	US-09-181-336-15	Sequence 15, Appl
878	35.5	34.5	182	1	US-08-127-954-171	Sequence 171, App	951	535	2	US-09-435-739-44	Sequence 44, Appl
879	35.5	34.5	182	1	US-08-127-954-172	Sequence 172, App	952	535	2	US-09-930-218-1	Sequence 1, Appl1
880	35.5	34.5	182	1	US-08-127-954-173	Sequence 173, App	953	535	2	US-09-988-113-44	Sequence 44, Appl
881	35.5	34.5	184	2	US-09-153-586-21	Sequence 21, Appl	954	535	2	US-10-384-450A-44	Sequence 44, Appl
882	35.5	34.5	184	2	US-09-585-580-21	Sequence 21, Appl	955	536	2	US-09-930-218-2	Sequence 2, Appl1
883	35.5	34.5	197	2	US-09-486-147-40	Sequence 40, Appl	956	539	1	US-09-949-016-6363	Sequence 6363, Ap
884	35.5	34.5	259	2	US-10-104-047-3455	Sequence 3455, Ap	957	543	1	US-08-922-170B-10	Sequence 10, Appl
885	35.5	34.5	274	1	US-08-222-851-1	Sequence 1, Appl1	958	543	2	US-09-071-739B-2	Sequence 2, Appl1
886	35.5	34.5	274	1	US-08-484-905-105	Sequence 105, App	959	543	2	US-09-181-336-13	Sequence 13, Appl
887	35.5	34.5	274	1	US-08-484-905-106	Sequence 106, App	960	543	2	US-09-260-038B-2	Sequence 2, Appl1
888	35.5	34.5	274	1	US-08-484-905-107	Sequence 107, App	961	543	2	US-09-635-923-3	Sequence 3, Appl1
889	35.5	34.5	274	1	US-08-484-905-108	Sequence 108, App	962	543	2	US-09-487-716A-2	Sequence 2, Appl1
890	35.5	34.5	274	2	US-08-481-985B-105	Sequence 105, App	963	543	2	US-09-322-977-2	Sequence 2, Appl1
891	35.5	34.5	274	2	US-08-481-985B-106	Sequence 106, App	964	543	2	US-09-186-200-1	Sequence 1, Appl1
892	35.5	34.5	274	2	US-08-481-985B-107	Sequence 107, App	965	543	2	US-09-435-739-10	Sequence 10, Appl
893	35.5	34.5	274	2	US-08-481-985B-108	Sequence 108, App	966	543	2	US-09-930-218-3	Sequence 3, Appl1
894	35.5	34.5	274	2	US-08-370-476-105	Sequence 105, App	967	543	2	US-09-704-772A-2	Sequence 2, Appl1
895	35.5	34.5	274	2	US-08-370-476-106	Sequence 106, App	968	543	2	US-09-988-113-10	Sequence 10, Appl
896	35.5	34.5	274	2	US-08-370-476-107	Sequence 107, App	969	543	2	US-09-944-602-2	Sequence 2, Appl1
897	35.5	34.5	274	2	US-08-370-476-108	Sequence 108, App	970	543	2	US-10-368-044A-1	Sequence 1, Appl1
898	35.5	34.5	281	2	US-09-949-016-7369	Sequence 7369, Ap	971	543	2	US-10-384-450A-10	Sequence 10, Appl
899	35.5	34.5	301	1	US-08-484-905-77	Sequence 77, Appl	972	545	2	US-09-899-440-18	Sequence 18, Appl
900	35.5	34.5	301	2	US-08-481-985B-77	Sequence 77, Appl	973	582	2	US-09-601-777-2	Sequence 2, Appl1
901	35.5	34.5	301	2	US-08-370-476-77	Sequence 77, Appl	974	592	2	US-09-435-739-14	Sequence 14, Appl
902	35.5	34.5	308	1	US-08-484-905-71	Sequence 71, Appl	975	592	2	US-09-988-113-14	Sequence 14, Appl
903	35.5	34.5	308	2	US-08-481-985B-71	Sequence 71, Appl	976	592	2	US-10-384-450A-14	Sequence 14, Appl

977 35.5 34.5 595 2 US-10-104-047-2714 Sequence 2714, Ap  
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979 35.5 34.5 763 2 US-09-949-016-7023 Sequence 7023, Ap  
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981 35.5 34.5 810 2 US-09-248-796A-15870 Sequence 15870, A  
982 35.5 34.5 878 2 US-09-735-934A-2 Sequence 2, Appli  
983 35.5 34.5 878 2 US-10-060-332-2 Sequence 2, Appli  
984 35.5 34.5 878 2 US-10-339-657-2 Sequence 2, Appli  
985 35.5 34.5 878 2 US-10-885-879-2 Sequence 2, Appli  
986 35.5 34.5 1479 2 US-08-840-062-4 Sequence 4, Appli  
987 35.5 34.5 2388 2 US-09-695-795A-2 Sequence 2, Appli  
988 35.5 34.5 3290 2 US-09-328-352-5486 Sequence 5486, Ap  
989 35 34.0 6 1 US-08-431-539-11 Sequence 11, Appli  
990 35 34.0 8 1 US-08-477-727A-7 Sequence 7, Appli  
991 35 34.0 8 1 US-08-477-727A-19 Sequence 19, Appli  
992 35 34.0 8 1 US-08-477-727A-32 Sequence 32, Appli  
993 35 34.0 8 1 US-08-477-727A-44 Sequence 44, Appli  
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995 35 34.0 12 2 US-09-548-409B-5 Sequence 5, Appli  
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997 35 34.0 19 1 US-08-310-912A-30 Sequence 30, Appli  
998 35 34.0 19 2 US-08-841-089-30 Sequence 30, Appli  
999 35 34.0 19 2 US-09-301-085-30 Sequence 30, Appli  
1000 35 34.0 19 4 PCT-US95-04570-30

## ALIGNMENTS

RESULT 1  
US-09-174-216-4  
; Sequence 4, Application US/09174216A  
; Patent No. 6335176  
; GENERAL INFORMATION:  
; APPLICANT: Ingelise, James  
; APPLICANT: Glickman, Joseph Fraser  
; TITLE OF INVENTION: Incorporation of Phosphorylation Sites  
; FILE REFERENCE: 1073.050  
; CURRENT APPLICATION NUMBER: US/09/174,216A  
; CURRENT FILING DATE: 1998-10-16  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Designed  
; OTHER INFORMATION: peptide to act as kinase substrate  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-09-174-216-4

Query Match 100.0%; Score 103; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEYAYGWMDF 17  
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Db 1 EGPWLEEEYAYGWMDF 17

RESULT 2  
US-09-623-548A-422  
; Sequence 422, Application US/09623548A  
; Patent No. 6849714  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter

; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623,548A  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 422  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-623-548A-422

Query Match 100.0%; Score 103; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEYAYGWMDF 17  
| | | | | | | | | | | | | | | | | |  
Db 1 EGPWLEEEYAYGWMDF 17

RESULT 3  
US-09-657-276-422  
; Sequence 422, Application US/09657276  
; Patent No. 6887470  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/657,276  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 422  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-657-276-422

Query Match 100.0%; Score 103; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEYAYGWMDF 17

Db 1 EGPWLEEEBAYGMDF 17  
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RESULT 4  
US-08-446-692-74  
; Sequence 74, Application US/08446692  
; Patent No. 5759551  
; GENERAL INFORMATION:  
; APPLICANT: Ladd, Anna  
; APPLICANT: Wang, Chang Yi  
; APPLICANT: Zamb, Timothy  
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Maria C.H. Lin  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10154-0053  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,692  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maria C.H. Lin  
; REGISTRATION NUMBER: 29,323  
; REFERENCE/DOCKET NUMBER: 1151-4146 US2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)415-8745  
; TELEFAX: (516)751-6849  
; INFORMATION FOR SEQ ID NO: 74:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-446-692-74

Query Match 97.1%; Score 100; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 4.4e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEBAYGMDF 17  
:|||||

Db 1 QGPWLEEEBAYGMDF 17  
:|||||

RESULT 5  
US-08-488-351A-74  
; Sequence 74, Application US/08488351A  
; Patent No. 5843446  
; GENERAL INFORMATION:  
; APPLICANT: Ladd, Anna  
; APPLICANT: Wang, Chang Yi  
; APPLICANT: Zamb, Timothy  
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Maria C.H. Lin  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10154-0053

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,351A  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/446,692  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/229,275  
; FILING DATE: 14-APR-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,166  
; FILING DATE: 27-APR-1992  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maria C.H. Lin  
; REGISTRATION NUMBER: 29,323  
; REFERENCE/DOCKET NUMBER: 1151-4146 US2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)415-8745  
; TELEFAX: (516)751-6849  
; INFORMATION FOR SEQ ID NO: 74:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-488-351A-74

Query Match 97.1%; Score 100; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 4.4e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEBAYGMDF 17  
:|||||

Db 1 QGPWLEEEBAYGMDF 17  
:|||||

RESULT 6  
US-09-079-372-17  
; Sequence 17, Application US/09079372  
; Patent No. 6165990  
; GENERAL INFORMATION:  
; APPLICANT: Singh, Pomila  
; APPLICANT: Wood, T.  
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN  
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079,372  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: US 08/634,546

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; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-372-17

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Query Match          97.1%; Score 100; DB 2; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.4e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EGPWLEEEEAAYGWDF 17
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Db 1 QGPWLEEEEAAYGWDF 17

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## RESULT 7

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US-09-079-372-10
; Sequence 10, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-372-10

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Query Match          97.1%; Score 100; DB 2; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.7e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EGPWLEEEEAAYGWDF 17
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Db 1 QGPWLEEEEAAYGWDF 17

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## RESULT 8

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US-09-079-372-15
; Sequence 15, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-372-15

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Query Match          97.1%; Score 100; DB 2; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.7e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EGPWLEEEEAAYGWDF 17
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Db 1 QGPWLEEEEAAYGWDF 17

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## RESULT 9

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US-09-079-372-12
; Sequence 12, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372

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;; FILING DATE: Concurrently Herewith  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA: US 08/634,546  
;; FILING DATE: 18-APR-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Hodgins, Daniel S.  
;; REGISTRATION NUMBER: 31,026  
;; REFERENCE/DOCKET NUMBER: UTSG:220  
;; INFORMATION FOR SEQ ID NO: 12:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 21 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
US-09-079-372-12

Query Match 97.1%; Score 100; DB 2; Length 21;  
Best Local Similarity 94.1%; Pred. No. 5.5e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17  
DB 5 QGPWLEEEERAYGWMDF 21  
:|||||

RESULT 10  
US-10-360-101-170  
; Sequence 170, Application US/10360101  
; Patent No. 6861236  
; GENERAL INFORMATION:  
; APPLICANT: Moll, Gert N.  
; APPLICANT: Leenhouts, Cornelis J.  
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way  
; FILE REFERENCE: 2183-5673  
; CURRENT APPLICATION NUMBER: US/10/360,101  
; PRIOR FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: EP 02077060.8  
; PRIOR FILING DATE: 2002-05-24  
; NUMBER OF SEQ ID NOS: 309  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 170  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: S8,C11-sequence of Big Gastrin-1  
US-10-360-101-170

Query Match 97.1%; Score 100; DB 2; Length 33;  
Best Local Similarity 94.1%; Pred. No. 9e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17  
DB 17 QGPWLEEEERAYGWMDF 33  
:|||||

RESULT 11  
US-08-446-692-69  
; Sequence 69, Application US/08446692  
; Patent No. 5759551  
; GENERAL INFORMATION:  
; APPLICANT: Ladd, Anna  
; APPLICANT: Wang, Chang Yi  
; APPLICANT: Zamb, Timothy  
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Maria C.H. Lin  
; STREET: 345 Park Avenue  
; CITY: New York

;; STATE: NY  
;; COUNTRY: US  
;; ZIP: 10154-0053  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/446,692  
;; FILING DATE: 7-JUN-1995  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Maria C.H. Lin  
;; REGISTRATION NUMBER: 29,323  
;; REFERENCE/DOCKET NUMBER: 1151-4146 US2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)415-8745  
;; TELEFAX: (516)751-6849  
;; INFORMATION FOR SEQ ID NO: 69:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 34 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-446-692-69

Query Match 97.1%; Score 100; DB 1; Length 34;  
Best Local Similarity 94.1%; Pred. No. 9.2e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17  
DB 18 QGPWLEEEERAYGWMDF 34  
:|||||

RESULT 12  
US-08-488-351A-69  
; Sequence 69, Application US/08488351A  
; Patent No. 5843446  
; GENERAL INFORMATION:  
; APPLICANT: Ladd, Anna  
; APPLICANT: Wang, Chang Yi  
; APPLICANT: Zamb, Timothy  
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Maria C.H. Lin  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10154-0053  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/488,351A  
;; FILING DATE: 7-JUN-1995  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/446,692  
;; FILING DATE: 7-JUN-1995  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/229,275  
;; FILING DATE: 14-APR-1994  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/057,166

1 FILING DATE: 27-APR-1992  
2 CLASSIFICATION: 424  
3 ATTORNEY/AGENT INFORMATION:  
4 NAME: Maria C.H. Lin  
5 REGISTRATION NUMBER: 29,323  
6 REFERENCE/DOCKET NUMBER: 1151-4146 US2  
7 TELECOMMUNICATION INFORMATION:  
8 TELEPHONE: (212)415-8745  
9 TELEFAX: (516)751-6849  
10 INFORMATION FOR SEQ ID NO: 69:  
11 SEQUENCE CHARACTERISTICS:  
12 LENGTH: 34 amino acids  
13 TYPE: amino acid  
14 TOPOLOGY: linear  
15 MOLECULE TYPE: peptide  
16 US-08-488-351A-69

Query Match 97.1%; Score 100; DB 1; Length 34;  
Best Local Similarity 94.1%; Pred. No. 9.2e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMD 17  
DB 18 QGPWLEEEERAYGWMD 34

RESULT 13  
US-09-079-372-9  
1 Sequence 9, Application US/09079372  
2 Patent No. 6165990  
3 GENERAL INFORMATION:  
4 APPLICANT: Singh, Pomila  
5 TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN  
6 TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER  
7 NUMBER OF SEQUENCES: 17  
8 CORRESPONDENCE ADDRESS:  
9 ADDRESSEE: Arnold, White & Durkee  
10 STREET: P.O. Box 4433  
11 CITY: Houston  
12 STATE: Texas  
13 COUNTRY: United States of America  
14 ZIP: 77210

15 COMPUTER READABLE FORM:  
16 MEDIUM TYPE: Floppy disk  
17 COMPUTER: IBM PC compatible  
18 OPERATING SYSTEM: PC-DOS/MS-DOS  
19 SOFTWARE: Patent In Release #1.0, Version #1.30  
20 CURRENT APPLICATION DATA:  
21 FILING DATE: Concurrently Herewith  
22 CLASSIFICATION:  
23 PRIOR APPLICATION DATA:  
24 APPLICATION NUMBER: US 08/634,546  
25 FILING DATE: 18-APR-1996  
26 ATTORNEY/AGENT INFORMATION:  
27 NAME: Hodgins, Daniel S.  
28 REGISTRATION NUMBER: 31,026  
29 REFERENCE/DOCKET NUMBER: UTSG:220  
30 INFORMATION FOR SEQ ID NO: 9:  
31 SEQUENCE CHARACTERISTICS:  
32 LENGTH: 34 amino acids  
33 TYPE: amino acid  
34 STRANDEDNESS:  
35 TOPOLOGY: linear

Query Match 97.1%; Score 100; DB 2; Length 34;  
Best Local Similarity 94.1%; Pred. No. 9.2e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMD 17  
DB 18 QGPWLEEEERAYGWMD 34

RESULT 14  
US-09-079-372-16  
1 Sequence 16, Application US/09079372  
2 Patent No. 6165990  
3 GENERAL INFORMATION:  
4 APPLICANT: Singh, Pomila  
5 APPLICANT: Wood, T.  
6 TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN  
7 TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER  
8 NUMBER OF SEQUENCES: 17  
9 CORRESPONDENCE ADDRESS:  
10 ADDRESSEE: Arnold, White & Durkee  
11 STREET: P.O. Box 4433  
12 CITY: Houston  
13 STATE: Texas  
14 COUNTRY: United States of America  
15 ZIP: 77210

16 COMPUTER READABLE FORM:  
17 MEDIUM TYPE: Floppy disk  
18 COMPUTER: IBM PC compatible  
19 OPERATING SYSTEM: PC-DOS/MS-DOS  
20 SOFTWARE: Patent In Release #1.0, Version #1.30  
21 CURRENT APPLICATION DATA:  
22 FILING DATE: Concurrently Herewith  
23 CLASSIFICATION:  
24 PRIOR APPLICATION DATA:  
25 APPLICATION NUMBER: US 08/634,546  
26 FILING DATE: 18-APR-1996  
27 ATTORNEY/AGENT INFORMATION:  
28 NAME: Hodgins, Daniel S.  
29 REGISTRATION NUMBER: 31,026  
30 REFERENCE/DOCKET NUMBER: UTSG:220  
31 INFORMATION FOR SEQ ID NO: 9:  
32 SEQUENCE CHARACTERISTICS:  
33 LENGTH: 34 amino acids  
34 TYPE: amino acid  
35 STRANDEDNESS:  
36 TOPOLOGY: linear

Query Match 97.1%; Score 100; DB 2; Length 34;  
Best Local Similarity 94.1%; Pred. No. 9.2e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMD 17  
DB 18 QGPWLEEEERAYGWMD 34

DB 18 QGPWLEEEERAYGWMD 34

RESULT 14  
US-09-079-372-16  
1 Sequence 16, Application US/09079372  
2 Patent No. 6165990  
3 GENERAL INFORMATION:  
4 APPLICANT: Singh, Pomila  
5 APPLICANT: Wood, T.  
6 TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN  
7 TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER  
8 NUMBER OF SEQUENCES: 17  
9 CORRESPONDENCE ADDRESS:  
10 ADDRESSEE: Arnold, White & Durkee  
11 STREET: P.O. Box 4433  
12 CITY: Houston  
13 STATE: Texas  
14 COUNTRY: United States of America  
15 ZIP: 77210

16 COMPUTER READABLE FORM:  
17 MEDIUM TYPE: Floppy disk  
18 COMPUTER: IBM PC compatible  
19 OPERATING SYSTEM: PC-DOS/MS-DOS  
20 SOFTWARE: Patent In Release #1.0, Version #1.30  
21 CURRENT APPLICATION DATA:  
22 APPLICATION NUMBER: US/09/079,372  
23 FILING DATE: Concurrently Herewith  
24 CLASSIFICATION:  
25 PRIOR APPLICATION DATA:  
26 APPLICATION NUMBER: US 08/634,546  
27 FILING DATE: 18-APR-1996  
28 ATTORNEY/AGENT INFORMATION:  
29 NAME: Hodgins, Daniel S.  
30 REGISTRATION NUMBER: 31,026  
31 REFERENCE/DOCKET NUMBER: UTSG:220  
32 INFORMATION FOR SEQ ID NO: 16:  
33 SEQUENCE CHARACTERISTICS:  
34 LENGTH: 34 amino acids  
35 TYPE: amino acid  
36 STRANDEDNESS:  
37 TOPOLOGY: linear

US-09-079-372-16  
Query Match 97.1%; Score 100; DB 2; Length 34;  
Best Local Similarity 94.1%; Pred. No. 9.2e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMD 17  
DB 18 QGPWLEEEERAYGWMD 34

RESULT 15  
US-09-623-548A-423  
1 Sequence 423, Application US/09623548A  
2 Patent No. 6849714  
3 GENERAL INFORMATION:  
4 APPLICANT: Conjuchem, Inc.  
5 APPLICANT: Bridon, Dominique  
6 APPLICANT: Ezrin, Alan  
7 APPLICANT: Milner, Peter  
8 APPLICANT: Holmes, Darren  
9 APPLICANT: Thibodeau, Karen  
10 TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
11 TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
12 COMPONENTS  
13 FILE REFERENCE: 2110  
14 CURRENT APPLICATION NUMBER: US/09/623,548A  
15 CURRENT FILING DATE: 2000-09-05  
16 PRIOR APPLICATION NUMBER: 60/134,406  
17 PRIOR FILING DATE: 1999-05-17  
18 PRIOR APPLICATION NUMBER: 60/153,406

Query Match 97.1%; Score 100; DB 2; Length 34;  
Best Local Similarity 94.1%; Pred. No. 9.2e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMD 17  
DB 18 QGPWLEEEERAYGWMD 34

RESULT 15  
US-09-623-548A-423  
1 Sequence 423, Application US/09623548A  
2 Patent No. 6849714  
3 GENERAL INFORMATION:  
4 APPLICANT: Conjuchem, Inc.  
5 APPLICANT: Bridon, Dominique  
6 APPLICANT: Ezrin, Alan  
7 APPLICANT: Milner, Peter  
8 APPLICANT: Holmes, Darren  
9 APPLICANT: Thibodeau, Karen  
10 TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
11 TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
12 COMPONENTS  
13 FILE REFERENCE: 2110  
14 CURRENT APPLICATION NUMBER: US/09/623,548A  
15 CURRENT FILING DATE: 2000-09-05  
16 PRIOR APPLICATION NUMBER: 60/134,406  
17 PRIOR FILING DATE: 1999-05-17  
18 PRIOR APPLICATION NUMBER: 60/153,406

;/ PRIOR FILING DATE: 1999-09-10  
;/ PRIOR APPLICATION NUMBER: 60/159,783  
;/ PRIOR FILING DATE: 1999-10-18  
;/ NUMBER OF SEQ ID NOS: 1617  
;/ SOFTWARE: PatentIn Ver. 2.1  
;/ SEQ ID NO 423  
;/ LENGTH: 34  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;/ OTHER INFORMATION: Peptide  
US-09-623-548A-423

Query Match 97.1%; Score 100; DB 2; Length 34;  
Best Local Similarity 94.1%; Pred. No. 9.2e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWMDF 17  
DB 18 QGPWLEEEBAYGWMDF 34

RESULT 16  
US-09-657-276-423  
; Sequence 423, Application US/09657276  
; Patent No. 6887470

;/ GENERAL INFORMATION:  
;/ APPLICANT: Conjugchem, Inc.  
;/ APPLICANT: Bridon, Dominique  
;/ APPLICANT: Ezrin, Alan  
;/ APPLICANT: Milner, Peter  
;/ APPLICANT: Holmes, Darren  
;/ APPLICANT: Thibaudau, Karen

;/ TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
;/ TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
;/ TITLE OF INVENTION: COMPONENTS  
;/ FILE REFERENCE: 2110

;/ CURRENT APPLICATION NUMBER: US/09/657,276  
;/ CURRENT FILING DATE: 2000-09-07  
;/ PRIOR APPLICATION NUMBER: 60/134,406  
;/ PRIOR FILING DATE: 1999-05-17  
;/ PRIOR APPLICATION NUMBER: 60/153,406  
;/ PRIOR FILING DATE: 1999-09-10  
;/ PRIOR APPLICATION NUMBER: 60/159,783  
;/ PRIOR FILING DATE: 1999-10-18  
;/ NUMBER OF SEQ ID NOS: 1617  
;/ SOFTWARE: PatentIn Ver. 2.1

;/ SEQ ID NO 423  
;/ LENGTH: 34  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;/ OTHER INFORMATION: Peptide  
US-09-657-276-423

Query Match 97.1%; Score 100; DB 2; Length 34;  
Best Local Similarity 94.1%; Pred. No. 9.2e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWMDF 17  
DB 18 QGPWLEEEBAYGWMDF 34

RESULT 17  
US-09-079-372-8  
; Sequence 8, Application US/09079372  
; Patent No. 6165990  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Singh, Pomila  
;/ APPLICANT: Wood, T.

;/ TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN  
;/ TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER  
;/ NUMBER OF SEQUENCES: 17  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSES: Arnold, White & Durkee  
;/ STREET: P.O. Box 4433  
;/ CITY: Houston  
;/ STATE: Texas  
;/ COUNTRY: United States of America  
;/ ZIP: 77210

;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/09/079,372  
;/ FILING DATE: Concurrently Herewith

;/ CLASSIFICATION:  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/634,546  
;/ FILING DATE: 18-APR-1996  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Hodgins, Daniel S.  
;/ REGISTRATION NUMBER: 31,026  
;/ REFERENCE/DOCKET NUMBER: UTSG:220  
;/ INFORMATION FOR SEQ ID NO: 8:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 35 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS:  
;/ TOPOLOGY: linear  
US-09-079-372-8

Query Match 97.1%; Score 100; DB 2; Length 35;  
Best Local Similarity 94.1%; Pred. No. 9.5e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWMDF 17  
DB 18 QGPWLEEEBAYGWMDF 34

RESULT 18

US-08-446-692-99  
; Sequence 99, Application US/08446692  
; Patent No. 5759551

;/ GENERAL INFORMATION:

;/ APPLICANT: Ladd, Anna  
;/ APPLICANT: Wang, Chang Yi  
;/ APPLICANT: Zamb, Timothy  
;/ TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
;/ TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
;/ NUMBER OF SEQUENCES: 114  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSES: Maria C.H. Lin  
;/ STREET: 345 Park Avenue  
;/ CITY: New York  
;/ STATE: NY  
;/ COUNTRY: US

;/ ZIP: 10154-0053

;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ OPERATING SYSTEM: IBM PC compatible  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/446,692  
;/ FILING DATE: 7-JUN-1995  
;/ CLASSIFICATION: 424  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Maria C.H. Lin  
;/ REGISTRATION NUMBER: 29,323

```
/
/ REFERENCE/DOCKET NUMBER: 1151-4146 US2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)415-8745
/ TELEFAX: (516)751-6849
/ INFORMATION FOR SEQ ID NO: 99:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 52 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-446-692-95

Query Match 97.1%; Score 100; DB 1; Length 52;
Best Local Similarity 94.1%; Pred. No. 1.5e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEYGNWDF 17
Db 36 QGPWLEEEEEEYGNWDF 52

RESULT 19
US-08-488-351A-99
; Sequence 99, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-95

Query Match 97.1%; Score 100; DB 1; Length 69;
Best Local Similarity 94.1%; Pred. No. 2e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEYGNWDF 17
Db 18 QGPWLEEEEEEYGNWDF 34

RESULT 21
US-08-488-351A-95
; Sequence 95, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
```

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Maria C.H. Lin  
;; STREET: 345 Park Avenue  
;; CITY: New York  
;; STATE: NY  
;; COUNTRY: US  
;; ZIP: 10154-0053  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/488,351A  
;; FILING DATE: 7-JUN-1995  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/446,692  
;; FILING DATE: 7-JUN-1995  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/229,275  
;; FILING DATE: 14-APR-1994  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/057,166  
;; FILING DATE: 27-APR-1992  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Maria C.H. Lin  
;; REGISTRATION NUMBER: 29,323  
;; REFERENCE/DOCKET NUMBER: 1151-4146 US2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)415-8745  
;; TELEFAX: (516)751-6849  
;; INFORMATION FOR SEQ ID NO: 95:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 69 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-488-351A-95

Query Match 97.1%; Score 100; DB 1; Length 69;  
Best Local Similarity 94.1%; Pred. No. 2e-07;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEAYGWDF 17  
Db 18 QGPWLEEEAYGWDF 34

RESULT 22  
US-09-079-372-7  
; Sequence 7, Application US/09079372  
; Patent No. 6165990  
; GENERAL INFORMATION:  
; APPLICANT: Singh, Pomila  
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN  
; NUMBER OF INVENTIONS: 17  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/079,372  
;; FILING DATE: Concurrently Herewith  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/634,546  
;; FILING DATE: 18-APR-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Hodgins, Daniel S.  
;; REGISTRATION NUMBER: 31,026  
;; REFERENCE/DOCKET NUMBER: UTSG:220  
;; INFORMATION FOR SEQ ID NO: 7:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 74 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
US-09-079-372-7

Query Match 97.1%; Score 100; DB 2; Length 74;  
Best Local Similarity 94.1%; Pred. No. 2.1e-07;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEAYGWDF 17  
Db 55 QGPWLEEEAYGWDF 71

RESULT 23  
US-09-079-372-14  
; Sequence 14, Application US/09079372  
; Patent No. 6165990  
; GENERAL INFORMATION:  
; APPLICANT: Singh, Pomila  
; APPLICANT: Wood, T.  
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN  
; NUMBER OF INVENTIONS: 17  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079,372  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/634,546  
; FILING DATE: 18-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hodgins, Daniel S.  
; REGISTRATION NUMBER: 31,026  
; REFERENCE/DOCKET NUMBER: UTSG:220  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 100 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-09-079-372-14

Query Match 97.1%; Score 100; DB 2; Length 100;  
Best Local Similarity 94.1%; Pred. No. 2.9e-07;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGFWLEEEAYGWMD 17  
:|||||  
Db 75 QGPWLEEEAYGWMD 91

## RESULT 24

US-09-949-016-11739  
; Sequence 11739, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11739  
; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-11739

Query Match 97.1%; Score 100; DB 2; Length 122;  
Best Local Similarity 94.1%; Pred. No. 3.6e-07;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGFWLEEEAYGWMD 17  
:|||||  
Db 97 QGPWLEEEAYGWMD 113

## RESULT 25

US-09-174-263-2  
; Sequence 2, Application US/09174263  
; Patent No. 6319898  
; GENERAL INFORMATION:  
; APPLICANT: Davies, J.  
; APPLICANT: Walters, B.  
; APPLICANT: Saxena, G.  
; TITLE OF INVENTION: METHOD FOR INHIBITING EUKARYOTIC PROTEIN KINASES  
; FILE REFERENCE: 9993-007  
; CURRENT APPLICATION NUMBER: US/09/174,263  
; CURRENT FILING DATE: 1998-10-16  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Biotinylated peptide substrate  
; NAME/KEY: SITE  
; LOCATION: (1)  
; OTHER INFORMATION: Xaa=Biotin-Glu  
US-09-174-263-2

Query Match 95.1%; Score 98; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.6e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GFWLEEEAYGWMD 17  
:|||||  
Db 2 GFWLEEEAYGWMD 17

## RESULT 26

US-09-623-548A-424  
; Sequence 424, Application US/09623548A  
; Patent No. 6849714  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623,548A  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 424  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-623-548A-424

Query Match 75.7%; Score 78; DB 2; Length 17;  
Best Local Similarity 82.4%; Pred. No. 6.4e-05;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGFWLEEEAYGWMD 17  
:|||||  
Db 1 ERPPWEEAYGWMD 17

## RESULT 27

US-09-657-276-424  
; Sequence 424, Application US/09657276  
; Patent No. 6887470  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/657,276  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 424  
; LENGTH: 17  
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-424

Query Match          75.7%; Score 78; DB 2; Length 17;
Best Local Similarity 82.4%; Pred. No. 6.4e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEEBEEAYGMDP 17
   | | | | | | | | | |
Db 1 ERPPMEEBEEAYGMDP 17

RESULT 28
US-08-127-351-3
; Sequence 3, Application US/08127351
; Patent No. 5449761
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT, P.C.
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 28-SEP-1993
; CLASSIFICATION: 534
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-127-351-3

Query Match          71.4%; Score 73.5; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 0.00028;
Matches 14; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 EGPWLEEEBEEAYGMD 16
   | | | | | | | | | |
Db 2 EGPWL-EEEBEAYGMD 16

RESULT 30
US-08-487-221A-3
; Sequence 3, Application US/08487221A
; Patent No. 5593656
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
US-08-480-367B-3

Query Match          71.4%; Score 73.5; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 0.00028;
Matches 14; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 EGPWLEEEBEEAYGMD 16
   | | | | | | | | | |
Db 2 EGPWL-EEEBEAYGMD 16

RESULT 30
US-08-487-221A-3
; Sequence 3, Application US/08487221A
; Patent No. 5593656
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
US-08-480-367B-3

Query Match          71.4%; Score 73.5; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 0.00028;
Matches 14; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 EGPWLEEEBEEAYGMD 16
   | | | | | | | | | |
Db 2 EGPWL-EEEBEAYGMD 16

RESULT 29
US-08-480-367B-3
; Sequence 3, Application US/08480367B
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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/487,221A
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/127,351
/ FILING DATE: 28-SEP-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Villacorta, Gilberto M.
/ REGISTRATION NUMBER: 34,038
/ REFERENCE/DOCKET NUMBER: 4980-004-44
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 413-3000
/ TELEFAX: (703) 413-2220
/ TELEX: 248855 OPAT UR
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
US-08-487-221A-3

Query Match 71.4%; Score 73.5; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 0.00028;
Matches 14; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 EGPWLEEEEEEYGWMD 16
Db 2 EGPWL-FEEYGWMD 16

RESULT 31
US-08-480-370-3
Sequence 3, Application US/08480370
Patent No. 5609847
GENERAL INFORMATION:
APPLICANT: BELINKA JR, BENJAMIN A.
APPLICANT: COUGHLIN, DANIEL J.
APPLICANT: ALVAREZ, VERNON L.
APPLICANT: WOOD, RICHARD
TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
TITLE OF INVENTION: CONSTRUCTS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
ADDRESSEE: NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,370
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,351
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-004-44
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
```

```
/ TELEFAX: (703) 413-2220
/ TELEX: 248855 OPAT UR
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
US-08-480-370-3

Query Match 71.4%; Score 73.5; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 0.00028;
Matches 14; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 EGPWLEEEEEEYGWMD 16
Db 2 EGPWL-FEEYGWMD 16

RESULT 32
US-08-652-971-10
Sequence 10, Application US/08652971
Patent No. 5814507
GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
PHOSPHATASE, PTP LAMBDA
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
STATE: California
COUNTRY: United States
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,971
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1033
TELECOMMUNICATION INFORMATION:
```

; TELEPHONE: (415) 225-3216  
; TELEFAX: (415) 952-9881  
; TELEX: 910 371-7168  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-652-971-10

Query Match 67.0%; Score 69; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00087;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEY 12  
Db 1 EGPWLEEEY 12

RESULT 34  
US-08-991-258A-10  
; Sequence 10, Application US/08991258A  
; Patent No. 5928887  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT, LLP  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/991.258A  
; FILING DATE: 17-DEC-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/652,971  
; FILING DATE: 24-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-63478-3/WH/NTK  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-991-258A-10

Query Match 67.0%; Score 69; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00087;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEY 12  
Db 1 EGPWLEEEY 12

Db 1 EGPWLEEEY 12  
RESULT 35  
US-08-769-399-10  
; Sequence 10, Application US/08769399  
; Patent No. 5976852  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd.  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/769,399  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Ginger R.  
; REGISTRATION NUMBER: 33,055  
; REFERENCE/DOCKET NUMBER: P1033  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 225-3216  
; TELEFAX: (415) 952-9881  
; TELEX: 910 371-7168  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-769-399-10

Query Match 67.0%; Score 69; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00087;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEY 12  
Db 1 EGPWLEEEY 12

RESULT 36  
US-08-991-953A-10  
; Sequence 10, Application US/08991953A  
; Patent No. 6083748  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT, LLP  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111  
; COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ FILING DATE: 16-DEC-1997  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION NUMBER: US/08/991,953A  
/ APPLICATION NUMBER: US 08/652,971  
/ FILING DATE: 24-MAY-1996  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Dreger, Walter H.  
/ REGISTRATION NUMBER: 24,190  
/ REFERENCE/DOCKET NUMBER: A-63478-3/WH/D/MTK  
/ TELEPHONE: (415) 781-1989  
/ TELEFAX: (415) 398-3249  
/ TELEX:  
/ INFORMATION FOR SEQ ID NO: 10:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 12 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS:  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
US-08-991-953A-10

Query Match 67.0%; Score 69; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00087;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEY 12  
Db 1 EGPWLEEEY 12

RESULT 37  
US-08-446-692-75  
; Sequence 75, Application US/08446692  
; Patent No. 5759551  
; GENERAL INFORMATION:  
; APPLICANT: Ladd, Anna  
; APPLICANT: Wang, Chang Yi  
; APPLICANT: Zamb, Timothy  
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Maria C.H. Lin  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10154-0053  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,692  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maria C.H. Lin  
; REGISTRATION NUMBER: 29,323  
; REFERENCE/DOCKET NUMBER: 1151-4146 US2  
; TELEPHONE: (212)415-8745  
; TELEFAX: (516)751-6849  
; INFORMATION FOR SEQ ID NO: 75:  
; SEQUENCE CHARACTERISTICS:

/ LENGTH: 12 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
US-08-446-692-75

Query Match 64.1%; Score 66; DB 1; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.0023;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEY 12  
Db 1 QGPWLEEEY 12

RESULT 38  
US-08-488-351A-75  
; Sequence 75, Application US/08488351A  
; Patent No. 5843446  
; GENERAL INFORMATION:  
; APPLICANT: Ladd, Anna  
; APPLICANT: Wang, Chang Yi  
; APPLICANT: Zamb, Timothy  
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Maria C.H. Lin  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10154-0053  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,351A  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/446,692  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/229,275  
; FILING DATE: 14-APR-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,166  
; FILING DATE: 27-APR-1992  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maria C.H. Lin  
; REGISTRATION NUMBER: 29,323  
; REFERENCE/DOCKET NUMBER: 1151-4146 US2  
; TELEPHONE: (212)415-8745  
; TELEFAX: (516)751-6849  
; INFORMATION FOR SEQ ID NO: 75:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-488-351A-75

Query Match 64.1%; Score 66; DB 1; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.0023;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEY 12  
:|||||  
Db 1 QGPWLEEEY 12

## RESULT 39

US-08-446-692-100  
; Sequence 100, Application US/08446692  
; Patent No. 5759551  
; GENERAL INFORMATION:  
; APPLICANT: Ladd, Anna  
; APPLICANT: Wang, Chang Yi  
; APPLICANT: Zamb, Timothy  
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Maria C.H. Lin  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10154-0053  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,692  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maria C.H. Lin  
; REGISTRATION NUMBER: 29,323  
; REFERENCE/DOCKET NUMBER: 1151-4146 US2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)415-8745  
; TELEFAX: (516)751-6849  
; INFORMATION FOR SEQ ID NO: 100:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 47 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-446-692-100

Query Match 64.1%; Score 66; DB 1; Length 47;  
Best Local Similarity 91.7%; Pred. No. 0.01;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEY 12  
:|||||  
Db 36 QGPWLEEEY 47

## RESULT 40

US-08-488-351A-100  
; Sequence 100, Application US/08488351A  
; Patent No. 5843446  
; GENERAL INFORMATION:  
; APPLICANT: Ladd, Anna  
; APPLICANT: Wang, Chang Yi  
; APPLICANT: Zamb, Timothy  
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Maria C.H. Lin  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: US

ZIP: 10154-0053  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,351A  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/446,692  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/229,275  
; FILING DATE: 14-APR-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,166  
; FILING DATE: 27-APR-1992  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maria C.H. Lin  
; REGISTRATION NUMBER: 29,323  
; REFERENCE/DOCKET NUMBER: 1151-4146 US2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)415-8745  
; TELEFAX: (516)751-6849  
; INFORMATION FOR SEQ ID NO: 100:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 47 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-488-351A-100

Query Match 64.1%; Score 66; DB 1; Length 47;  
Best Local Similarity 91.7%; Pred. No. 0.01;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEY 12  
:|||||  
Db 36 QGPWLEEEY 47

## RESULT 41

US-08-178-570-69  
; Sequence 69, Application US/08178570  
; Patent No. 5532167  
; GENERAL INFORMATION:  
; APPLICANT: Lewis C. Cantley  
; APPLICANT: Zhou Song Yang  
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 STATE STREET, suite 510  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/178,570  
; FILING DATE: JANUARY 7, 1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A., Jr.

```
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-004
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-178-570-69

Query Match 52.4%; Score 54; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EEEAYGWMD 16
Db 1 EEEAYGWMD 9

RESULT 42
US-08-369-643-69
; Sequence 69, Application US/08369643A
; Patent No. 6004757
; GENERAL INFORMATION:
; APPLICANT: Cantley, Lewis C.
; APPLICANT: Songyang, Zhou
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; FILE REFERENCE: CNS-001CP
; CURRENT APPLICATION NUMBER: US/08/369,643A
; CURRENT FILING DATE: 1995-01-06
; EARLIER APPLICATION NUMBER: US 08/178,570
; EARLIER FILING DATE: 1994-01-07
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Gastrin
US-08-369-643-69

Query Match 52.4%; Score 54; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EEEAYGWMD 16
Db 1 EEEAYGWMD 9

RESULT 43
PCT-US95-00147-69
; Sequence 69, Application PC/TUS9500147
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
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; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00147
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,570
; FILING DATE: JANUARY 7, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-004CPPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US95-00147-69

Query Match 52.4%; Score 54; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EEEAYGWMD 16
Db 1 EEEAYGWMD 9

RESULT 44
US-08-151-219-1
; Sequence 1, Application US/08151219
; Patent No. 5468494
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,219
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE: N-terminal  
 US-08-151-219-1

Query Match 52.4%; Score 54; DB 1; Length 16;  
 Best Local Similarity 81.8%; Pred. No. 0.17;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEEEA 11  
 ||||| :  
 Db 1 EGPWLEEESS 11

## RESULT 45

PCT-US94-13205-1  
 ; Sequence 1, Application PC/TUS9413205

; GENERAL INFORMATION:  
 ; APPLICANT: Gevas, Philip C.  
 ; APPLICANT: Grimes, Stephen  
 ; APPLICANT: Karr, Stephen  
 ; APPLICANT: Michaeli, Dov  
 ; APPLICANT: Scibienski, Robert  
 ; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dimitrios T. Drivas, White and Case  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 100036

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/13205  
 ; FILING DATE: 12-NOV-1993  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Drivas, Dimitrios T.  
 ; REGISTRATION NUMBER: 32,218  
 ; REFERENCE/DOCKET NUMBER: 1102865-028  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 819-8286  
 ; TELEFAX: (212) 354-8113  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 16 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE: N-terminal  
 PCT-US94-13205-1

Query Match 52.4%; Score 54; DB 4; Length 16;  
 Best Local Similarity 81.8%; Pred. No. 0.17;  
 Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 EGPWLEEEEA 11  
 ||||| :  
 Db 1 EGPWLEEESS 11

## RESULT 46

US-08-151-219-2  
 ; Sequence 2, Application US/08151219

; Patent No. 5468494  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gevas, Philip C.  
 ; APPLICANT: Grimes, Stephen  
 ; APPLICANT: Karr, Stephen  
 ; APPLICANT: Michaeli, Dov  
 ; APPLICANT: Scibienski, Robert  
 ; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dimitrios T. Drivas, White and Case  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 100036

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/151,219  
 ; FILING DATE: 12-NOV-1993  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Drivas, Dimitrios T.  
 ; REGISTRATION NUMBER: 32,218  
 ; REFERENCE/DOCKET NUMBER: 1102865-028  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 819-8286  
 ; TELEFAX: (212) 354-8113  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE: N-terminal  
 US-08-151-219-2

Query Match 51.5%; Score 53; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEER 9  
 ||||| :  
 Db 1 EGPWLEEEE 9

## RESULT 47

PCT-US94-13205-2  
 ; Sequence 2, Application PC/TUS9413205

; GENERAL INFORMATION:  
 ; APPLICANT: Gevas, Philip C.  
 ; APPLICANT: Grimes, Stephen  
 ; APPLICANT: Karr, Stephen  
 ; APPLICANT: Michaeli, Dov  
 ; APPLICANT: Scibienski, Robert  
 ; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dimitrios T. Drivas, White and Case  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 100036

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13205
; FILING DATE: 12-NOV-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; PCT-US94-13205-2

Query Match 51.5%; Score 53; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

RESULT 48
US-08-151-219-4
; Sequence 4, Application US/08151219
; Patent No. 5468494
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13205
; FILING DATE: 12-NOV-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; PCT-US94-13205-4

Query Match 51.5%; Score 53; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9
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```
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-151-219-4

Query Match 51.5%; Score 53; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

RESULT 49
PCT-US94-13205-4
; Sequence 4, Application PC/TUS9413205
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13205
; FILING DATE: 12-NOV-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; PCT-US94-13205-4

Query Match 51.5%; Score 53; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9
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RESULT 50
US-09-270-767-45243
; Sequence 45243, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45243
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45243

Query Match      50.5%; Score 52; DB 2; Length 307;
Best Local Similarity 50.0%; Pred. No. 7.6;
Matches      8; Conservative      5; Mismatches      3; Indels      0; Gaps      0;

Qy      1 EGPWLEEEYAYGMD 16
Db      133 DAPVQEEHHGWIE 148

Search completed: January 3, 2006, 09:19:39
Job time : 41.1667 secs
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:05 ; Search time 171.619 Seconds  
(without alignments)  
43.523 Million cell updates/sec

Title: US-10-759-832-1  
Perfect score: 103  
Sequence: 1 EGPWLEEEBAYGWDP 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	100.0	17	2 AAW65184	Aaw65184 Gastrin f
2	103	100.0	17	2 AAW24398	Aaw24398 Carboxy-a
3	103	100.0	17	4 AAU05580	Aau05580 Human Jan
4	103	100.0	17	4 AAB91246	Aab91246 Gastrin r
5	103	100.0	17	4 AAB59273	Aab59273 KS2-pepti
6	103	100.0	17	5 AAU76504	Aau76504 Protein k
7	103	100.0	17	7 ADF72769	Adf72769 Chemosele
8	103	100.0	17	8 ADF72934	Adf72934 Biotinyla
9	103	100.0	17	8 ADH10240	Adh10240 Peptide s
10	103	100.0	17	8 ADH89206	Adh89206 Gastrin G
11	103	100.0	17	8 ADK00577	Adk00577 Immunogen
12	103	100.0	17	8 ADL02105	Adl02105 Phosphope
13	103	100.0	17	8 ADN03334	Adn03334 Exemplary
14	103	100.0	17	8 ADK42169	Adk42169 Gastrin r
15	103	100.0	17	8 ADT49596	Adt49596 Human mat
16	103	100.0	17	8 ADU48549	Adu48549 Gastrin-1
17	103	100.0	17	9 ADV16301	Adv16301 Human gas
18	103	100.0	17	9 ADW00242	Adw00242 Human wil
19	103	100.0	17	9 ADW71906	Adw71906 Non-phosp
20	103	100.0	17	9 AEA08308	Aea08308 PTK domai
21	103	100.0	17	9 AEA52649	Aea52649 Kinase bi
22	103	100.0	17	9 AEB25345	Aeb25345 Peptide u
23	103	100.0	17	9 AEB77639	Aeb77639 Gastrin-1
24	103	100.0	17	9 AEC05671	Aec05671 Gastrin p

25	103	100.0	18	2 AAW24397	Aaw24397 Glycine-e
26	103	100.0	18	8 ADH89207	Adh89207 Glycine e
27	103	100.0	18	8 ADT49597	Adt49597 Human gas
28	103	100.0	18	9 AEC05677	Aec05677 Gastrin p
29	103	100.0	34	8 ADT49598	Adt49598 Human gas
30	103	100.0	35	8 ADT49599	Adt49599 Human gas
31	100	97.1	17	2 AAR62739	Aar62739 Gastrin h
32	100	97.1	17	4 AAY72387	Aay72387 Human ami
33	100	97.1	17	8 ADU48550	Adu48550 Gastrin-1
34	100	97.1	17	8 ADU24445	Adu24445 Novel glu
35	100	97.1	17	8 ADU46719	Adu46719 Gastrin 1
36	100	97.1	17	9 ADV16302	Adv16302 Human gas
37	100	97.1	17	9 ADW00243	Adw00243 Human var
38	100	97.1	17	9 ADZ71375	Adz71375 N-termina
39	100	97.1	17	9 AEB92577	Aeb92577 Glutamin
40	100	97.1	18	2 AAW31639	Aaw31639 Human gly
41	100	97.1	18	4 AAY72381	Aay72381 Human pro
42	100	97.1	18	4 AAY72385	Aay72385 Human gly
43	100	97.1	21	2 AAW31641	Aaw31641 Gastrin p
44	100	97.1	21	4 AAY72383	Aay72383 Human pro
45	100	97.1	33	7 ABR83022	Abr83022 Gastrin-r
46	100	97.1	33	8 ADL92093	Adl92093 Big gastr
47	100	97.1	33	9 ADW00233	Adw00233 Human wil
48	100	97.1	34	2 AAR62734	Aar62734 Gastrin h
49	100	97.1	34	2 AAW31638	Aaw31638 Amidated
50	100	97.1	34	4 AAB91247	Aab91247 Gastrin r
51	100	97.1	34	4 AAY72380	Aay72380 Human pro
52	100	97.1	34	4 AAY72386	Aay72386 Human ami
53	100	97.1	34	5 ABB82195	Abb82195 Gastrin 3
54	100	97.1	34	7 ADJ68390	Adj68390 Human hea
55	100	97.1	34	8 ADU70137	Adu70137 Gastrin p
56	100	97.1	34	8 ADU48547	Adu48547 Gastrin-3
57	100	97.1	34	9 ADV16299	Adv16299 Human gas
58	100	97.1	34	9 ADU77732	Adu77732 Gastrin p
59	100	97.1	34	9 ADW00240	Adw00240 Human wil
60	100	97.1	34	9 AEB77640	Aeb77640 Big gastr
61	100	97.1	34	9 AEB98013	Aeb98013 Gastrin 3
62	100	97.1	35	2 AAW31637	Aaw31637 Amidated
63	100	97.1	35	4 AAY72379	Aay72379 Human pro
64	100	97.1	52	2 AAR62749	Aar62749 Immunogen
65	100	97.1	52	9 AEB98018	Aeb98018 Gastrin 5
66	100	97.1	59	2 AAR62745	Aar62745 Immunogen
67	100	97.1	74	2 AAW31636	Aaw31636 Human pro
68	100	97.1	74	4 AAY72378	Aay72378 Human pro
69	100	97.1	80	8 ADT54946	Adt54946 Human pro
70	100	97.1	100	4 AAY72384	Aay72384 Human pre
71	100	97.1	101	1 AAP90331	Aap90331 Recombina
72	100	97.1	101	8 ADU48551	Adu48551 Gastrin-3
73	100	97.1	101	9 ADU77736	Adu77736 Gastrin p
74	100	97.1	101	9 AEB98017	Aeb98017 Gastrin 7
75	98	95.1	16	3 AAB13767	Aab13767 Tyrosine
76	98	95.1	16	9 ADW00235	Adw00235 Human wil
77	98	95.1	17	5 ABB82194	Abb82194 Gastrin 1
78	98	95.1	17	8 ADU70139	Adu70139 Gastrin p
79	98	95.1	17	8 ADT54950	Adt54950 Human pro
80	98	95.1	17	9 ADU77734	Adu77734 Gastrin p
81	98	95.1	17	9 AEB98015	Aeb98015 Gastrin 1
82	98	95.1	18	8 ADT54949	Adt54949 Human pro
83	97	94.2	17	9 AEA36970	Aea36970 Phosphoty
84	97	94.2	33	8 ADW00234	Adw00234 Human var
85	97	94.2	34	8 ADU70138	Adu70138 Gastrin p
86	97	94.2	34	8 ADU48548	Adu48548 Gastrin-3
87	97	94.2	34	9 ADV16300	Adv16300 Human gas
88	97	94.2	34	9 ADU77733	Adu77733 Gastrin p
89	97	94.2	34	9 ADW00241	Adw00241 Human var
90	97	94.2	34	9 AEB98014	Aeb98014 Gastrin 3
91	96	93.2	17	9 AEA51268	Aea51268 Ligand-co
92	96	93.2	19	5 AAU74405	Aau74405 Lys3-Gast
93	96	93.2	19	7 ADF45101	Adf45101 Kemptide .
94	96	93.2	19	9 ADW76494	Adw76494 Peptide #
95	95	92.2	16	9 ADW00236	Adw00236 Human var
96	95	92.2	17	8 ADU70140	Adu70140 Gastrin p
97	95	92.2	17	9 ADU77735	Adu77735 Gastrin p

98	95	92.2	17	9	AEB98016	Aeb98016	Gastrin 1	171	46.5	45.1	1453	4	ABG21028	Abg21028	Novel hum
99	92	89.3	17	8	ADT54959	Adt54959	Human pro	172	46.5	45.1	1537	4	ABG21029	Abg21029	Novel hum
100	92	89.3	18	8	ADT54956	Adt54956	Human pro	173	46.5	45.1	1565	8	ADN99207	Adn99207	Desmulin
101	92	89.3	18	8	ADT54955	Adt54955	Human pro	174	46.5	45.1	1614	7	ADN95277	Adn95277	Human BEC
102	90	87.4	16	1	AAP71246	Aap71246	Non-radio	175	46.5	45.1	3648	8	ADP30076	Adp30076	Human sec
103	88.5	85.9	18	8	ADN29118	Adn29118	Human bio	176	46.5	45.1	3776	8	ADP30075	Adp30075	Human sec
104	86	83.5	17	8	ADT54960	Adt54960	Human pro	177	46.5	45.1	5373	4	AAU14603	Aau14603	Novel bon
105	85	82.5	14	9	AEB98019	Aeb98019	Gastrin 1	178	46.5	45.1	5373	7	ADJ68935	Adj68935	Human hea
106	80.5	78.2	18	8	ADO51612	Ado51612	Phosphory	179	46.5	45.1	5430	9	ADZ85102	Adz85102	Full-length
107	80	77.7	18	8	ADT54957	Adt54957	Human pro	180	46.5	45.1	5447	4	AAU14697	Aau14697	Novel bon
108	78	75.7	17	4	ABP91248	Abp91248	Gastrin r	181	46	44.7	9	8	ADT54961	Adt54961	Human pro
109	75	72.8	34	4	AA846553	Aa846553	Synthetic	182	46	44.7	37	2	AAW04956	Aaw04956	Partial p
110	74	71.8	14	8	ADT54954	Adt54954	Human pro	183	46	44.7	204	2	AAW53970	Aaw53970	Myccelioph
111	70.5	68.4	27	9	AEC05676	Aec05676	Gastrin T	184	46	44.7	205	8	ADO26418	Ado26418	H insoln
112	70	68.0	13	8	ADT54965	Adt54965	Human pro	185	46	44.7	205	8	ADO26420	Ado26420	H insoln
113	70	68.0	13	8	ADT54966	Adt54966	Human pro	186	46	44.7	205	8	ADO26419	Ado26419	H insoln
114	69	67.0	12	2	AA806245	Aa806245	Antigenic	187	46	44.7	205	8	ADO26416	Ado26416	H insoln
115	69	67.0	13	9	ADY37657	Ady37657	Human G17	188	46	44.7	206	9	AEA35114	Aea35114	S. coccoc
116	68	66.0	18	8	ADT54958	Adt54958	Human pro	189	46	44.7	206	9	ABE69296	Abe69296	Surfactan
117	66	64.1	12	2	AAR62740	Aar62740	Gastrin h	190	46	44.7	223	5	AAO15070	Aao15070	Humicola
118	66	64.1	12	9	ADY37667	Ady37667	Human G17	191	46	44.7	223	5	AAO15070	Aao15070	Humicola
119	66	64.1	47	2	AAR62750	Aar62750	Immunogen	192	46	44.7	223	9	AEA35117	Aea35117	S. coccoc
120	62	60.2	11	9	ADW00245	Adw00245	Human wil	193	46	44.7	225	2	AAW04925	Aaw04925	Cellulyti
121	62	60.2	34	5	AAU85979	Aau85979	Modified	194	46	44.7	225	3	AAW04925	Aaw04925	Amino aci
122	60	58.3	10	4	AA846952	Aa846952	Synthetic	195	46	44.7	225	4	ABW00707	Abw00707	Chrysoopo
123	59	57.3	17	8	ADH89223	Adh89223	Gastrin G	196	46	44.7	225	7	ABW00707	Abw00707	Chrysoopo
124	59	57.3	28	9	ADW00244	Adw00244	Human wil	197	46	44.7	282	1	AAU09405	Aau09405	Human phe
125	58	56.3	10	8	ADH89213	Adh89213	Gastrin G	198	46	44.7	282	6	ABU09405	Abu09405	Human phe
126	58	56.3	19	9	AEC05672	Aec05672	Gastrin t	199	46	44.7	282	8	ADH13186	Adh13186	Human mal
127	57.5	55.8	19	9	AEC05674	Aec05674	Gastrin t	200	46	44.7	282	9	AEA15073	Aea15073	Human pol
128	57.5	55.8	20	9	AEC05675	Aec05675	Gastrin t	201	46	44.7	282	9	AEA08357	Aea08357	Human phe
129	57	55.3	11	8	ADT54952	Adt54952	Human pro	202	46	44.7	297	2	AAW04933	Aaw04933	Chimeric
130	55	53.4	9	8	ADT49601	Adt49601	Human G17	203	46	44.7	308	2	AAW04934	Aaw04934	Chimeric
131	54	52.4	9	2	AAR79712	Aar79712	EGF recep	204	46	44.7	332	5	ABB07514	Abb07514	Human dru
132	54	52.4	9	3	AAV67913	Aav67913	Gastrin p	205	46	44.7	367	3	AAW04934	Aaw04934	Arabidops
133	54	52.4	10	7	ABR83037	AbR83037	Gastrin-r	206	46	44.7	367	3	AAW04934	Aaw04934	Arabidops
134	54	52.4	15	7	ABR83042	AbR83042	Gastrin-r	207	46	44.7	367	3	AAW04934	Aaw04934	Arabidops
135	54	52.4	15	7	ABR83043	AbR83043	Gastrin-l	208	46	44.7	367	8	ADT43505	Adt43505	Plant tra
136	54	52.4	16	2	AAV74295	Aav74295	Human gas	209	46	44.7	367	8	ADO01719	Ado01719	Thalecres
137	54	52.4	16	3	AAV49309	Aav49309	Human hep	210	46	44.7	367	9	ASA26741	Asa26741	Stress to
138	54	52.4	16	6	ABP73035	Abp73035	Peptide s	211	46	44.7	367	9	ASA26741	Asa26741	Stress to
139	54	52.4	458	7	ADM26800	Adm26800	Hyperther	212	46	44.7	373	3	AAW04934	Aaw04934	Arabidops
140	53.5	51.9	13	4	AA837631	Aa837631	Cholesteryl	213	46	44.7	373	3	AAW04934	Aaw04934	Arabidops
141	53	51.5	9	2	AAW24399	Aaw24399	Anti-gaet	214	46	44.7	471	4	ABG10785	Abg10785	Novel hum
142	53	51.5	9	3	AAV59434	Aav59434	Antigastri	215	45.5	44.2	489	3	AAV84603	Aav84603	Amino aci
143	53	51.5	9	3	AAV51305	Aav51305	Human gas	216	45.5	44.2	612	6	ABU18437	Abu18437	Pseudomon
144	53	51.5	9	8	ADH89212	Adh89212	Gastrin G	217	45	43.7	7	1	AAV50373	Aav50373	Protein e
145	53	51.5	10	9	AEC05673	Aec05673	Gastrin p	218	45	43.7	8	2	AAV50373	Aav50373	Protein e
146	53	51.5	15	2	AAV74297	Aav74297	Human gas	219	45	43.7	8	2	AAV62741	Aav62741	Gastrin h
147	52	50.5	999	4	AB858837	Ab858837	Drosophil	220	45	43.7	21	8	ADR41103	Adr41103	Cyclic KD
148	52	50.5	1000	8	ADP56594	Adp56594	Drosophil	221	45	43.7	21	8	ADR51151	Adr51151	Duo bindi
149	50	48.5	8	1	AAV50374	Aav50374	Gastric a	222	45	43.7	21	8	ADU40146	Adu40146	Kinase do
150	50	48.5	238	5	AAU93061	Aau93061	Arabidops	223	45	43.7	70	8	ADP45238	Adp45238	Human INP
151	50	48.5	238	7	ADP30031	Adp30031	Plant yle	224	45	43.7	117	8	ADQ65620	Adq65620	Wheat LLS
152	50	48.5	238	8	ADT44105	Adt44105	Plant tra	225	45	43.7	144	3	AAW23464	Aaw23464	Wheat LLS
153	50	48.5	238	8	ADT61441	Adt61441	A. thalia	226	45	43.7	250	2	AAV38794	Aav38794	Monoglyce
154	50	48.5	238	8	ADO02415	Ado02415	Thalecres	227	45	43.7	368	8	ADY25276	Ady25276	Plant ful
155	50	48.5	766	8	ADY22351	Ady22351	Plant ful	228	45	43.7	375	6	ABU40398	Abu40398	Protein e
156	49	47.6	8	2	AAV79689	Aav79689	pp60(c-8r	229	45	43.7	511	8	ADP45240	Adp45240	Human INP
157	49	47.6	8	3	AAV57990	Aav57990	Gastrin p	230	45	43.7	516	6	ADM68879	Adm68879	Bacterial
158	49	47.6	308	8	ADM66914	Adm66914	Plant ful	231	45	43.7	899	8	ADN98031	Adn98031	Phototrab
159	48	46.6	8	8	ADH89211	Adh89211	Gastrin G	232	45	43.7	1082	6	ABW70317	Abw70317	Pengue vi
160	48	46.6	210	7	ABG74059	Abg74059	Pseudomon	233	45	43.7	3396	2	AAV43662	Aav43662	DEN1-S275
161	48	46.6	759	4	ABG25868	Abg25868	Novel hum	234	44.5	43.2	121	8	ADQ66204	Adq66204	Novel hum
162	48	46.6	759	4	ABG29793	Abg29793	Novel hum	235	44.5	43.2	417	7	ABM88463	Abm88463	Rice abio
163	48	46.6	820	4	ABG08556	Abg08556	Novel hum	236	44.5	43.2	460	9	ABM96390	Abm96390	M. xanthu
164	47	45.6	303	4	ABGL0786	Abgl0786	Novel hum	237	44	42.7	7	1	AAV40033	Aav40033	Sequence
165	46.5	45.1	135	4	ABGL12791	Abgl12791	Novel hum	238	44	42.7	7	3	AAV51308	Aav51308	Human gas
166	46.5	45.1	1062	8	ADR09311	Adr09311	Human pro	239	44	42.7	8	2	AAW21347	Aaw21347	Gastrin p
167	46.5	45.1	1253	7	ADJ70041	Adj70041	Human hea	240	44	42.7	8	9	ADW39615	Adw39615	HMG CoA r
168	46.5	45.1	1253	9	ADY54967	Ady54967	Chronic v	241	44	42.7	14	2	AAW06249	Aaw06249	Antigenic
169	46.5	45.1	1374	7	ADB75269	Adb75269	Prostate	242	44	42.7	14	9	ADY37666	Ady37666	Human G17
170	46.5	45.1	1402	5	ABF43694	Abf43694	Human mRN	243	44	42.7	103	9	ABM94723	Abm94723	M. xanthu

244	44	42.7	131	3	RAY77146	Ray77146 Pinctada	317	43	41.7	334	8	ADX91745	Adx91745 Plant ful
245	44	42.7	131	3	RAY77148	Ray77148 Pinctada	318	43	41.7	335	9	ADM17421	Adm17421 Eucalyptu
246	44	42.7	131	3	RAY77149	Ray77149 Pinctada	319	43	41.7	339	8	ADW17422	Adw17422 Eucalyptu
247	44	42.7	274	5	ABB49300	Abb49300 Listeria	320	43	41.7	340	8	ADY10688	Ady10688 Plant ful
248	44	42.7	304	8	ADX77578	Adx77578 Plant ful	321	43	41.7	342	3	AGG26270	Agg26270 Arabidops
249	44	42.7	316	8	ADX90115	Adx90115 Plant ful	322	43	41.7	374	8	ADX72635	Adx72635 Plant ful
250	44	42.7	344	7	ABO61832	AbO61832 Klebsiell	323	43	41.7	396	5	ABP28665	Abp28665 Streptoco
251	44	42.7	400	6	ADA34160	Ada34160 Acinetoba	324	43	41.7	396	8	ADU69534	AdU69534 S agalact
252	44	42.7	424	5	ABP47762	Abp47762 Protein #	325	43	41.7	396	8	ADV87856	Adv87856 Streptoco
253	44	42.7	424	5	ABP47762	Abp47762 Protein #	326	43	41.7	396	8	ADV79109	Adv79109 Streptoco
254	44	42.7	637	9	ABE39871	AbE39871 L. pneumo	327	43	41.7	396	8	ADV81308	Adv81308 Streptoco
255	44	42.7	642	9	ABE36461	AbE36461 L. pneumo	328	43	41.7	444	9	ABE39950	AbE39950 L. pneumo
256	44	42.7	1100	8	ADN46390	Adn46390 Thermoco	329	43	41.7	453	9	ABE36556	AbE36556 L. pneumo
257	44	42.7	1105	1	APF71667	Apf71667 Translati	330	43	41.7	491	7	ADM26057	Adm26057 Hyperther
258	44	42.7	1150	7	ABM85422	Abm85422 Mouse pro	331	43	41.7	495	7	ADG76091	Adg76091 Human NOV
259	44	42.7	1150	7	ABM85422	Abm85422 Mouse pro	332	43	41.7	510	8	ADL83282	Adl83282 Human PRO
260	44	42.7	1413	5	ABE21729	AbE21729 Human PKI	333	43	41.7	510	8	ABM80328	Abm80328 Tumour-as
261	44	42.7	1460	7	ADC59465	AdC59465 Novel hum	334	43	41.7	560	8	ABM84746	Abm84746 Human dia
262	43.5	42.2	1460	8	ADU04632	AdU04632 Human KIA	335	43	41.7	560	8	ABM84744	Abm84744 Human dia
263	43.5	42.2	2105	8	ADO44170	AdO44170 Structura	336	43	41.7	560	8	ABM84747	Abm84747 Human dia
264	43.5	42.2	2649	7	ADP79929	Adp79929 Human put	337	43	41.7	560	8	ABM84748	Abm84748 Human dia
265	43.5	42.2	2649	8	ADQ14317	AdQ14317 Human bul	338	43	41.7	569	5	ABR97213	AbR97213 Novel hum
266	43.5	42.2	2649	8	ADR41699	AdR41699 Human bul	339	43	41.7	569	8	ADR67096	Adr67096 Human can
267	43.5	42.2	2649	9	ABE77779	AbE77779 Human bul	340	43	41.7	579	8	ABM84742	Abm84742 Human dia
268	43.5	42.2	3215	8	ADS11060	AdS11060 Human the	341	43	41.7	579	8	ABM84745	Abm84745 Human dia
269	43.5	42.2	3227	8	ADS11061	AdS11061 Human the	342	43	41.7	580	4	ABB74666	Abb74666 Mouse hig
270	43.5	42.2	5171	7	ADJ70881	AdJ70881 Human hea	343	43	41.7	580	4	ABY74664	AbY74664 Rat high
271	43	41.7	7	8	ADH89210	AdH89210 Gastrin G	344	43	41.7	580	4	ABY72388	AbY72388 Mouse P4P
272	43	41.7	10	1	APF50992	Apf50992 Cholecyst	345	43	41.7	580	7	ADD50641	Add50641 Mouse hig
273	43	41.7	10	1	APF50993	Apf50993 Cholecyst	346	43	41.7	580	7	ADD50661	Add50661 Mouse hig
274	43	41.7	10	1	APF50991	Apf50991 Cholecyst	347	43	41.7	580	7	ADD50643	Add50643 Rat high-
275	43	41.7	10	1	APF50991	Apf50991 Cholecyst	348	43	41.7	580	9	ADV77901	Adv77901 Rat high-
276	43	41.7	57	3	ABR33331	AbR33331 Eucalyptu	349	43	41.7	580	9	ADV77899	Adv77899 Mouse hig
277	43	41.7	64	3	ABR33338	AbR33338 Eucalyptu	350	43	41.7	580	9	ADV77919	Adv77919 Mouse hig
278	43	41.7	75	2	AAW04940	Aaw04940 Partial X	351	43	41.7	590	4	ABA848374	Aab48373 Human SEC
279	43	41.7	90	5	ABP32822	Abp32822 Human ORF	352	43	41.7	596	4	ABA848374	Aab48373 Human SEC
280	43	41.7	94	2	AAV31902	AAv31902 Soybean c	353	43	41.7	623	8	ABM84741	Abm84741 Human dia
281	43	41.7	108	8	ADW74718	AdW74718 Plant ful	354	43	41.7	624	4	ABA848378	Aab48378 Human SEC
282	43	41.7	130	5	ADK36663	AdK36663 Novel hum	355	43	41.7	626	8	ADP83519	Adp83519 Breast sp
283	43	41.7	154	6	ABU17002	Abu17002 Protein e	356	43	41.7	634	7	ADD18234	Add18234 Human mol
284	43	41.7	159	7	ADCO1314	AdC01314 Enterohae	357	43	41.7	634	7	ADG76089	Adg76089 Human NOV
285	43	41.7	161	4	ABBS2823	AbB52823 Escherich	358	43	41.7	638	7	ADD18239	Add18239 Human mol
286	43	41.7	161	7	ADC00191	AdC00191 Enterohae	359	43	41.7	638	7	ADD18237	Add18237 Human mol
287	43	41.7	162	3	AAAB33249	AAb33249 Eucalyptu	360	43	41.7	638	7	ADG76097	Adg76097 Human NOV
288	43	41.7	163	6	ADA34878	Ada34878 Acinetoba	361	43	41.7	638	7	ADG76095	Adg76095 Human NOV
289	43	41.7	191	3	AAAB33222	AAb33222 Eucalyptu	362	43	41.7	652	8	ABM84740	Abm84740 Human dia
290	43	41.7	205	8	ADJ48497	AdJ48497 Maize oil	363	43	41.7	652	8	ABM84743	Abm84743 Human dia
291	43	41.7	260	8	ADM78378	AdM78378 Plant ful	364	43	41.7	654	9	ADX26333	Adx26333 Novel cel
292	43	41.7	262	9	ABM96555	Abm96555 M. xanthu	365	43	41.7	662	7	ABM90165	Abm90165 Rice abio
293	43	41.7	264	4	AAAB90778	AAb90778 Human she	366	43	41.7	671	8	ABM80948	Abm80948 Tumour-as
294	43	41.7	264	5	ADZ58739	Adz58739 Human NNM	367	43	41.7	688	2	AAW06316	Aaw06316 TRP-1 pro
295	43	41.7	264	6	ADP58089	Adp58089 Human nic	368	43	41.7	704	3	ADC00981	AdC00981 Enterohae
296	43	41.7	264	7	ADN95843	Adn95843 Human BEC	369	43	41.7	714	3	AAAB42266	Aab42266 Human ORF
297	43	41.7	264	8	ADM67198	Adm67198 Human adi	370	43	41.7	718	9	ADX06699	Adx06699 Cyclin-de
298	43	41.7	264	8	ADN97330	Adn97330 Human nic	371	43	41.7	721	5	ADC97372	AdC97372 E. faeciu
299	43	41.7	264	8	ADQ75755	AdQ75755 Nicotinam	372	43	41.7	785	5	ABU60951	Abu60951 Lung spec
300	43	41.7	264	8	ADR11776	AdR11776 Human N-m	373	43	41.7	785	6	ABU18435	AbJ18435 Breast sp
301	43	41.7	264	8	ABM81310	Abm81310 Tumour-as	374	43	41.7	792	8	ADN27045	Adn27045 Bacterial
302	43	41.7	264	8	ADU18092	AdU18092 Human can	375	43	41.7	794	8	ADR67098	Adr67098 Human can
303	43	41.7	264	9	ADV70247	Adv70247 Tumour-as	376	43	41.7	805	5	ABBS98402	Abb98402 Human NOV
304	43	41.7	266	3	AAAB43845	AAb43845 Human can	377	43	41.7	833	4	AAE03640	Aae03640 Human ext
305	43	41.7	274	8	ADX73048	AdX73048 Plant ful	378	43	41.7	833	5	AAE18214	Aae18214 Human MOL
306	43	41.7	280	8	ADX79361	AdX79361 Plant ful	379	43	41.7	833	5	AAE18215	Aae18215 Human MOL
307	43	41.7	292	4	AAAG92580	AAg92580 C glutami	380	43	41.7	833	5	AAE18213	Aae18213 Human MOL
308	43	41.7	292	7	ADC08061	AdC08061 Rice prot	381	43	41.7	833	5	ADJ128039	AdJ128039 ECMCAD pr
309	43	41.7	303	2	RAR24300	Ar24300 Glycopept	382	43	41.7	833	7	ADD18208	Add18208 Human mol
310	43	41.7	303	8	ADX66564	Adx66564 Plant ful	383	43	41.7	833	7	ADD18206	Add18206 Human mol
311	43	41.7	308	6	ABU40749	Abu40749 Protein e	384	43	41.7	833	7	ADD18204	Add18204 Human mol
312	43	41.7	309	6	ABU28074	Abu28074 Protein e	385	43	41.7	833	7	ADG76093	Adg76093 Human NOV
313	43	41.7	309	8	ADP94465	AdP94465 Plant ful	386	43	41.7	833	7	ADG76099	Adg76099 Human NOV
314	43	41.7	318	7	ADP04129	AdP04129 Bacterial	387	43	41.7	833	7	ADR67100	Adr67100 Human can
315	43	41.7	329	8	ADX72849	Adx72849 Plant ful	388	43	41.7	886	5	ABBS97963	Abb97963 Human pro
316	43	41.7	332	8	ADX93398	Adx93398 Plant ful	389	43	41.7	886	8	ADR67094	Adr67094 Human can

390	43	41.7	895	8	ADP83518	Breast ep	463	42	40.8	463	8	ADR88663	Adr88663 Human glu
391	43	41.7	1159	6	ABU42581	Protein e	464	42	40.8	463	9	ADY60819	Ady60819 Human glu
392	43	41.7	1162	5	ADP39163	Staphyloc	465	42	40.8	463	9	ADY73567	Ady73567 Glucagon
393	43	41.7	1162	8	ADSO6520	Staphyloc	466	42	40.8	463	9	AEA50193	AEA50193 GLP1R. 8/
394	43	41.7	2408	2	AAR24307	Translati	467	42	40.8	463	9	AE832309	AE832309 Human pro
395	42.5	41.3	103	4	AAR82530	Human imm	468	42	40.8	477	5	AAE23674	AAE23674 SLG proce
396	42.5	41.3	197	6	ADA35499	Acinetoba	469	42	40.8	481	3	AAAG31200	AAAG31200 Arabidops
397	42.5	41.3	220	7	ABP71000	Ring fing	470	42	40.8	485	9	ABEB2344	ABEB2344 Human pro
398	42.5	41.3	248	6	ABM74373	DNA clone	471	42	40.8	502	4	ABEB2813	ABEB2813 Drosophil
399	42.5	41.3	255	9	ADY17863	PRO polyp	472	42	40.8	542	3	ABM96322	ABM96322 M. xanthu
400	42.5	41.3	274	4	ABG22354	Novel hum	473	42	40.8	563	3	AAAG31199	AAAG31199 Arabidops
401	42.5	41.3	274	4	AAU31494	Novel hum	474	42	40.8	580	4	AAAB74665	AAAB74665 Human hig
402	42.5	41.3	281	7	ADJ22713	Human dis	475	42	40.8	580	4	AAAB86837	AAAB86837 Human CHO
403	42.5	41.3	287	8	ADJ32715	Human nuc	476	42	40.8	580	6	ABU08979	ABU08979 Human hig
404	42.5	41.3	297	6	ADA54180	Human pro	477	42	40.8	580	7	ADD50649	ADD50649 High-affi
405	42.5	41.3	302	8	ADY12633	Plant ful	478	42	40.8	580	7	ADD50639	ADD50639 Human hig
406	42.5	41.3	329	7	ADP30602	Plant yie	479	42	40.8	580	7	ADD50648	ADD50648 High-affi
407	42.5	41.3	329	8	ADI44107	Plant tra	480	42	40.8	580	7	ADD50647	ADD50647 High-affi
408	42.5	41.3	329	8	ADI61445	A. thalia	481	42	40.8	580	7	ADJ69339	ADJ69339 Human hea
409	42.5	41.3	329	8	ADJ602419	Thalecres	482	42	40.8	580	9	ADV77897	ADV77897 Human hig
410	42.5	41.3	357	8	ADT60162	Plant pol	483	42	40.8	580	9	ADV77905	ADV77905 Human hig
411	42.5	41.3	393	8	ADX95226	Plant ful	484	42	40.8	580	9	ADV77907	ADV77907 Human hig
412	42.5	41.3	393	8	ADT59670	Plant pol	485	42	40.8	580	9	ADV77906	ADV77906 Human hig
413	42.5	41.3	530	9	AE806261	Amino aci	486	42	40.8	589	7	ABM86950	ABM86950 Rice abio
414	42.5	41.3	711	8	ADR86405	Aspergill	487	42	40.8	602	8	ADQ97488	ADQ97488 Mouse can
415	42	40.8	1	1	AAPE50994	Cholecyet	488	42	40.8	630	3	AAAG31198	AAAG31198 Arabidops
416	42	40.8	41	3	AAAB19611	Glucagon-	489	42	40.8	740	7	ADC87605	ADC87605 Human GPC
417	42	40.8	78	8	ABO54993	Human gen	490	42	40.8	758	7	ABM85268	ABM85268 Mouse pro
418	42	40.8	103	5	ABP55156	Human pro	491	42	40.8	818	8	ADU82879	ADU82879 Ligand up
419	42	40.8	124	3	AAAB19612	Glucagon-	492	42	40.8	842	7	ABM85494	ABM85494 Mouse pro
420	42	40.8	129	3	AAAT77150	Pinctada	493	42	40.8	961	8	ADS73342	ADS73342 Arabidops
421	42	40.8	129	3	AAAT77152	Pinctada	494	42	40.8	1282	8	ABM88185	ABM88185 Rice abio
422	42	40.8	129	3	AAAT77151	Pinctada	495	42	40.8	1282	8	ADI45253	ADI45253 Rice isop
423	42	40.8	129	3	AAAT77147	Pinctada	496	42	40.8	1431	9	ADV97898	ADV97898 Murine pr
424	42	40.8	179	8	ADQ99476	Chicken (	497	42	40.8	4868	8	ADM68813	ADM68813 Mosquito
425	42	40.8	179	8	ADQ99476	Chicken (	498	41.5	40.3	45	4	ABG09615	ABG09615 Novel hum
426	42	40.8	179	8	ADQ99476	Chicken (	499	41.5	40.3	66	6	ADA57071	ADA57071 Human sec
427	42	40.8	179	8	ADQ99476	Chicken (	500	41.5	40.3	66	6	ADA40923	ADA40923 Human sec
428	42	40.8	208	9	ADP16929	Chicken (	501	41.5	40.3	66	6	ABR47837	ABR47837 Human sec
429	42	40.8	221	8	ADP39781	HIV Nef p	502	41.5	40.3	66	6	ABR47837	ABR47837 Human sec
430	42	40.8	221	8	ADP39781	HIV Nef p	503	41.5	40.3	66	6	ABR47837	ABR47837 Human sec
431	42	40.8	221	8	ADP39781	HIV Nef p	504	41.5	40.3	66	6	ABR47837	ABR47837 Human sec
432	42	40.8	234	7	ABO72949	Pseudomon	505	41.5	40.3	67	2	AAAT36241	AAAT36241 Human sec
433	42	40.8	235	5	AAE20636	Human gen	506	41.5	40.3	67	6	ADAL1659	ADAL1659 Human nov
434	42	40.8	235	5	AAE20636	Human alb	507	41.5	40.3	91	6	ADAL12015	ADAL12015 Human nov
435	42	40.8	235	8	ADL78509	Albumin f	508	41.5	40.3	101	5	ABP32743	ABP32743 Human ORF
436	42	40.8	254	8	ADP73346	Adiantum	509	41.5	40.3	146	4	AAAB3599	AAAB3599 Human pol
437	42	40.8	268	4	AAAT79590	Corynebac	510	41.5	40.3	146	7	ABM89788	ABM89788 Rice abio
438	42	40.8	268	4	AAAT79590	Corynebac	511	41.5	40.3	146	8	ADM24620	ADM24620 Human PRO
439	42	40.8	287	7	ABO73882	Pseudomon	512	41.5	40.3	288	6	ABJ25996	ABJ25996 Aspergill
440	42	40.8	301	3	AAAG41485	Arabidops	513	41.5	40.3	288	6	ABJ25396	ABJ25396 Aspergill
441	42	40.8	301	8	ADN73669	Thale cre	514	41.5	40.3	375	6	ABU17034	ABU17034 Protein e
442	42	40.8	304	4	AAE02541	A. thalia	515	41.5	40.3	378	6	ADA36891	ADA36891 Acinetoba
443	42	40.8	304	5	AAU92294	Arabidops	516	41.5	40.3	410	8	ADR31329	ADR31329 Aspergill
444	42	40.8	304	7	ADD30740	Plant yie	517	41.5	40.3	492	7	ABR84659	ABR84659 Human tru
445	42	40.8	304	8	ADJ37249	Plant yie	518	41.5	40.3	492	7	ABO74647	ABO74647 Pseudomon
446	42	40.8	304	8	ADJ37249	Plant yie	519	41.5	40.3	567	7	ABD85487	ABD85487 Human egg
447	42	40.8	304	8	ADJ37249	Plant yie	520	41.5	40.3	586	5	ABP33791	ABP33791 Herbicida
448	42	40.8	304	9	AEA27069	Stress to	521	41.5	40.3	628	7	ABD85485	ABD85485 Human egg
449	42	40.8	310	8	ADJ49001	Oil-assoc	522	41.5	40.3	722	2	AAAT35095	AAAT35095 C. pneumo
450	42	40.8	318	3	AAAG41484	Arabidops	523	41.5	40.3	752	7	ABD85483	ABD85483 Human egg
451	42	40.8	318	5	ABP60935	Zymomonas	524	41.5	40.3	753	7	ABD85481	ABD85481 Human egg
452	42	40.8	349	6	ADA15583	A. thalia	525	41.5	40.3	763	7	ABD85492	ABD85492 Human egg
453	42	40.8	349	7	ADD55756	Thalecres	526	41.5	40.3	776	8	ADK16939	ADK16939 Nanaorch
454	42	40.8	349	8	ADQ01721	Thalecres	527	41.5	40.3	785	9	ABM90774	ABM90774 M. xanthu
455	42	40.8	379	8	ADQ09200	Plant ful	528	41.5	40.3	816	4	ABG25783	ABG25783 Novel hum
456	42	40.8	463	2	AAR70006	Human glu	529	41.5	40.3	816	4	ABG04035	ABG04035 Novel hum
457	42	40.8	463	4	AAAT1871	Human glu	530	41.5	40.3	872	4	ABB62201	ABB62201 Drosophil
458	42	40.8	463	6	ABP81957	Human glu	531	41.5	40.3	929	3	AAAB41226	AAAB41226 Human ORF
459	42	40.8	463	6	ABR58078	Human GPC	532	41.5	40.3	930	2	AAW75426	AAW75426 Human egg
460	42	40.8	463	7	ADC86429	Human GPC	533	41.5	40.3	930	2	AAW75426	AAW75426 Human egg
461	42	40.8	463	7	ADL13188	GLP-1 rec	534	41.5	40.3	930	7	ABD85503	ABD85503 Human egg
462	42	40.8	463	8	ADO29357	Human GPC	535	41.5	40.3	930	8	ADQ17600	ADQ17600 Human sof

536	41.5	40.3	930	8	ADR99240	Adr99240	ADAMTS5.	609	41	39.8	584	3	AAG39955	Aag39955	Arabidops
537	41	39.8	6	8	ADO70141	Ado70141	Gastrin p	610	41	39.8	600	3	AAG39907	Aag39907	Arabidops
538	41	39.8	6	9	ADV16303	Adv16303	Human gas	611	41	39.8	612	3	AAG31134	Aag31134	Arabidops
539	41	39.8	6	9	ADW00246	Adw00246	Human wil	612	41	39.8	615	5	ABB93850	Abb93850	Herbicida
540	41	39.8	6	9	ADW00237	Adw00237	Human wil	613	41	39.8	628	3	AAG31133	Aag31133	Arabidops
541	41	39.8	6	9	AEb98020	Aeb98020	Gastrin 6	614	41	39.8	628	5	ABB93106	Abb93106	Herbicida
542	41	39.8	6	9	AEb98025	Aeb98025	Modified	615	41	39.8	632	3	AAG39954	Aag39954	Arabidops
543	41	39.8	7	8	ADT49603	Adt49603	Gastrin 3	616	41	39.8	632	6	ABU41415	Abu41415	Protein e
544	41	39.8	7	8	ADT54953	Adt54953	Human pro	617	41	39.8	633	4	AAU33714	Aau33714	Pseudomon
545	41	39.8	8	8	ADR48674	Adr48674	Cosmetic	618	41	39.8	633	6	ABU15635	Abu15635	Protein e
546	41	39.8	65	4	AAE06085	Aae06085	Human gen	619	41	39.8	635	8	ADN72239	Adn72239	Thale cre
547	41	39.8	65	5	ABG33907	Abg33907	Human sec	620	41	39.8	637	4	ABG08113	Abg08113	Novel hum
548	41	39.8	66	3	AAy87108	Aay87108	Human sec	621	41	39.8	648	3	AAG39953	Aag39953	Arabidops
549	41	39.8	95	3	AAy87195	Aay87195	Human sec	622	41	39.8	648	3	AAG39906	Aag39906	Arabidops
550	41	39.8	95	4	AAE06172	Aae06172	Human gen	623	41	39.8	659	7	ABO74194	AbO74194	ABO74194
551	41	39.8	95	5	ABG33996	Abg33996	Human sec	624	41	39.8	664	3	AAG39905	Aag39905	Arabidops
552	41	39.8	99	4	ABB15846	Abb15846	Human ner	625	41	39.8	690	3	AAG16506	Aag16506	Arabidops
553	41	39.8	103	4	ABR88410	AbR88410	Human mem	626	41	39.8	699	8	ADN21871	Adn21871	Bacterial
554	41	39.8	103	5	ABR40424	AbR40424	Human sec	627	41	39.8	705	8	ADN24630	Adn24630	Bacterial
555	41	39.8	103	5	ABR40500	AbR40500	Human sec	628	41	39.8	711	7	ADG75747	Adg75747	Human pro
556	41	39.8	103	6	ABO14011	AbO14011	Novel hum	629	41	39.8	715	8	ADX95897	Adx95897	Plant ful
557	41	39.8	103	8	ADNG60708	Adng60708	Human sec	630	41	39.8	724	7	ADC85131	Adc85131	Ion trans
558	41	39.8	103	9	ADY63183	Ady63183	Human clo	631	41	39.8	724	7	ADC37435	Adc37435	Human tra
559	41	39.8	104	2	AAy27606	Aay27606	Human sec	632	41	39.8	724	8	ADM91339	Adm91339	Human org
560	41	39.8	104	8	ADG78417	Adg78417	Human sec	633	41	39.8	724	8	ADR10186	Adr10186	Human pro
561	41	39.8	123	4	AAG91649	Aag91649	C glutami	634	41	39.8	724	8	ADR40143	Adr40143	Human OAT
562	41	39.8	123	4	AAG91231	Aag91231	C glutami	635	41	39.8	729	2	AAW47538	Aaw47538	Homo sapi
563	41	39.8	149	4	ABG29930	Abg29930	Novel hum	636	41	39.8	729	8	ADF61818	Adf61818	Human BRC
564	41	39.8	168	8	ABO58496	AbO58496	Human gen	637	41	39.8	729	3	ADL23955	Adl23955	Deubiquit
565	41	39.8	194	4	ABG08111	Abg08111	Novel hum	638	41	39.8	733	8	AAG16505	Aag16505	Arabidops
566	41	39.8	203	3	AAG57345	Aag57345	Arabidops	639	41	39.8	739	8	ADY23655	Ady23655	Plant ful
567	41	39.8	209	3	AAy69193	Aay69193	Monocyte-	640	41	39.8	748	7	ADJ21187	Adj21187	Novel hum
568	41	39.8	209	7	ADH30238	Adh30238	Human mon	641	41	39.8	748	9	AEb77268	Aeb77268	Human hea
569	41	39.8	209	8	ADO00827	Ado00827	Human mon	642	41	39.8	750	8	ADX96695	Adx96695	Plant ful
570	41	39.8	234	6	ABU11793	Abu11793	Human MDP	643	41	39.8	779	6	ABU19870	Abu19870	Protein e
571	41	39.8	236	4	ABG05373	Abg05373	Novel hum	644	41	39.8	788	8	ADY73315	Ady73315	Rice 3 Rm
572	41	39.8	248	7	ADC01289	Adc01289	Euterohae	645	41	39.8	818	8	ADN22915	Adn22915	Bacterial
573	41	39.8	250	8	ADT71530	Adt71530	Human CGD	646	41	39.8	865	4	ABB60350	Abb60350	Drosophil
574	41	39.8	262	8	ADX92011	Adx92011	Plant ful	647	41	39.8	890	4	ABG21937	Abg21937	Novel hum
575	41	39.8	270	3	AAG57344	Aag57344	Arabidops	648	41	39.8	934	4	ABB67315	Abb67315	Drosophil
576	41	39.8	271	7	ADC08052	Adc08052	Rice prot	649	41	39.8	934	4	ABB67315	Abb67315	Drosophil
577	41	39.8	273	2	AAy05831	Aay05831	Arabidops	650	41	39.8	934	8	ADY73298	Ady73298	Rice 3 Rm
578	41	39.8	273	7	ABO43112	AbO43112	A. thalia	651	41	39.8	993	8	ADY73319	Ady73319	Tobacco 3
579	41	39.8	273	8	ADO01749	Ado01749	Thalecres	652	41	39.8	1042	8	ADQ39272	Adq39272	Human myo
580	41	39.8	276	3	AAG57343	Aag57343	Arabidops	653	41	39.8	1079	8	ADQ39270	Adq39270	Human myo
581	41	39.8	276	8	ADN72875	Adn72875	Thale cre	654	41	39.8	1088	3	ADH30236	Adh30236	Human mon
582	41	39.8	314	4	AAm93516	Aam93516	Human pol	655	41	39.8	1088	7	ADH30236	Adh30236	Human mon
583	41	39.8	314	8	ADL31208	Adl31208	Human pro	656	41	39.8	1088	8	ADQ00825	Ado00825	Human mon
584	41	39.8	326	4	AAE92794	Aae92794	Human pro	657	41	39.8	1088	8	ADP25157	Adp25157	PRO polyp
585	41	39.8	332	7	ABM88586	Abm88586	Rice abio	658	41	39.8	1088	8	ADQ39273	Adq39273	Human myo
586	41	39.8	335	8	ADU02576	Adu02576	Novel hum	659	41	39.8	1088	8	ADQ39270	Adq39270	Human myo
587	41	39.8	365	4	ABG03322	Abg03322	Novel hum	660	41	39.8	1097	8	ADQ39271	Adq39271	Human myo
588	41	39.8	392	4	ABG09051	Abg09051	Novel hum	661	41	39.8	1119	5	AAE97825	Aae97825	Thermus a
589	41	39.8	401	8	ADG21074	Adg21074	Bacterial	662	41	39.8	1119	5	AAE14716	Aae14716	Thermus a
590	41	39.8	418	4	ABE12127	AbE12127	Human sec	663	41	39.8	1129	5	ABG70894	Abg70894	T. aquati
591	41	39.8	420	8	ADU02411	Adu02411	Novel hum	664	41	39.8	1229	6	ABU35793	Abu35793	Protein e
592	41	39.8	436	7	ADE71271	AdE71271	Novel hum	665	41	39.8	1233	6	ABU34207	Abu34207	Protein e
593	41	39.8	440	4	ABG29931	Abg29931	Novel hum	666	41	39.8	1233	8	ADQ66727	Adq66727	Novel hum
594	41	39.8	442	7	ABO82757	AbO82757	Pseudomon	667	41	39.8	1233	9	ADY15098	Ady15098	PRO polyp
595	41	39.8	459	1	AAp96202	Aap96202	Human mus	668	41	39.8	2106	7	ADJ70287	Adj70287	Human hea
596	41	39.8	464	4	ABG23368	Abg23368	Novel hum	669	41	39.8	2137	9	ADX06608	Adx06608	Cyclin-d
597	41	39.8	502	4	AAO06616	Aao06616	Human pol	670	41	39.8	2141	6	ABR41636	AbR41636	Human DIT
598	41	39.8	502	7	ADC33275	Adc33275	Human nov	671	41	39.8	3392	4	AAE07981	Aae07981	Attenuate
599	41	39.8	505	8	ADY33343	Ady33343	Arabidops	672	41	39.8	3392	4	AAE07980	Aae07980	Wild-type
600	41	39.8	513	7	ADE16054	AdE16054	G-coupled	673	41	39.8	4010	4	ABE61520	AbE61520	Drosophil
601	41	39.8	513	8	ADL93993	Adl93993	Human-G-c	674	40.5	39.3	172	7	ABO66349	AbO66349	Klebsiell
602	41	39.8	537	6	ABU25070	Abu25070	Protein e	675	40.5	39.3	297	7	ADJ30462	Adj30462	Plant vie
603	41	39.8	559	3	AAG16507	Aag16507	Arabidops	676	40.5	39.3	297	8	ADU44435	Adu44435	Amino aci
604	41	39.8	564	3	AAG31135	Aag31135	Arabidops	677	40.5	39.3	433	8	ADU07725	Adu07725	Novel hum
605	41	39.8	566	4	AAm93845	Aam93845	Human pol	678	40.5	39.3	608	7	ADN99924	Adn99924	Sorangium
606	41	39.8	566	8	ADL31892	Adl31892	Human pro	679	40.5	39.3	3785	7	ADC26984	Adc26984	Sorangium
607	41	39.8	566	8	ADO20199	Ado20199	Human PRO	680	40.5	39.3	5087	4	AAU10700	Aau10700	Amino aci
608	41	39.8	566	8	ABM82293	Abm82293	Tumour-ab	681	40.5	39.3	9334	7	ADC26980	Adc26980	Sorangium

682	40	38.8	10	1	AAP50995	Aap50995	Cholecyst	755	40	38.8	326	8	ADY11691	Ady11691	Plant ful
683	40	38.8	10	1	AAP50996	Aap50996	Cholecyst	756	40	38.8	328	4	AAm25666	Aam25666	Human pro
684	40	38.8	10	1	AAP50997	Aap50997	Cholecyst	757	40	38.8	331	8	ADx77848	Adx77848	Plant ful
685	40	38.8	10	1	AAP50990	Aap50990	Cholecyst	758	40	38.8	335	9	ADz75744	Adz75744	Xanthomon
686	40	38.8	30	8	ABO60123	AbO60123	Human gen	759	40	38.8	342	8	ADY11688	Ady11688	Plant ful
687	40	38.8	62	5	ABF01522	AbF01522	Human ORF	760	40	38.8	347	8	ADY22771	Ady22771	Plant ful
688	40	38.8	64	4	AAU51593	Aau51593	Propionib	761	40	38.8	348	9	ADW17200	Adw17200	E Grandis
689	40	38.8	64	6	ABM48112	Abm48112	Propionib	762	40	38.8	362	3	AAAG40441	Aag40441	Arabidops
690	40	38.8	60	4	ABG04742	Abg04742	Novel hum	763	40	38.8	364	8	ADx68045	Adx68045	Plant ful
691	40	38.8	106	3	AGS59284	Ags59284	Arabidops	764	40	38.8	370	3	AAV99428	Aav99428	Human PRO
692	40	38.8	122	5	ABG60002	Abg60002	Human DIT	765	40	38.8	370	4	AAb66177	Abb66177	Protein o
693	40	38.8	125	8	ADx97072	Adx97072	Plant ful	766	40	38.8	370	4	AAU29198	Aau29198	Human PRO
694	40	38.8	148	6	ABU38788	Abu38788	Protein e	767	40	38.8	370	6	ABU58574	Abu58574	Human PRO
695	40	38.8	160	6	ABU07428	Abu07428	Protein d	768	40	38.8	370	6	ABU88122	Abu88122	Novel hum
696	40	38.8	164	8	ADJ48845	Adj48845	Oil -assoc	769	40	38.8	370	6	ABU84437	Abu84437	Human sec
697	40	38.8	169	6	ABO01280	AbO01280	Growth de	770	40	38.8	370	6	ABR66311	AbR66311	Human sec
698	40	38.8	173	2	AAJ31739	Aaj31739	Human B5T	771	40	38.8	370	6	ABR65701	AbR65701	Human sec
699	40	38.8	173	2	AAJ31738	Aaj31738	Mouse B5T	772	40	38.8	370	6	ABU99641	Abu99641	Human sec
700	40	38.8	173	2	AAJ31737	Aaj31737	Rat B5T o	773	40	38.8	370	6	ABU82880	Abu82880	Human PRO
701	40	38.8	177	7	ABO78054	AbO78054	Pseudomon	774	40	38.8	370	6	ABU90001	Abu90001	Novel hum
702	40	38.8	181	8	ADO42989	AdO42989	Mouse DOR	775	40	38.8	370	6	ABR68250	AbR68250	Human sec
703	40	38.8	182	4	AAU16252	Aau16252	Human nov	776	40	38.8	370	6	ABU96303	Abu96303	Novel hum
704	40	38.8	182	6	AAU55321	Aau55321	Human nov	777	40	38.8	370	6	ABU92734	Abu92734	Human sec
705	40	38.8	188	4	AAU23356	Aau23356	Novel hum	778	40	38.8	370	6	ABO08811	AbO08811	Human sec
706	40	38.8	194	4	AAm86073	Aam86073	Human imm	779	40	38.8	370	6	ABO02863	AbO02863	Human sec
707	40	38.8	197	5	AAE20628	Aae20628	Human gen	780	40	38.8	370	6	ABR75017	AbR75017	Human sec
708	40	38.8	197	5	ABG65244	Abg65244	Human alb	781	40	38.8	370	6	ABR94779	AbR94779	Human sec
709	40	38.8	197	8	ADL78511	Adl78511	Albumin f	782	40	38.8	370	6	ABU85752	Abu85752	Human PRO
710	40	38.8	199	8	ADO42990	AdO42990	Rat diabe	783	40	38.8	370	6	ABU98912	Abu98912	Novel hum
711	40	38.8	200	7	ABM85970	Abm85970	Rice abio	784	40	38.8	370	6	ABU98127	Abu98127	Novel hum
712	40	38.8	202	7	ADC71544	AdC71544	Human NOV	785	40	38.8	370	6	ABU91833	Abu91833	Novel hum
713	40	38.8	202	8	ADN33955	Adn33955	Human nov	786	40	38.8	370	6	ABU89526	Abu89526	Human PRO
714	40	38.8	202	8	ADO42311	AdO42311	Human NOV	787	40	38.8	370	6	ABU86367	Abu86367	Human sec
715	40	38.8	203	8	ADS22097	AdS22097	Bacterial	788	40	38.8	370	6	ABU67580	Abu67580	Human sec
716	40	38.8	203	8	ADx91109	Adx91109	Plant ful	789	40	38.8	370	6	ABU80608	Abu80608	Human PRO
717	40	38.8	209	5	ABR89412	AbR89412	Human pol	790	40	38.8	370	6	ABR99526	AbR99526	Human sec
718	40	38.8	209	8	ADJ71948	Adj71948	Human PWM	791	40	38.8	370	6	ABR98916	AbR98916	Human sec
719	40	38.8	210	3	AAAB42100	AaB42100	Human ORF	792	40	38.8	370	6	ABO16439	AbO16439	Human sec
720	40	38.8	210	4	AAW79872	Aam79872	Human pro	793	40	38.8	370	6	ABR92339	AbR92339	Human sec
721	40	38.8	211	6	ABR41442	AbR41442	Human DIT	794	40	38.8	370	6	ABO18980	AbO18980	Human sec
722	40	38.8	213	7	ADL22757	Adl22757	Human dis	795	40	38.8	370	6	ABR78401	AbR78401	Human sec
723	40	38.8	216	4	AAO04182	Aae04182	Human gen	796	40	38.8	370	6	ABU85137	Abu85137	Novel hum
724	40	38.8	221	8	ADO42991	AdO42991	Mouse DOR	797	40	38.8	370	6	ABO00276	AbO00276	Novel hum
725	40	38.8	234	3	AAAB42859	Aab42859	Human ORF	798	40	38.8	370	6	ABO11608	AbO11608	Human sec
726	40	38.8	243	5	ABR40550	AbR40550	Human sec	799	40	38.8	370	6	ABO02253	AbO02253	Human sec
727	40	38.8	260	4	ABR62860	AbB62860	Drosophil	800	40	38.8	370	6	ABU88827	Abu88827	Novel hum
728	40	38.8	263	8	ADT59968	Aag159968	Plant pol	801	40	38.8	370	6	ABU83522	Abu83522	Human sec
729	40	38.8	267	3	AGI17722	Aag17722	Arabidops	802	40	38.8	370	6	ABO06323	AbO06323	Novel hum
730	40	38.8	269	4	ABR65529	Abb65529	Drosophil	803	40	38.8	370	6	ABR59359	AbR59359	Human sec
731	40	38.8	278	2	AAW37811	Aaw37811	Tobacco M	804	40	38.8	370	6	ABO09421	AbO09421	Human sec
732	40	38.8	284	4	ABG26687	Abg26687	Novel hum	805	40	38.8	370	6	ABO19285	AbO19285	Novel hum
733	40	38.8	296	8	ADX89305	Adx89305	Plant ful	806	40	38.8	370	6	ABO11303	AbO11303	Human sec
734	40	38.8	299	8	ADL61439	Adl61439	A. thalia	807	40	38.8	370	6	ABR66921	AbR66921	Human sec
735	40	38.8	299	8	ADO02411	AdO02411	Thalecres	808	40	38.8	370	6	ABO16134	AbO16134	Human sec
736	40	38.8	300	8	ADN43537	Adn43537	Bacterial	809	40	38.8	370	6	ABO13840	AbO13840	Human sec
737	40	38.8	303	4	AAAB73519	AbB73519	Human tra	810	40	38.8	370	6	ABU65743	Abu65743	Human sec
738	40	38.8	303	9	ADW17415	Adw17415	Eucalyptu	811	40	38.8	370	6	ABO07591	AbO07591	Human PRO
739	40	38.8	304	8	ADX71311	Adx71311	Plant ful	812	40	38.8	370	6	ABO03778	AbO03778	Human sec
740	40	38.8	314	3	AGI17721	Aag17721	Arabidops	813	40	38.8	370	6	ABR67226	AbR67226	Human sec
741	40	38.8	314	7	ADM03980	Adm03980	Human pro	814	40	38.8	370	6	ABO15829	AbO15829	Human sec
742	40	38.8	315	3	AAAG40442	Aag40442	Arabidops	815	40	38.8	370	6	ABU56110	Abu56110	Human sec
743	40	38.8	315	8	ADN17560	Adn17560	Bacterial	816	40	38.8	370	6	ABU65438	Abu65438	Human PRO
744	40	38.8	319	6	ADA15491	Ada15491	A. thalia	817	40	38.8	370	6	ABU95383	Abu95383	Novel hum
745	40	38.8	319	8	ADO01755	AdO01755	Thalecres	818	40	38.8	370	6	ABU71286	Abu71286	Human PRO
746	40	38.8	319	8	ADX70903	Adx70903	Plant ful	819	40	38.8	370	6	ABO07896	AbO07896	Human PRO
747	40	38.8	321	9	AEB39583	Aeb39583	L. pneumo	820	40	38.8	370	6	ABR70137	AbR70137	Human sec
748	40	38.8	321	9	AEB36160	Aeb36160	L. pneumo	821	40	38.8	370	6	ABR69470	AbR69470	Human sec
749	40	38.8	323	8	ADS27757	AdS27757	Bacterial	822	40	38.8	370	6	ABO01611	AbO01611	Human PRO
750	40	38.8	325	7	ADD30244	AdD30244	Plant yle	823	40	38.8	370	6	ABU81413	Abu81413	Human PRO
751	40	38.8	325	8	ADI44101	Adi44101	Plant tra	824	40	38.8	370	6	ABR60210	AbR60210	Human sec
752	40	38.8	325	8	ADJ49247	Adj49247	Oil-assoc	825	40	38.8	370	6	ABR67945	AbR67945	Human sec
753	40	38.8	325	8	ADO02405	AdO02405	Thalecres	826	40	38.8	370	6	ABR65333	AbR65333	Human sec
754	40	38.8	326	3	AGI17720	Aag17720	Arabidops	827	40	38.8	370	6	ABR68555	AbR68555	Human sec

828 40 38.8 370 6 ABR71967 Human sec  
829 40 38.8 370 6 ABU85447 Human PRO  
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ABM07146 Human sec  
ABM21240 Human sec  
ABM09586 Human sec  
ABO41456 Human sec  
ABO36271 Human PRO  
ABO43800 Human sec  
ABM76500 Human sec  
ABM76196 Human sec  
ABM25815 Human sec  
ABM26120 Human sec  
ABO03473 Human sec  
ABO02558 Human sec  
ABR90729 Human sec  
ABR73797 Human sec  
ABO17049 Human sec  
ABR94474 Human sec  
ABR75981 Human sec  
ABR71357 Human sec  
ABR93254 Human sec  
ABR93559 Human sec  
ABR87984 Human sec  
ABR93670 Novel hum  
ABO33670 Human sec  
ABO30119 Human sec  
ABO33328 Human PRO  
ABM05016 Human sec  
ABM08976 Human sec  
ABO36576 Human sec  
ABO35661 Human PRO  
ABO39626 Human sec  
ABM10501 Human sec  
ABM12026 Human sec  
ABO52172 Human PRO  
ABO52477 Human PRO  
ABO23795 Human sec  
ABR97281 Human sec  
ABR97069 Human sec  
ABM11111 Human sec  
ABM28255 Human sec  
ABO32254 Human sec  
ABM15381 Human sec  
ABM06536 Human sec  
ABM04347 Human sec  
ABM22460 Human sec  
ABM07756 Human sec  
ABO40846 Human sec  
ABM35493 Human sec  
ABM33256 Human sec  
ABO52782 Human PRO  
ABO50342 Human sec  
ABU99336 Human sec

974 40 38.8 370 6 ABO04388 Human sec  
975 40 38.8 370 6 ABO06018 Human sec  
976 40 38.8 370 6 ABM18558 Human sec  
977 40 38.8 370 6 ABR97586 Human sec  
978 40 38.8 370 6 ABR80686 Human sec  
979 40 38.8 370 6 ABR01297 Human sec  
980 40 38.8 370 6 ABR88899 Human sec  
981 40 38.8 370 6 ABM13551 Human sec  
982 40 38.8 370 6 ABM20935 Human sec  
983 40 38.8 370 6 ABO42066 Human sec  
984 40 38.8 370 6 ABO42676 Human sec  
985 40 38.8 370 6 ABM10196 Human sec  
986 40 38.8 370 6 ABO38711 Human sec  
987 40 38.8 370 6 ABM32951 Human sec  
988 40 38.8 370 6 ABM22765 Human sec  
989 40 38.8 370 6 ABM74976 Human sec  
990 40 38.8 370 6 ADA79894 Human sec  
991 40 38.8 370 6 ABR96366 Human sec  
992 40 38.8 370 6 ABM02517 Human sec  
993 40 38.8 370 6 ABR86459 Human sec  
994 40 38.8 370 6 ABR86764 Human sec  
995 40 38.8 370 6 ABM16728 Human sec  
996 40 38.8 370 6 ABM29780 Human sec  
997 40 38.8 370 6 ABO29204 Human sec  
998 40 38.8 370 6 ABM233985 Human sec  
999 40 38.8 370 6 ABM23375 Human sec  
1000 40 38.8 370 6 ABM22155 Human sec

## ALIGNMENTS

RESULT 1  
AAW65184  
ID AAW65184 standard; peptide; 17 AA.  
XX AAW65184;  
XX  
DT 02-OCT-1998 (first entry)  
XX  
DE Gastrin fragment analogue.  
XX  
KW Bradykinin; N-benzylglycine; agonist; receptor study; antagonist;  
KW achiral; analgesic; angiotensin II; gastrin.  
XX Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "Pyroglutamic acid"  
FT Modified-site 17 /note= "C-terminal amide"  
FT  
XX  
PN US5527882-A.  
XX  
PD 18-JUN-1996.  
XX  
XX 07-NOV-1994; 94US-00335202.  
XX  
PR 07-JUL-1989; 89US-00376839.  
PR 16-SEP-1992; 92US-00945664.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Young JD, Mitchell AR;  
XX  
DR WPI; 1996-299898/30.  
XX  
PT New bradykinin analogues contg. N-benzyl-glycine - useful as bradykinin  
PT agonists or antagonists, useful e.g. as analgesics.  
XX  
PS Disclosure; Col 7-8; 15pp; English.  
XX

CC The invention relates to the obtaining of a potent agonist or antagonist  
CC peptide by the replacement of selected amino acids with synthetic achiral  
CC amino acids. The present sequence represents a gastrin fragment analogue,  
CC where at least one of Tyr12 and Phe17 is intended to be replaced by N-  
CC benzylglycine, N-cyclohexylmethylglycine or the ring substituted  
CC derivatives thereof  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 103; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EGPWLEEEERAYGWMDF 17  
|||||  
DB 1 EGPWLEEEERAYGWMDF 17  
|||||  
RESULT 2  
AAW24398  
ID AAW24398 standard; peptide; 17 AA.  
XX  
AC AAW24398;  
XX  
DT 13-MAR-1998 (first entry)  
XX  
DE Carboxy-amidated gastrin-17.  
XX  
KW Carboxy-amidated gastrin-17; gastrointestinal tumour; immunogen;  
KW colorectal adenocarcinoma; antibody; progastrin;  
KW cholecystochinin B. anti-gastrin-17; anti-G-17.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 17 /note= "C-terminal amide"  
FT  
XX  
PN WO9728821-A1.  
XX  
PD 14-AUG-1997.  
XX  
PF 07-FEB-1997; 97WO-US002029.  
XX  
PR 08-FEB-1996; 96US-0011411P.  
XX  
PA (APHT-) APHTON CORP.  
XX  
PI Gevas PC, Karr SL, Grimes S, Michaeli D, Watson SA;  
XX  
DR WPI; 1997-415075/38.  
XX  
PT Treatment of glycine-extended gastrin-17-dependent gastrointestinal  
PT tumours - using anti-G17 immunogenic composition, especially for  
PT treatment of colorectal adenocarcinomas.  
XX  
PS Example 1; Fig 1B; 37pp; English.  
XX  
CC The present sequence represents carboxy-amidated gastrin-17. Treatment of  
CC gastrin-17-dependent gastrointestinal tumours comprises administering to  
CC a mammal an anti-gastrin 17 (G17) immunogenic composition. Anti-G17  
CC immunogens raise antibodies which bind both the amidated and glycine-  
CC extended forms of G17. Neutralisation of progastrin G17-Gly prohormone by  
CC the antibodies inhibits the growth of tumour cells dependent on  
CC progastrin G17-Gly as growth stimulator or inducer. The method is  
CC especially for the treatment of colorectal adenocarcinomas in humans.  
CC This novel method is non-invasive, selectively reversible, does not  
CC damage normal tissue, does not require frequent repeated treatments and  
CC does not cross the blood brain barrier  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 103; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17  
| | | | | | | | | | | | | | | | | |  
Db 1 EGPWLEEEERAYGWMDF 17

RESULT 3  
AAU05580  
ID AAU05580 standard; peptide; 17 AA.

AC AAU05580;

XX 24-OCT-2001 (first entry)

DE Human Janus kinase 3 (JAK3) biotinylated peptide substrate GAS1.

XX Janus kinase 3; JAK3; JAK/STAT inhibitor; peptide substrate;  
KW signal transducer and activator of transcription; osteoarthritis;  
KW degenerative joint disease; rheumatoid arthritis; leprosy; asthma;  
KW cancer; tumour; leukaemia.

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 1 /note= "Glu is biotinylated"

FT Modified-site 17 /note= "Phe is amidated"

XX WO200152892-A2.

XX 26-JUL-2001.

XX 22-JAN-2001; 2001WO-US002033.

XX 24-JAN-2000; 2000US-0177872P.

XX 28-NOV-2000; 2000US-00723490.

XX (GENZ ) GENZYME CORP.

XX Vasios G;

XX WPI; 2001-465338/50.

XX Use of inhibitors of Janus kinase/signal transducers and activators of  
PT transcription for inhibiting onset and progression of degenerative joint  
PT diseases or disorders such as osteoarthritis, rheumatoid arthritis.

XX Example 6; Page 18; 55pp; English.

XX The sequence represents a synthetic biotinylated peptide substrate for  
CC human Janus kinase 3 (JAK3). The invention relates to the use of JAK/STAT  
CC (Janus kinase/signal transducer and activator of transcription)  
CC inhibitors other than debromohymenialdisine (DBH) and hymenialdisine (H)  
CC for inhibiting the progression or the likelihood of developing diseases  
CC involving cartilage degradation, and for regulating the expression of pro  
CC -inflammatory agents or cytokines in a chondrocyte, and cartilage  
CC degrading enzymes in a cell. A JAK3/STAT inhibitor of the invention is  
CC useful for inhibiting progression or likelihood of developing  
CC osteoarthritis or rheumatoid arthritis. The inhibitor is also useful for  
CC treating other JAK/STAT-mediated diseases or disorders, including T cell-  
CC mediated disorders, mast cell-mediated disorders, type 2 (cytokine  
CC hypersensitivity) disorders, B cell lymphoma, and myeloid diseases. T  
CC cell-mediated disorders include human T cell leukaemia/lymphoma virus  
CC (HTLV)-1, Sclery's syndrome, C-abl transformation, natural killer-like T  
CC cell lymphomas (NK-like tumours) and Graft-vs-host disease; cytokine  
CC hypersensitivity disorders include leishmaniasis, leprosy, allergy and  
CC viral infections; mast cell-mediated disorders include hay fever, asthma,  
CC hives and anaphylaxis; and leukaemias and lymphomas include acute  
CC lymphocytic and lymphoblastic leukaemias, B cell lymphomas and leukaemias  
CC of myeloid origin. DBH and H are useful as therapeutic agents in cancers

CC in which JAK3 plays a role in the initiation or progression of  
CC tumourigenesis

XX Sequence 17 AA;

Query Match 100.0%; Score 103; DB 4; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17

Db 1 EGPWLEEEERAYGWMDF 17

RESULT 4

AAAB91246

ID AAB91246 standard; peptide; 17 AA.

XX AAB91246;

XX 22-JUN-2001 (first entry)

DE Gastrin releasing peptide (GRP) SEQ ID NO:422.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
KW blood component; modification; succinimidyl; maleimido group; amino;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

XX 10-SEP-1999; 99US-0153406P.

XX 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents  
PT peptidase degradation, useful for increasing length of in vivo activity.

XX Disclosure; Page 336; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (III) and a  
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
CC a less therapeutically active amino acid region (IV), which covalently  
CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity in  
CC vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB92441 represent inventions which can be used in the  
CC exemplification of the present invention

XX Sequence 17 AA;

Query Match 100.0%; Score 103; DB 4; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMDP 17  
DB 1 EGPWLEEEEEEAYGWMDP 17

RESULT 5  
AAB59273  
ID AAB59273 standard; peptide; 17 AA.  
XX  
AC AAB59273;  
DT 27-MAR-2001 (first entry)  
XX  
DE KS2-peptide substrate.  
XX  
KW Phosphorylation; kinase; insulin.  
XX  
OS Unidentified.  
XX  
PN WO200075167-A2.  
XX  
PD 14-DEC-2000.  
XX  
PF 09-JUN-2000; 2000WO-US016025.  
XX  
PR 09-JUN-1999; 99US-0138311P.  
XX  
PR 10-JUN-1999; 99US-0138438P.  
XX  
PR 08-JUL-1999; 99US-00349733.  
XX  
PR 28-APR-2000; 2000US-0200594P.  
XX  
PA (LJLB-) LJL BIOSYSTEMS INC.  
XX  
PI Sportsman JR, Hoekstra MF, Lee SK, Cairns N, Kauvar LM;  
XX  
DR WPI; 2001-091201/10.  
XX  
PT Assay for detecting phosphorylation and dephosphorylation modification of  
PT proteins by contacting luminescence peptide with a binding partner and  
PT measuring change in luminescence polarization.  
XX  
PS Claim 70; Page 70; 89pp; English.  
XX  
CC The present invention relates to detecting addition or removal of a  
CC phosphate group to or from a substrate. The method involves contacting a  
CC luminescent peptide with a binding partner that binds specifically to a  
CC phosphorylated peptide without regard to the particular amino acid  
CC sequence of the peptide. The method is useful for detecting  
CC phosphorylation and dephosphorylation modifications of proteins,  
CC including kinases and phosphatases. The methods can be used to study the  
CC kinase activity of different receptors e.g. the insulin receptor and to  
CC find agonists and antagonists of these receptors  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 103; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMDP 17  
DB 1 EGPWLEEEEEEAYGWMDP 17

RESULT 6  
AAU76504  
ID AAU76504 standard; peptide; 17 AA.  
XX  
AC AAU76504;  
XX  
DT 05-JUN-2002 (first entry)

XX  
XX Protein kinase A (PKA) substrate #3.  
XX  
KW Protein kinase A; phosphorylation.  
XX  
OS Synthetic.  
XX  
XX  
XX Key Location/Qualifiers  
FT Modified-site 1  
FT /label= OTHER  
FT /note= "Pyroglutamic acid"  
XX  
PN US6335176-B1.  
XX  
PD 01-JAN-2002.  
XX  
PF 16-OCT-1998; 98US-00174216.  
XX  
PR 16-OCT-1998; 98US-00174216.  
XX  
PA (PHAR-) PHARMACOEIA INC.  
XX  
PI Inglese J, Glickman JF;  
XX  
XX WPI; 2002-194620/25.  
XX  
DR  
XX  
PT Reagent for phosphorylating a compound, comprises a moiety that is  
PT specifically reactive with reactive site chain of the compound, a linking  
PT moiety and a peptide sequence comprising kinase substrate.  
XX  
XX Disclosure; Col 8; 26pp; English.  
XX  
CC The invention relates to a reagent (I) for incorporation of a  
CC phosphorylation site by reaction with a reactive side chain of a compound  
CC to be phosphorylated. (I) comprises a structure A-B-C, where A is a  
CC moiety that is specifically reactive with a reactive side chain, C is a  
CC peptide sequence comprising kinase substrate, and B is a linking moiety  
CC selected from any one of the 19 compounds given in the specification e.g.  
CC N-gamma-maleimidobutyryloxy-succinamide ester. (I) is useful for  
CC phosphorylation, by reacting (I) with a compound to be phosphorylated  
CC (e.g. protein or polypeptide) and then phosphorylating the resulting  
CC product using a protein kinase under phosphorylating conditions  
CC comprising 32P-phosphate or 33P-phosphate. The phosphorylated compounds  
CC are useful in assays such as drug discovery. The method is suitable for  
CC radioactively phosphorylating already synthesised proteins, without the  
CC need to carry out recombinant methods to incorporate an amino acid  
CC sequence. The method is highly adaptable and can be used to phosphorylate  
CC a broad variety of compounds that contain reactive site groups. (I)  
CC avoids production of proteins having an inaccessible kinase substrate  
CC sequence as can result from known recombinant methods. Introduction of  
CC multiple phosphorylation sites in proteins is possible merely by  
CC increasing the ratio of reagent to protein, and the method of  
CC phosphorylating does not interfere with the protein's function or become  
CC inaccessible as a result of protein folding. The method allows labeled  
CC products to be obtained that have a higher specific activity than is  
CC normally obtained with recombinant methods. The present sequence  
CC represents a protein kinase A (PKA) peptide substrate used in examples  
CC that demonstrate the method of the invention  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 103; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMDP 17  
DB 1 EGPWLEEEEEEAYGWMDP 17

RESULT 7  
ADF27269  
ID ADF27269 standard; peptide; 17 AA.

XX AC ADF72769;  
 XX DT 26-FEB-2004 (first entry)  
 XX DE  
 XX DE Chemoselective self-assembled monolayer binding peptide.  
 XX KW immobilizing; functional organic molecule; predetermined density;  
 KW mixed monolayer surface; MMS; reducing end; peracetylated sugar;  
 KW chemoselective; self-assembled monolayer; SAM.  
 XX OS Unidentified.  
 XX OS  
 XX PN WO2003018854-A2.  
 XX PD 06-MAR-2003.  
 XX PF 27-AUG-2002; 2002WO-US027195.  
 XX PR 27-AUG-2001; 2001US-0315261P.  
 PR 28-AUG-2001; 2001US-0315544P.  
 PR 15-FEB-2002; 2002US-0356765P.  
 PR 15-FEB-2002; 2002US-0358412P.  
 PR 19-FEB-2002; 2002US-0357136P.  
 PR 20-FEB-2002; 2002US-0375023P.  
 PR 26-APR-2002; 2002US-0380259P.  
 XX PA (SURF-) SURFACE LOGIX INC.  
 XX PI  
 XX PI Hodneland C, Campbell S, Duffy D, Agosto M, Wang B;  
 XX DT WPI; 2003-393250/37.  
 XX DR  
 XX PT Immobilizing functional organic molecule in a predetermined density on a  
 PT mixed monolayer surface, by contacting the surface with the organic  
 PT molecule to form a covalent bond and to immobilize the organic molecule.  
 XX PS Disclosure; Fig 40; 234pp; English.  
 XX CC The invention relates to a novel method for immobilizing a functional  
 CC organic molecule in a predetermined density on a mixed monolayer surface  
 CC (MMS). The novel method comprises a first monolayer moiety (MM1) having a  
 CC covalent bond forming reactive group and a second monolayer moiety (MM2)  
 CC having an inert group. The method involves contacting MMS with the  
 CC functional organic molecule to form a covalent bond between the  
 CC functional organic molecule and MM1 to immobilize the functional organic  
 CC molecule. The novel method of the invention is useful for immobilizing a  
 CC functional organic molecule in a predetermined density on a mixed  
 CC monolayer surface, where the functional organic molecule is selected from  
 CC oligopeptides, peptides, polypeptides, oligonucleotides,  
 CC oligonucleosides, carbohydrates, proteins, nucleosides, nucleotides,  
 CC enzymes, enzyme substrates, ligands, receptors, antibodies, antigens,  
 CC lipids, and small molecules, but preferably a carbohydrate. The  
 CC carbohydrate comprises a reducing end, the reducing end comprises a  
 CC paracetylated sugar having an n-pentenyl group. This sequence represents  
 CC a peptide which binds to the chemoselective self-assembled monolayer's  
 CC (SAM's) at the E-terminal, relating to the novel method of the invention.  
 XX SQ Sequence 17 AA;  
 Query Match 100.0%; Score 103; DB 7; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEERAYGWMP 17  
 DB 1 EGPWLEEEERAYGWMP 17  
 RESULT 8  
 ADF72934  
 ID ADF72934 standard; peptide; 17 AA.  
 XX

AC ADF72934;  
 XX DT 26-FEB-2004 (first entry)  
 XX DE  
 XX DE Biotinylated substrate biotin.  
 XX KW bisubstituted pyrazine compounds; Antiallergic; Antiasthmatic;  
 KW Antiinflammatory; Dermatological; Antirheumatic; Antiarthritic;  
 KW immunosuppressive; Antidiabetic; Antithyroid; Nootropic; Neuroprotective;  
 KW Virucide; Hepatotropic; Anti-HIV; Cytostatic;  
 KW JAK-2 tyrosine protein kinase inhibitor.  
 XX OS Synthetic.  
 XX OS  
 XX PN WO2003099796-A1.  
 XX PD 04-DEC-2003.  
 XX PF 23-MAY-2003; 2003WO-AU000629.  
 XX PR 23-MAY-2002; 2002AU-00002515.  
 PR 26-JUL-2002; 2002US-0399070P.  
 XX PA (CYTO-) CYTOPIA PTY LTD.  
 XX PI Burns CJ, Bu X, Wilks AP;  
 XX PI WPI; 2004-053219/05.  
 XX PT New disubstituted pyrazine useful for treating a protein kinase  
 PT associated disorders e.g. allergic asthma, rheumatic disease, systemic  
 PT lupus erythematosus and rheumatoid arthritis.  
 XX PS Disclosure; SEQ ID NO 7; 42pp; English.  
 XX CC The present invention relates to bisubstituted pyrazine compounds. The  
 CC compounds potentially modulates protein kinase signal transduction by  
 CC affecting the enzymatic activity of RTKs, CKs and/or STKs mediated  
 CC signal transduction pathways. The present sequence represents  
 CC biotinylated substrate biotin.  
 XX SQ Sequence 17 AA;  
 Query Match 100.0%; Score 103; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEERAYGWMP 17  
 DB 1 EGPWLEEEERAYGWMP 17  
 RESULT 9  
 ADH10240  
 ID ADH10240 standard; peptide; 17 AA.  
 XX AC ADH10240;  
 XX DT 11-MAR-2004 (first entry)  
 XX DE Peptide substrate used in kinase assays.  
 XX KW Pyrazine; protein kinase; signal transduction; Janus kinase; TYK2;  
 KW antiallergic; antiasthmatic; antiinflammatory; dermatological;  
 KW antirheumatic; antiarthritic; immunosuppressive; muscular; antidiabetic;  
 KW antithyroid; nootropic; neuroprotective; virucide; hepatotropic;  
 KW anti-HIV; cytostatic; tyrosine protein kinase.  
 XX OS Synthetic.  
 XX OS  
 XX PN WO2003099811-A1.  
 XX PD 04-DEC-2003.  
 XX

XX 23-MAY-2003; 2003WO-AU000628.  
 PF 23-MAY-2002; 2002AU-00002514.  
 PR 26-JUL-2002; 2002US-039898P.  
 XX (CYTO-) CYTOPIA PTY LTD.  
 PA Wilks AF, Bu X, Burns CJ;  
 XX WPI; 2004-081905/08.  
 DR New disubstituted pyrazines useful for treating protein kinase associated  
 XX disorders, e.g. allergic asthma, rheumatic disease, systemic lupus  
 PT erythematous and rheumatoid arthritis.  
 PT Example 61; Page 73; 53pp; English.  
 PS  
 CC The invention relates to disubstituted pyrazines of specified formula.  
 CC The novel compounds are potent modulators of protein kinases (such as  
 CC tyrosine kinase and serine/threonine kinase) mediated signal transduction  
 CC pathways. They are used for treating a protein kinase (such as a receptor  
 CC tyrosine kinase (e.g. EGF, HER2, HER3, HER4, IR, IGF-1R, IIR, PDGFR-  
 CC alpha, PDGFR-beta, CSFIR, C-Kit, C-fms, Flk-1R, Flk4, KDR/Flk-1, Flt-1,  
 CC FkR, Btk, Csk, Abi, ZAP70, Fes/Fps, Pak, Ack, Yes, Fyn, Lyn, Lck, Blk,  
 CC Hck, Fgr and Yrk), a tyrosine kinase (e.g. JAK1 - JAK3, TYK2) and a  
 CC serine/threonine kinase (e.g. ERK2, c-jun, p38MAPK, PKA, PKB, PKC, a  
 CC cyclin-dependent kinase, CDK1 - CDK11) associated disease state e.g.  
 CC atopy (e.g. allergic asthma, atopic dermatitis (Eczema), allergic  
 CC rhinitis); cell mediated hypersensitivity (e.g. allergic contact  
 CC dermatitis and hypersensitivity pneumonitis); rheumatic disease (e.g.  
 CC systemic lupus erythematosus, rheumatoid arthritis, juvenile arthritis,  
 CC Sjogren's syndrome, scleroderma, polymyositis, ankylosing spondylitis,  
 CC psoriatic arthritis), other autoimmune disease (e.g. type I diabetes,  
 CC autoimmune thyroid disorders, and Alzheimer's disease), viral disease  
 CC (e.g. Epstein Barr Virus (EBV), hepatitis B, hepatitis C, HIV, HTLV 1,  
 CC Varicella-Zoster virus, human papilloma virus), and cancer (e.g.  
 CC leukemia, lymphoma and prostate cancer). The present sequence represents  
 CC a peptide substrate used in kinase assays.  
 XX Sequence 17 AA;  
 SQ

Query Match 100.0%; Score 103; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EGPWLEEEEEEAYGWMDP 17  
 |||||  
 DB 1 EGPWLEEEEEEAYGWMDP 17

RESULT 10  
 ADH89206  
 ID ADH89206 standard; peptide; 17 AA.  
 AC ADH89206;  
 XX  
 DT 06-MAY-2004 (first entry)  
 DE Gastrin G-17 peptide, SEQ ID 1.  
 DE  
 KW Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;  
 KW gastrin G-34; gonadotropin releasing hormone; GnRH;  
 KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;  
 KW thyroid cancer; lung cancer; reproductive system cancer.  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "Pyroglutamic acid"  
 FT Modified-site 17

FT /note= "C-terminal amide"  
 XX WO2004004687-A2.  
 PN 15-JAN-2004.  
 PD  
 XX 03-JUL-2003; 2003WO-US021176.  
 PF  
 XX 03-JUL-2002; 2002US-0394179P.  
 PR  
 XX (APHT-) APTON CORP.  
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 XX Michaeli D, Grines S, Barenholz Y, Even-Chen S;  
 XX WPI; 2004-099340/10.  
 DR  
 XX Injectible liposomal composition for delivery of a water-soluble  
 PT substance e.g. vaccine for preventing pregnancy, comprises several  
 PT liposomal vesicles comprising a high weight ratio of lipid to  
 PT encapsulated water-soluble substance.  
 XX Claim 14; SEQ ID NO 1; 73pp; English.  
 PS  
 XX The present invention relates to injectable liposomal compositions (I)  
 CC for delivery of a water-soluble substance e.g. immunomimic peptides. (I)  
 CC comprises several liposomal vesicles comprising a high weight ratio of a  
 CC lipid to an encapsulated water-soluble substance so as to achieve a high  
 CC efficiency of encapsulation. The immunomimic peptide is chosen from  
 CC gastrin G-17 (ADH89206 to ADH89213 and ADH89223), gastrin G-34 (ADH89217-  
 CC ADH89219), gonadotropin releasing hormone (GnRH) peptide (ADH89220 and  
 CC ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-  
 CC ADH89222 and ADH89225). (I) comprising vaccines directed against hormone  
 CC or hormone cognate receptors, where the vaccine comprises at least one:  
 CC hormone-immunomimic peptide such as gastrin G-17 or G-34 is useful for:  
 CC treating gastrointestinal malignancy, and non-gastrointestinal tumors  
 CC such as thyroid and lung cancer; or GnRH or hCG immunomimic peptide is  
 CC useful as contraceptive and for treating cancers in male and female  
 CC reproductive systems.  
 XX Sequence 17 AA;  
 SQ

Query Match 100.0%; Score 103; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EGPWLEEEEEEAYGWMDP 17  
 |||||  
 DB 1 EGPWLEEEEEEAYGWMDP 17

RESULT 11  
 ADK00577  
 ID ADK00577 standard; peptide; 17 AA.  
 XX  
 AC ADK00577;  
 XX  
 DT 06-MAY-2004 (first entry)  
 DE Immunogenic lipopeptide of the invention #113.  
 DE  
 KW T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;  
 KW Antinfertility; Vaccine; antibody.  
 XX Synthetic.  
 OS  
 XX WO2004014956-A1.  
 PN 19-FEB-2004.  
 PD  
 XX 12-AUG-2003; 2003WO-AU001018.  
 PF 12-AUG-2002; 2002US-040283P.  
 PR

XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.  
 XX PI Jackson D, Zeng W;  
 XX DR WPI; 2004-238735/22.  
 XX PT Novel lipopeptide comprising polypeptide having amino acid sequence of T  
 PT helper cell epitope and B cell epitope, conjugated to lipid moieties,  
 PT useful for eliciting immune response against group A Streptococcus  
 PT antigen.  
 XX PS Claim 36; SEQ ID NO 113; 194pp; English.  
 XX CC The present invention relates to a lipopeptide comprising polypeptide  
 CC conjugated to lipid moieties, where polypeptide contains amino acid  
 CC sequence of T helper cell epitope and B cell epitope, where amino acid  
 CC sequences are different, and internal lysine residues or internal lysine  
 CC analog residues for covalent attachment of each of lipid moieties through  
 CC  $\epsilon$  group; amino group or terminal side chain group of lysine or lysine  
 CC analog. The peptides are useful in eliciting the production of antibody  
 CC against an antigenic B cell epitope in a subject, and are useful for  
 CC antibody production, synthetic vaccine production, diagnostic method  
 CC employing antibodies and antibody ligands and immunotherapy for  
 CC veterinary and human medicine. The method efficiently elicits the  
 CC production of antibody against antigenic B cell epitope. The present  
 CC sequence represents a novel immunogenic lipopeptide comprising T helper  
 CC and B cell epitopes.  
 XX SQ Sequence 17 AA;  
 Query Match 100.0%; Score 103; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEERAYGWMPF 17  
 DB 1 EGPWLEEEERAYGWMPF 17  
 RESULT 12  
 ADL02105  
 ID ADL02105 standard; peptide; 17 AA.  
 XX AC ADL02105;  
 XX DT 20-MAY-2004 (first entry)  
 XX DE Phosphopeptide.  
 XX KW phosphopeptide; binding solution; high-throughput screening;  
 KW cellular phosphoprotein status; signal transduction; mitosis;  
 KW cell proliferation; phosphoprotein expression profile.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "N-terminal biotinyl"  
 FT Modified-site 17 /note= "C-terminal amidated"  
 FT US2004038306-A1.  
 XX PD 26-FEB-2004.  
 XX PP 02-MAY-2003; 2003US-00428192.  
 XX PR 03-MAY-2002; 2002US-0377733P.  
 PR 28-JUN-2002; 2002US-0393059P.  
 PR 30-AUG-2002; 2002US-0407255P.  
 PR 14-JAN-2003; 2003US-0440252P.  
 XX

PA (AGNE/) AGNEW B.  
 PA (BEEC/) BEECHEM J.  
 PA (GEEK/) GEE K.  
 PA (HAUG/) HAUGLAND R.  
 PA (LIU/) LIU J.  
 PA (MART/) MARTIN V.  
 PA (PATT/) PATTON W.  
 PA (STEL/) STEINBERG T.  
 XX Agnew B, Beechem J, Gee K, Haugland R, Liu J, Martin V;  
 PI Patton W, Steinberg T;  
 XX WPI; 2004-267637/25.  
 XX CC Binding solution useful for binding, detecting and isolating  
 PT phosphorylated target molecules, comprises metal chelating part or  
 PT phosphate-binding compound having chemical part, linker and metal-  
 PT chelating part, salt and acid.  
 XX Example 29; Page 51; 83pp; English.  
 XX CC The invention relates to a binding solution (BS), comprising a 1,2-bis(2-  
 CC aminophenoxy-)ethane-N,N',N'-tetraacetic acid (BAPTA) metal chelating  
 CC part or a phosphate-binding compound having a chemical part, linker and  
 CC metal-chelating part, salt comprising trivalent metal ions and an acid.  
 CC The (BS) is useful for binding a phosphorylated target molecule in a  
 CC sample, detecting an immobilised phosphorylated target molecule in a  
 CC sample and isolating phosphorylated target molecule from a sample. The  
 CC (BS) is also useful in the field of proteomics, molecular biology, high-  
 CC throughput screening and diagnostics. The (BS) is useful for analysis and  
 CC monitoring of phosphorylated target molecules. The (BS) is useful to  
 CC generate data that are used as reference point for human patients or  
 CC animal sample for diagnosis of disease, progression of disease, and/or  
 CC predisposition for disease. The (BS) is useful for gaining valuable  
 CC information of the effects of various drugs and compounds on the cellular  
 CC phosphoprotein status. The (BS) is useful for studying biological  
 CC phenomena such as signal transductions, mitosis, cell proliferation, etc.  
 CC The (BS) is useful for generating a comprehensive phosphoprotein  
 CC expression profile from any cell type or biological fluid of interest.  
 CC The (BS) specifically detects, isolates and/or quantitates phosphorylated  
 CC target molecules. The (BS) allows for rapid, sensitive, and non-  
 CC radioactive detection of variety of selected kinases and phosphatases.  
 CC The (BS) allows for high-throughput screening. The present sequence  
 CC represents the amino acid sequence of a phosphopeptide.  
 XX SQ Sequence 17 AA;  
 Query Match 100.0%; Score 103; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEERAYGWMPF 17  
 DB 1 EGPWLEEEERAYGWMPF 17  
 RESULT 13  
 ADN03334  
 ID ADN03334 standard; peptide; 17 AA.  
 XX AC ADN03334;  
 XX DT 17-JUN-2004 (first entry)  
 XX DE Exemplary peptide ligand for proteome analysis #60.  
 XX KW Peptide ligand; proteome; capture compound; mass spectrometry;  
 KW protein separation;  
 KW matrix assisted laser desorption ionisation-time of flight; MALDI-TOF.  
 XX OS Unidentified.  
 XX PN US2003119021-A1.



XX (APHT-) APHTON CORP.  
 PA (HUNT-) HUNTINGDON LIFE SCI LTD.  
 XX  
 XX  
 PI Grimes S, Little J, McLoughlin L;  
 XX  
 XX WPI, 2004-719280/70.  
 DR  
 XX Determining total or free amount of gastrin hormone in a biological fluid  
 PT sample comprises incubating the sample in the presence of an N-terminal  
 PT sequence gastrin peptide for binding to a C-terminal specific antibody.  
 XX  
 XX Disclosure; SEQ ID NO 1; 24pp; English.  
 PS  
 XX The invention relates to determining the total amount of gastrin or free  
 CC gastrin hormone in a biological fluid sample. The method involves (a)  
 CC obtaining a biological fluid sample comprising a gastrin hormone from a  
 CC patient; (b) providing an immobilized antibody that selectively binds a C  
 CC -terminal epitope of the gastrin hormone; (c) incubating the sample in  
 CC the presence of an N-terminal sequence gastrin peptide under conditions  
 CC for binding of the gastrin hormone in the sample to the antibody to  
 CC produce an immobilized complex of the antibody bound to the gastrin  
 CC hormone; (d) washing the immobilized complex to remove unbound antibody  
 CC and N-terminal sequence gastrin peptide, and incubating the complex with  
 CC a detectable marker-conjugated antibody that selectively binds an N-  
 CC terminal epitope of gastrin hormone to form an immobilized detectable  
 CC marker-conjugated antibody complex; (e) washing the immobilized  
 CC detectable marker-conjugated antibody complex, and incubating with a  
 CC development reagent; and (f) measuring the developed reagent to determine  
 CC the total amount of (free) gastrin hormone in the biological fluid  
 CC sample. The C-terminal selective antibody and/or the N-terminal selective  
 CC antibody is a monoclonal antibody. The gastrin hormone is gastrin-17  
 CC (G17) or glycine extended G17 (G17-Gly) and the C-terminal selective  
 CC antibody and the N-terminal selective antibody bind G17. The method is  
 CC useful for detecting and/or quantifying free or total amount of gastric  
 CC hormone peptides including antibody-bound, in a biological fluid. The  
 CC present sequence represents the amino acid sequence of mature G17, the  
 CC predominant form of little gastrins in human.  
 XX  
 XX Sequence 17 AA;  
 SQ  
 Query Match 100.0%; Score 103; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEERAYGWMDF 17  
 DB 1 EGPWLEEEERAYGWMDF 17  
 RESULT 16  
 ADU48549  
 ID ADU48549 standard; protein; 17 AA.  
 XX  
 AC ADU48549;  
 XX  
 XX 27-JAN-2005 (first entry)  
 DT  
 XX Gastrin-17 amino acid sequence.  
 DB  
 XX KGF; FGF; keratinocyte growth factor; gastrin-17; antilipaeamic;  
 KW antidiabetic; vasotropic; cerebroprotective; cardiant; antiarrhythmic;  
 KW antibacterial; immunosuppressive; antiinflammatory; gastrointestinal;  
 KW antitumor; hypotensive; nootropic; neuroprotective; anorectic;  
 KW dermatological; endocrine; respiratory; hepatotropic; gene therapy;  
 KW cell therapy; fibroblast growth factor.  
 XX  
 OS Unidentified.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "pyroglutamic acid"  
 FT  
 XX

PN WO2004096853-A1.  
 XX  
 PD 11-NOV-2004.  
 XX  
 XX 30-APR-2004; 2004WO-CA0000648.  
 PF  
 XX 30-APR-2003; 2003US-0509068P.  
 PR  
 XX (WARA-) WARATAH PHARM INC.  
 PA  
 XX Brand SU, Cruz A;  
 PI  
 XX WPI; 2004-804727/79.  
 DR  
 XX New pharmaceutical composition comprising a keratinocyte growth factor  
 FT (KGF) agonist and a gastrin compound, useful in treating or preventing  
 FT diabetes, hypertension, heart failure and obesity.  
 PT  
 XX Disclosure; SEQ ID NO 7; 58pp; English.  
 PS  
 XX The invention relates to a pharmaceutical composition comprising a  
 CC keratinocyte growth factor (KGF) agonist and a gastrin compound that  
 CC provides beneficial effects relative to each compound alone, and  
 CC optionally a carrier, excipient, or vehicle. The composition provides  
 CC sustained beneficial effects, and is in a form that provides normal blood  
 CC glucose levels in a subject that persist for a prolonged period of time  
 CC after administration. The composition further comprises amounts of a KGF  
 CC agonist and a gastrin compound in a form for chronic or acute therapy of  
 CC a subject in need, where the amounts are suboptimal relative to the  
 CC amount of each compound administered alone for treatment of diabetes. The  
 CC beneficial effects are reduced or absent islet inflammation, decreased  
 CC disease progression, increased survival, or decreased symptoms of a  
 CC disease or condition, and/or are sustained beneficial effects that  
 CC persist for a prolonged period of time after termination of treatment.  
 CC The composition is useful for the preparation of a medicament for the  
 CC treatment of a condition or disease, such as dyslipidaemia,  
 CC hyperglycaemia, severe hypoglycaemic episodes, stroke, left ventricular  
 CC hypertrophy, arrhythmia, bacteraemia, septicemia, irritable bowel  
 CC syndrome, functional dyspepsia, diabetes, catabolic changes after  
 CC surgery, stress induced hyperglycaemia, gastric ulcers, myocardial  
 CC infarction, impaired glucose tolerance, hypertension, Alzheimer's disease  
 CC and other central and peripheral neurodegenerative conditions, chronic  
 CC heart failure, fluid retentive states, metabolic syndrome and related  
 CC diseases, and disorders and obesity. The composition is also used to  
 CC promote and/or enhance soft tissue growth and regeneration, such as in  
 CC epidermolysis bullosa, chemotherapy induced alopecia, male-pattern  
 CC baldness, hyaline membrane disease and hepatic cirrhosis. The present  
 CC sequence represents a little gastrin (gastrin-17) peptide sequence.  
 XX  
 XX Sequence 17 AA;  
 SQ  
 Query Match 100.0%; Score 103; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEERAYGWMDF 17  
 DB 1 EGPWLEEEERAYGWMDF 17  
 RESULT 17  
 ADV16301  
 ID ADV16301 standard; peptide; 17 AA.  
 XX  
 AC ADV16301;  
 XX  
 XX 10-FEB-2005 (first entry)  
 DT  
 XX Human gastrin-17 wild-type peptide.  
 DB  
 XX Gastrin-17; diabetes mellitus; insulin dependent diabetes;  
 KW Gastrin receptor modulator; CCK receptor modulator.  
 XX

```

OS Homo sapiens.
XX Key Location/Qualifiers
FH Modified-site 1
FT Modified-site /note= "pyroglutamic acid, optionally absent"
FT Modified-site 17
FT Modified-site /note= "C-terminal amide"
XX
XX
XX US2004229810-A1.
XX
XX 18-NOV-2004.
XX
XX 03-DEC-2003; 2003US-00728082.
XX
XX 22-OCT-2002; 2002US-0420187P.
XX 22-OCT-2002; 2002US-0420399P.
XX 21-NOV-2002; 2002US-0428100P.
XX 21-NOV-2002; 2002US-0428100P.
XX 22-DEC-2002; 2002US-0430590P.
XX 03-DEC-2002; 2002US-0428562P.
XX 22-OCT-2003; 2003US-00691123.
XX
XX (CRUZ/) CRUZ A.
XX
XX Cruz A;
XX
XX WPI; 2005-037040/04.
XX
XX Pharmaceutical composition for treating subject with diabetes, has
XX gastrin compound having extended activity upon administration to subject
XX in comparison with native gastrin.
XX
XX Claim 2; SEQ ID NO 3; 24pp; English.
XX
XX The invention relates to a novel pharmaceutical composition comprising a
XX gastrin compound having an extended activity, upon administration to a
XX subject, in comparison with native gastrin. The compounds of the
XX invention may be useful for treating a subject having diabetes. This
XX involves measuring a physiological indicator of islet neogenesis and
XX fasting blood glucose (FBG). The method further involves decreasing
XX insulin dependency. Furthermore, the compounds may be useful for
XX maintaining an increase in gastrin serum level for an extended period of
XX time. The current sequence is that of the human gastrin-17 wild-type
XX peptide of the invention which may act as a stimulator of the gastrin or
XX CCK receptor.
XX
XX Sequence 17 AA;
XX
XX Query Match 100.0%; Score 103; DB 9; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 3.1e-08;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EGPWLEEEERAYGWMDP 17
XX |||||
XX Db 1 EGPWLEEEERAYGWMDP 17
XX
XX RESULT 18
XX ADW00242
XX ID ADW00242 standard; peptide; 17 AA.
XX
XX AC ADW00242;
XX
XX 24-MAR-2005 (first entry)
XX
XX Human wild type gastrin-17 peptide.
XX
XX antidiabetic; gastrin receptor; cholecystokinin receptor;
XX gastrin receptor modulator; CCK receptor modulator; gastrin; diabetes;
XX fasting blood glucose; insulin.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers

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```

FT Modified-site 1 /note= "pyroglutamic acid"
FT Modified-site 17 /note= "amidated C-terminus"
XX
XX US200426682-A1.
XX
XX 30-DEC-2004.
XX
XX 21-NOV-2003; 2003US-00719450.
XX
XX 22-OCT-2002; 2002US-0420187P.
XX 22-OCT-2002; 2002US-0420399P.
XX 21-NOV-2002; 2002US-0428100P.
XX 22-NOV-2002; 2002US-0428562P.
XX 03-DEC-2002; 2002US-0430590P.
XX 22-OCT-2003; 2003US-00691123.
XX 14-NOV-2003; 2003US-0519933P.
XX
XX (CRUZ/) CRUZ A.
XX
XX Cruz A;
XX
XX WPI; 2005-074216/08.
XX
XX Pharmaceutical composition useful for treating diabetes, comprises a
XX gastrin compound having an extended activity upon administration to a
XX subject in comparison with native gastrin.
XX
XX Disclosure; Page 4; 25pp; English.
XX
XX The invention relates to a pharmaceutical composition (I) comprising a
XX gastrin compound (C1) having an extended activity upon administration to
XX a subject in comparison with native gastrin. (I) or C1 is useful for
XX treating a subject having diabetes, which involves administering C1 or a
XX modified gastrin capable of covalently reacting with a serum protein,
XX where the frequency of administering the gastrin compound is less than
XX frequency of administration of a native gastrin. The method further
XX involves measuring a physiological indicator of islet neogenesis,
XX measuring fasting blood glucose (FBG), and decreasing insulin dependency.
XX The modified gastrin comprises a sequence of native gastrin capable of
XX binding to the gastrin/CCK receptor and an amino terminal cysteine or
XX lysine. (I) or C1 is useful for maintaining for an extended period of
XX time an increased gastrin serum level compared with the serum level of a
XX peptide having an amino acid sequence of a native gastrin, which involves
XX administering C1. (I) Contains gastrin compositions having longer active
XX function than native gastrin peptides, and has a longer half-life in
XX circulation in a subject. This sequence corresponds to the wild type
XX gastrin-17 peptide used in the invention. (Note: this sequence differs
XX from sequence denoted as SEQ ID NO: 3 as given in the Sequence Listing of
XX the specification).
XX
XX Sequence 17 AA;
XX
XX Query Match 100.0%; Score 103; DB 9; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 3.1e-08;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EGPWLEEEERAYGWMDP 17
XX |||||
XX Db 1 EGPWLEEEERAYGWMDP 17
XX
XX RESULT 19
XX ADW71906
XX ID ADW71906 standard; peptide; 17 AA.
XX
XX AC ADW71906;
XX
XX 07-APR-2005 (first entry)
XX
XX Non-phosphopeptide used in detection assay.
XX
XX

```

```
KW High throughput screening; diagnostic.
XX Unidentified.
OS
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Biotinyl glutamic acid"
FT Modified-site 17
FT Modified-site 17 /note= "amidated residue"
XX
XX WO2005047290-A2.
XX
XX 26-MAY-2005.
XX
XX 10-NOV-2004; 2004WO-US037433.
XX
XX 11-NOV-2003; 2003US-0519311P.
XX
XX (CELL-) CELLULAR GENOMICS INC.
XX
XX Currie KS, Desimone RW, Pippin DA, Darrow JW, Mitchell SA;
XX WPI; 2005-386327/39.
XX
XX New imidazo(1,2-a)pyrazin-8-ylamine derivatives, useful to treat e.g.
XX cancer, autoimmune condition, inflammatory condition, psoriasis,
XX atherosclerosis, Parkinson's disease, diabetes and septic shock, are
XX kinase modulators.
XX
XX Example 4; SEQ ID NO 10; 236pp; English.
XX
XX This invention describes novel imidazo[1,2-a]pyrazin-8-ylamine
XX derivatives and their salts, solvates, crystal forms, diastereomers and
XX prodrugs. The invention also describes 1) a method for identifying a
XX kinase comprising contacting an organism, cell or preparation comprising
XX contacting the kinase with a novel imidazo[1,2-a]pyrazin-8-ylamine
XX derivative and detecting modulation of an activity of a kinase and 2) a
XX method for identifying Btk comprising contacting the organism cell or
XX preparation comprising the contacting kinase with a imidazo[1,2-a]pyrazin
XX -8-ylamine derivative and detecting modulation of an activity of Btk. The
XX derivatives can be used for the treatment of cancer when administered
XX with at least one antitumor therapeutic (preferably a chemotherapeutic
XX agent and especially mitomycin C, carboplatin, taxol, cisplatin,
XX paclitaxel, etoposide or doxorubicin or a radiotherapeutic agent. The
XX derivatives are useful for manufacture of a medicament for the treatment
XX of kinase (Btk) implicated condition, preferably cancer, an autoimmune
XX and/or inflammatory condition, in a mammal (preferably human, dog or
XX cat). The derivatives are also useful to treat conditions, diseases
XX and/or disorders such as psoriasis, cancer (especially chronic
XX myelogenous leukemia, gastrointestinal stromal tumors, non-small cell
XX lung cancer, breast cancer, ovarian cancer, recurrent ovarian cancer,
XX prostate cancer such as hormonal refractory prostate cancer, kidney
XX cancer, head and neck cancer or colorectal cancer), immunoregulation
XX (e.g. graft rejection), atherosclerosis, rheumatoid arthritis,
XX Parkinson's disease, Alzheimer's disease, diabetes (especially insulin
XX resistance or diabetic retinopathy) and septic shock. The imidazo[1,2-
XX a]pyrazin-8-ylamine derivatives have effective pharmacological properties
XX such as oral bioavailability, low toxicity, low serum protein binding and
XX desirable in vitro and in vivo half-lives. This sequence represents a
XX biotinylated and amidated peptide which is a substrate for a PTK domain
XX assay.
XX
XX Sequence 17 AA;
XX
XX Query Match 100.0%; Score 103; DB 9; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 3.1e-08;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 EGPWLEEREAYGWMDF 17
XX |||||
XX Db 1 EGPWLEEREAYGWMDF 17
XX
XX RESULT 20
XX AEA08308
XX ID AEA08308 standard; peptide; 17 AA.
XX
XX AC AEA08308;
XX
XX 28-JUL-2005 (first entry)
XX
XX PTK domain substrate peptide SEQ ID NO 10.
XX
XX imidazo[1,2-a]pyrazin-8-ylamine; kinase; Btk kinase; cancer; neoplasm;
XX cycostatic; immunosuppressive; antiinflammatory; antipsoriatic;
XX immunomodulator; antiarteriosclerotic; antiarthritic; antirheumatic;
XX antiparkinsonian; neuroprotective; nootropic; antidiabetic;
XX antibacterial; anticancer; immune disorder; autoimmune disease;
XX inflammation; psoriasis; chronic myelocytic leukemia;
XX gastrointestinal tumor; lung tumor; breast tumor; ovary tumor;
XX prostate tumor; renal tumor; head and neck tumor; colorectal tumor;
```

## RESULT 21

AEA52649

ID AEA52649 standard; peptide; 17 AA.

XX AC

XX AEA52649;

XX AC

XX 25-AUG-2005 (first entry)

XX AC

XX Kinase biotinylated substrate peptide.

XX DE

XX Pharmacological; kinase; atopy; hypersensitivity; rheumatism;  
 KW autoimmune disease; viral infection; cancer; neurodegenerative disease;  
 KW cardiovascular disease; inflammation; infection; PCR; primer; ss;  
 KW dermatological; anti-allergic; immunosuppressive; anti-rheumatic; virucide;  
 KW cytostatic; neuroprotective; cardiovascular-gen.; anti-inflammatory;  
 KW antimicrobial; enzyme inhibition.

XX XX

XX Synthetic.

XX OS

XX Key Location/Qualifiers

XX FH

XX Modified-site 1

XX FT /note= "Biotinylated residue"

XX FT

XX Modified-site 17

XX FT

XX FT /note= "C-terminal amide"

XX XX

XX WO2005054230-A1.

XX XX

XX 16-JUN-2005.

XX PD

XX 03-DEC-2004; 2004WO-AU001690.

XX PF

XX 03-DEC-2003; 2003AU-00906686.

XX PR

XX 20-APR-2004; 2004AU-00902060.

XX PR

XX (CYTO-) CYTOPIA RES PTY LTD.

XX PA

XX Burns CJ, Wilks AP, Bu X;

XX XX

XX WPI; 2005-466876/47.

XX DR

XX New pyrazine derivatives are protein tyrosine kinase inhibitors useful to

XX PT

XX treat e.g. rheumatic diseases, atopy, other autoimmune diseases/viral  
 PT diseases, cancer, inflammation, neurodegenerative diseases and  
 PT cardiovascular diseases.

XX PT

XX Disclosure; Page 42; 75pp; English.

XX PS

XX The invention relates to pyrazine derivatives and their prodrugs, salts,  
 CC hydrates, solvates, crystal forms and diastereomers. The pyrazine  
 CC derivatives are useful for treating tyrosine kinase-associated diseases  
 CC involving janus kinase (JAK) 1, JAK2, JAK3 or TYK2 (particularly atopy,  
 CC cell mediated hypersensitivity, rheumatic diseases, other autoimmune  
 CC diseases/viral diseases), cancer, neurodegenerative diseases and  
 CC cardiovascular diseases), in medicaments for treating JAK-associated  
 CC disease states and for treating diseases and conditions associated with  
 CC inflammation and infection. This sequence represents a kinase  
 CC biotinylated substrate peptide used in the scope of the invention.

XX XX

XX Sequence 17 AA;

XX SQ

Query Match 100.0%; Score 103; DB 9; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY

1 EGPWLEEEEAAYGWMDF 17

XX Db

1 EGPWLEEEEAAYGWMDF 17

XX XX

XX RESULT 22

XX AEB25345

ID

XX

XX AC

XX AEB25345;

XX XX

XX 08-SEP-2005 (first entry)

XX DT

XX DE

XX Peptide used in protein kinase inhibitor assay.

XX XX

XX Cancer; neoplasm; inflammation; gastrointestinal disorder;  
 KW Alzheimers disease; neurological disease; degeneration; dementia;  
 KW psychiatric disorder; cognitive disorder; arthritis; cytostatic;  
 KW gastrointestinal-gen.; anti-inflammatory; antipsoriatic;  
 KW immunosuppressive; neuroprotective; anticonvulsant; nootropic;  
 KW antiparkinsonian; cerebroprotective; CNS-gen.; vasotropic; vulnary;  
 KW neuroleptic; antidepressant; endocrine-gen.; contraceptive;  
 KW antiarthritic.

XX XX

XX Synthetic.

XX OS

XX FH

XX Key

XX Modified-site 1

XX FT

XX Location/Qualifiers

XX FT

XX /note= "N-terminal biotin label"

XX XX

XX WO2005061519-A1.

XX PN

XX XX

XX 07-JUL-2005.

XX PD

XX 17-DEC-2004; 2004WO-US042631.

XX PF

XX 19-DEC-2003; 2003US-0531202P.

XX PR

XX (SYRR-) SYRRX INC.

XX PA

XX Gangloff AR, Nowakowski J, Paraselli BR, Stafford JA, Tennant MG;

XX XX

XX WPI; 2005-497745/50.

XX DR

XX New indole-containing derivatives useful for treating e.g. Kaposi's

XX PT

XX sarcoma, Parkinson's disease, stroke, depression or hair loss.

XX PT

XX Example; Page 87; 179pp; English.

XX XX

XX The present invention relates to novel indole-containing derivatives that

XX CC

XX act as protein kinase inhibitors. These compounds are useful for

XX CC

XX treating: cancer (e.g. non small-cell lung, bladder, head, neck, ovarian,

XX CC

XX prostate, breast, colorectal, small-cell lung, genitourinary,

XX CC

XX gastrointestinal cancer, squamous cell carcinoma, astrocytoma, Kaposi's

XX CC

XX sarcoma, glioblastoma, melanoma or glioma); inflammation, inflammatory

XX CC

XX bowel disease, psoriasis, or transplant rejection; for preventing or

XX CC

XX treating dementia related diseases (e.g. frontotemporal dementia

XX CC

XX Parkinson's type, Parkinson dementia complex of Guam, HIV dementia,

XX CC

XX diseases with associated neurofibrillar tangle pathologies, predemented

XX CC

XX dementia and dementia pugilistica), Alzheimer's disease and conditions

XX CC

XX associated with kinases; for preventing or treating amyotrophic lateral

XX CC

XX sclerosis, corticobasal degeneration, Down syndrome, Huntington's

XX CC

XX disease, Parkinson's disease, postencephalic parkinsonism, progressive

XX CC

XX supranuclear palsy, Pick's disease, Niemann-Pick's disease, stroke, head

XX CC

XX trauma and other chronic neurodegenerative diseases, bipolar disease, hair

XX CC

XX loss and contraceptive medication; mild cognitive impairment, age-

XX CC

XX associated memory impairment, age-related cognitive decline, cognitive

XX CC

XX impairment no dementia, mild cognitive decline, mild neurocognitive

XX CC

XX decline, late-life forgetfulness, memory impairment and cognitive

XX CC

XX impairment and androgenetic alopecia; or for treating arthritis (all

XX CC

XX claimed). The present sequence is that of a peptide used in a time-

XX CC

XX resolved fluorescence resonance energy transfer detection method to

XX CC

XX compounds of the invention.

XX SQ

XX Sequence 17 AA;

XX Query Match 100.0%; Score 103; DB 9; Length 17;

XX Homo sapiens.

```

PN WO9728821-A1.
XX
XX PD 14-AUG-1997.
XX
XX PF 07-FEB-1997; 97WO-US002029.
XX
XX PR 08-FEB-1996; 96US-0011411P.
XX
XX PA (APHT-) APHTON CORP.
XX
XX PI Gevas PC, Karr SL, Grimes S, Michaeli D, Watson SA;
XX
XX DR WPI; 1997-415075/38.
XX
XX PT Treatment of glycine-extended gastrin-17-dependent gastrointestinal
XX
XX PT tumours - using anti-G17 immunogenic composition, especially for
XX
XX PT treatment of colorectal adenocarcinomas.
XX
XX PS Example 1; Fig 1A; 37pp; English.
XX
XX CC The present sequence represents glycine-extended gastrin-17. Treatment of
XX
XX CC glycine-extended gastrin-17 (G17-Gly)-dependent gastrointestinal tumours
XX
XX CC comprises administering an anti-gastrin 17 (anti-G17) immunogenic
XX
XX CC composition. Anti-G17 immunogens raise antibodies which bind both the
XX
XX CC amidated and glycine-extended forms of G17. Neutralisation of progastrin
XX
XX CC G17-Gly pro hormone by the antibodies inhibits the growth of tumour cells
XX
XX CC dependent on progastrin G17-Gly as growth stimulator or inducer. The
XX
XX CC method is especially for the treatment of colorectal adenocarcinomas in
XX
XX CC humans. This novel method is non-invasive, selectively reversible, does
XX
XX CC not damage normal tissue, does not require frequent repeated treatments
XX
XX CC and does not cross the blood brain barrier
XX
XX SQ Sequence 18 AA;

Query Match 100.0%; Score 103; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEREAYGWMDP 17
Db 1 EGPWLEEEEREAYGWMDP 17

RESULT 26
ADH89207
ID ADH89207 standard; peptide; 18 AA.
XX
XX AC ADH89207;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Glycine extended gastrin G-17 precursor peptide, SEQ ID 2.
XX
XX KW Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;
XX
XX KW gastrin G-34; gonadotropin releasing hormone; GnRH;
XX
XX KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;
XX
XX KW thyroid cancer; lung cancer; reproductive system cancer.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX
XX FT Modified-site 1 /note= "Pyroglutamic acid"
XX
XX FT /label= pGlu
XX
XX FT /note= "pyroglutamic acid"
XX
XX PN WO2004004687-A2.
XX
XX PD 15-JAN-2004.
XX
XX PF 03-JUL-2003; 2003WO-US021176.
XX
XX PR 03-JUL-2002; 2002US-0394179P.
XX
XX PA (APHT-) APHTON CORP.

PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
XX PI Michaeli D, Grimes S, Barenholz Y, Even-Chen S;
XX
XX DR WPI; 2004-099340/10.
XX
XX PT Injectable liposomal composition for delivery of a water-soluble
XX
XX PT substance e.g. vaccine for preventing pregnancy, comprises several
XX
XX PT liposomal vesicles comprising a high weight ratio of lipid to
XX
XX PT encapsulated water-soluble substance.
XX
XX PS Disclosure; SEQ ID NO 2; 73pp; English.
XX
XX CC The present invention relates to injectable liposomal compositions (I)
XX
XX CC for delivery of a water-soluble substance e.g. immunomimic peptides. (I)
XX
XX CC comprises several liposomal vesicles comprising a high weight ratio of a
XX
XX CC lipid to an encapsulated water-soluble substance so as to achieve a high
XX
XX CC efficiency of encapsulation. The immunomimic peptide is chosen from
XX
XX CC gastrin G-17 (ADH89206 to ADH89213 and ADH89223), gastrin G-34 (ADH89217-
XX
XX CC ADH89219), gonadotropin releasing hormone (GnRH) peptide (ADH89220 and
XX
XX CC ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-
XX
XX CC ADH89222 and ADH89225). (I) comprising vaccines directed against hormone
XX
XX CC or hormone cognate receptors, where the vaccine comprises at least one:
XX
XX CC hormone-immunomimic peptide such as gastrin G-17 or G-34 is useful for
XX
XX CC treating gastrointestinal malignancy, and non-gastrointestinal tumors
XX
XX CC such as thyroid and lung cancer; or GnRH or hCG immunomimic peptide is
XX
XX CC useful as contraceptive and for treating cancers in male and female
XX
XX CC reproductive systems.
XX
XX SQ Sequence 18 AA;

Query Match 100.0%; Score 103; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEREAYGWMDP 17
Db 1 EGPWLEEEEREAYGWMDP 17

RESULT 27
ADT49597
ID ADT49597 standard; peptide; 18 AA.
XX
XX AC ADT49597;
XX
XX DT 30-DEC-2004 (first entry)
XX
XX DE Human gastrin 17 (G17)-Gly amino acid sequence.
XX
XX KW G17; gastrin; hormone; human; G17-Gly; gastrin 17.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX
XX FT Modified-site 1 /label= pGlu
XX
XX FT /note= "pyroglutamic acid"
XX
XX PN WO2004088326-A2.
XX
XX PD 14-OCT-2004.
XX
XX PF 29-MAR-2004; 2004WO-US009666.
XX
XX PR 28-MAR-2003; 2003US-0458244P.
XX
XX PA (APHT-) APHTON CORP.
XX
XX PA (HUNT-) HUNTINGDON LIFE SCI LTD.
XX
XX PI Grimes S, Little J, McLoughlin L;
XX
XX DR WPI; 2004-719280/70.

```

XX Determining total or free amount of gastrin hormone in a biological fluid  
PT sample comprises incubating the sample in the presence of an N-terminal  
PT sequence gastrin peptide for binding to a C-terminal specific antibody.  
XX  
XX Disclosure; SEQ ID NO 2; 24pp; English.

XX The invention relates to determining the total amount of gastrin or free  
CC gastrin hormone in a biological fluid sample. The method involves (a)  
CC obtaining a biological fluid sample comprising a gastrin hormone from a  
CC patient; (b) providing an immobilized antibody that selectively binds a C  
CC -terminal epitope of the gastrin hormone; (c) incubating the sample in  
CC the presence of an N-terminal sequence gastrin peptide under conditions  
CC for binding of the gastrin hormone in the sample to the antibody to  
CC produce an immobilized complex of the antibody bound to the gastrin  
CC hormone; (d) washing the immobilized complex to remove unbound antibody  
CC and N-terminal sequence gastrin peptide, and incubating the complex with  
CC a detectable marker- conjugated antibody that selectively binds an N-  
CC terminal epitope of gastrin hormone to form an immobilized detectable  
CC marker-conjugated antibody complex; (e) washing the immobilized  
CC detectable marker-conjugated antibody complex, and incubating with a  
CC development reagent; and (f) measuring the developed reagent to determine  
CC the total amount of (free) gastrin hormone in the biological fluid  
CC sample. The C-terminal selective antibody and/or the N-terminal selective  
CC antibody is a monoclonal antibody. The gastrin hormone is gastrin-17  
CC (G17) or glycine extended G17 (G17-Gly) and the C-terminal selective  
CC antibody and the N-terminal selective antibody bind G17. The method is  
CC useful for detecting and/or quantifying free or total amount of gastric  
CC hormone peptides including antibody-bound, in a biological fluid. The  
CC present sequence represents the amino acid sequence of G17-Gly, an  
CC incomplete processed form of gastrin found as a minor component of little  
CC gastrins in human.

XX Sequence 18 AA;

Query Match 100.0%; Score 103; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.3e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17  
|||||  
DB 1 EGPWLEEEERAYGWMDF 17

RESULT 28

AEC05677  
ID AEC05677 standard; peptide; 18 AA.

XX  
AC AEC05677;

XX 20-OCT-2005 (first entry)

XX Gastrin peptide.

XX Vaccine; development; antibody production; immunogenicity; gastrin;  
XX hormone.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "Pyroglutamic acid"

FT Modified-site 18 /note= "Biotinylated C-terminal amide"

XX EP1564554-A1.

XX 17-AUG-2005.

XX 12-FEB-2004; 2004EP-00075439.

XX 12-FEB-2004; 2004EP-00075439.

PA (PEPS-) PEPSAN SYSTEMS BV.  
PA (UYUT-) UNIV UTRECHT HOLDING BV.

XX Akresterijn GJ, Hensen EJ, Scibelli A, Van Der Most RG, Meloen RH;  
PI Turkstra JA;

XX WPI; 2005-573732/59.

XX Affinity-binding assay for selecting antigen specific immune cells, by  
PT contacting cell having four copies of target molecule with two labeled  
PT binding molecules, detecting cells staining with each label, selecting  
XX cells binding both labels.

XX Example 1; Page 6; 45pp; English.

XX The present invention relates to an affinity-binding assay for selecting  
CC antigen specific immune cells. The method involves contacting particle  
CC such as a cell having four copies of target molecule with two binding  
CC molecules specific for the target molecule, where first of the binding  
CC molecules is associated with a first label, and a second of the binding  
CC molecules is associated with a second label, detecting cells staining  
CC with each label and selecting cells binding both labels. The invention  
CC also provides a method for detection of early B cell populations in  
CC vaccine development. The invention is useful for the preparation of an  
CC antibody. The present sequence is a gastrin peptide. This sequence is an  
CC immunogenic peptide used as a vaccine.

XX Sequence 18 AA;

Query Match 100.0%; Score 103; DB 9; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.3e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17

|||||  
DB 1 EGPWLEEEERAYGWMDF 17

RESULT 29

ADT49598

ID ADT49598 standard; peptide; 34 AA.

XX  
AC ADT49598;

XX 30-DEC-2004 (first entry)

XX Human gastrin 34 (G34) amino acid sequence.

XX G34; gastrin; hormone; human; gastrin 34; gastrin 17.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 1 /label= pGlu

FT Modified-site 34 /note= "Pyroglutamic acid"

FT Modified-site 34 /note= "C-terminal amide"

XX WO2004088326-A2.

XX 14-OCT-2004.

XX 29-MAR-2004; 2004WO-US009666.

XX 28-MAR-2003; 2003US-0458244P.

XX (APHT-) APHTON CORP.

XX (HUNT-) HUNTINGDON LIFE SCI LTD.

XX Grimes S, Little J, McLoughlin L;

XX WPI; 2004-719280/70.

XX Determining total or free amount of gastrin hormone in a biological fluid  
 PT sample comprises incubating the sample in the presence of an N-terminal  
 PT sequence gastrin peptide for binding to a C-terminal specific antibody.  
 XX  
 PS Disclosure; SEQ ID NO 3; 24pp; English.  
 XX  
 CC The invention relates to determining the total amount of gastrin or free  
 CC gastrin hormone in a biological fluid sample. The method involves (a)  
 CC obtaining a biological fluid sample comprising a gastrin hormone from a C  
 CC patient; (b) providing an immobilized antibody that selectively binds a C  
 CC terminal epitope of the gastrin hormone; (c) incubating the sample in  
 CC the presence of an N-terminal sequence gastrin peptide under conditions  
 CC for binding of the gastrin hormone in the sample to the antibody to  
 CC produce an immobilized complex of the antibody bound to the gastrin  
 CC hormone; (d) washing the immobilized complex to remove unbound antibody  
 CC and N-terminal sequence gastrin peptide, and incubating the complex with  
 CC a detectable marker- conjugated antibody that selectively binds an N-  
 CC terminal epitope of gastrin hormone to form an immobilized detectable  
 CC marker-conjugated antibody complex; (e) washing the immobilized  
 CC detectable marker-conjugated antibody complex, and incubating with a  
 CC development reagent; and (f) measuring the developed reagent to determine  
 CC the total amount of (free) gastrin hormone in the biological fluid  
 CC sample. The C-terminal selective antibody and/or the N-terminal selective  
 CC antibody is a monoclonal antibody. The gastrin hormone is gastrin-17  
 CC (G17) or glycine extended G17 (G17-Gly) and the C-terminal selective  
 CC antibody and the N-terminal selective antibody bind G17. The method is  
 CC useful for detecting and/or quantifying free or total amount of gastric  
 CC hormone peptides including antibody-bound, in a biological fluid. The  
 CC present sequence represents the amino acid sequence of gastrin 34 (G34),  
 CC the predominant form of big gastrins in human.  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 103; DB 8; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYGWDF 17  
 |||||  
 DB 18 EGPWLEEEAYGWDF 34

RESULT 30  
 ADT49599  
 ID ADT49599 standard; peptide; 35 AA.  
 XX  
 AC ADT49599;  
 XX  
 DT 30-DEC-2004 (first entry)  
 XX  
 XX Human gastrin 34 (G34)-Gly amino acid sequence.  
 DE  
 XX G34; gastrin; hormone; human; gastrin 34; gastrin 17.  
 KW  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH  
 FT Modified-site 1  
 FT /label= pGlu  
 FT /note= "pyroglutamic acid"  
 XX  
 XX WO2004088326-A2.  
 PN  
 XX 14-OCT-2004.  
 PD  
 XX 29-MAR-2004; 2004WO-US009666.  
 PF  
 XX 28-MAR-2003; 2003US-0458244P.  
 PR  
 XX (APHT-) APHTON CORP.  
 PA (HUNT-) HUNTINGDON LIFE SCI LTD.  
 XX

PI Grimes S, Little J, McLoughlin L;  
 XX  
 DR WPI; 2004-719280/70.  
 XX  
 PT Determining total or free amount of gastrin hormone in a biological fluid  
 PT sample comprises incubating the sample in the presence of an N-terminal  
 PT sequence gastrin peptide for binding to a C-terminal specific antibody.  
 XX  
 PS Disclosure; SEQ ID NO 4; 24pp; English.  
 XX  
 CC The invention relates to determining the total amount of gastrin or free  
 CC gastrin hormone in a biological fluid sample. The method involves (a)  
 CC obtaining a biological fluid sample comprising a gastrin hormone from a C  
 CC patient; (b) providing an immobilized antibody that selectively binds a C  
 CC terminal epitope of the gastrin hormone; (c) incubating the sample in  
 CC the presence of an N-terminal sequence gastrin peptide under conditions  
 CC for binding of the gastrin hormone in the sample to the antibody to  
 CC produce an immobilized complex of the antibody bound to the gastrin  
 CC hormone; (d) washing the immobilized complex to remove unbound antibody  
 CC and N-terminal sequence gastrin peptide, and incubating the complex with  
 CC a detectable marker- conjugated antibody that selectively binds an N-  
 CC terminal epitope of gastrin hormone to form an immobilized detectable  
 CC marker-conjugated antibody complex; (e) washing the immobilized  
 CC detectable marker-conjugated antibody complex, and incubating with a  
 CC development reagent; and (f) measuring the developed reagent to determine  
 CC the total amount of (free) gastrin hormone in the biological fluid  
 CC sample. The C-terminal selective antibody and/or the N-terminal selective  
 CC antibody is a monoclonal antibody. The gastrin hormone is gastrin-17  
 CC (G17) or glycine extended G17 (G17-Gly) and the C-terminal selective  
 CC antibody and the N-terminal selective antibody bind G17. The method is  
 CC useful for detecting and/or quantifying free or total amount of gastric  
 CC hormone peptides including antibody-bound, in a biological fluid. The  
 CC present sequence represents the amino acid sequence of glycine-extended  
 CC gastrin 34 (G34-Gly).  
 XX  
 SQ Sequence 35 AA;

Query Match 100.0%; Score 103; DB 8; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYGWDF 17  
 |||||  
 DB 18 EGPWLEEEAYGWDF 34

RESULT 31  
 AAR62739  
 ID AAR62739 standard; peptide; 17 AA.  
 XX  
 AC AAR62739;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 21-SEP-1995 (first entry)  
 XX  
 DE Gastrin haptens.  
 XX  
 KW Helper T cell epitope; universal immune stimulator; invasin; haptens;  
 KW gastrin; peptic ulcers; gastrin-stimulated tumours.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9425060-A1.  
 PN  
 XX 10-NOV-1994.  
 PD  
 XX 28-APR-1994; 94WO-US004832.  
 PF  
 XX 27-APR-1993; 93US-00057166.  
 PR 14-APR-1994; 94US-00229275.  
 XX  
 XX (LADD/) LADD A B.  
 PA (WANG/) WANG C Y.  
 PA

PA (ZAMB/) ZAMB T.  
 XX Ladd AB, Wang CY, Zamb T;  
 XX WPI; 1994-357910/44.  
 XX  
 XX Immunogenic luteinising hormone releasing hormone peptide(s) - that  
 PT suppress LHRH activity in males and females.  
 XX  
 XX Claim 27, 37; Page 96; 213pp; English.  
 XX  
 XX Synthetic immunogenic peptides are provided in which a universal immune  
 CC stimulator is linked to a peptide or protein hapten containing B cell  
 CC and/or cytotoxic T lymphocyte epitopes, giving a product which causes  
 CC potent immune responses to the coupled peptide or protein. The stimulator  
 CC consists of (A) a promiscuous helper T cell epitope (Th) which elicits an  
 CC immune response to the coupled peptide in members of a heterogeneous  
 CC population expressing diverse HLA phenotypes, and (B) an adjuvant peptide  
 CC sequence from the invasins protein of Yersinia. Spacer amino acid  
 CC sequences (e.g. Gly-Gly) can be provided between the invasins and Th  
 CC domains and between the immune stimulator and hapten components. When the  
 CC hapten is LHRH, then optionally the invasins domain can be omitted from  
 CC the immune stimulator component. The present sequence is an example of a  
 CC gastrin hapten which can be bound to the immune stimulator to form a  
 CC vaccine for treating peptic ulcer disease or gastrin-stimulated tumours.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 17 AA;

Query Match 97.1%; Score 100; DB 2; Length 17;  
 Best Local Similarity 94.1%; Pred. NO. 8.5e-08; Indels 0; Gaps 0;  
 Mismatches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMP 17  
 :|||||  
 Db 1 QGPWLEEEERAYGWMP 17

RESULT 32  
 AAY72387  
 ID AAY72387 standard; peptide; 17 AA.  
 XX  
 XX AAY72387;  
 XX  
 XX 24-APR-2001 (first entry)  
 DT  
 XX Human amidated gastrin peptide #2.  
 DE  
 XX Human; cytostatic; antisense construct; amidated gastrin; therapy;  
 KW colon cancer; tumour.  
 XX  
 XX Homo sapiens.  
 OS  
 XX US6165990-A.  
 PN  
 XX 26-DEC-2000.  
 PD  
 XX 15-MAY-1998; 98US-00079372.  
 PF  
 XX 18-APR-1996; 96US-00634546.  
 PR  
 XX (TEXA) UNIV TEXAS SYSTEM.  
 PA  
 XX Singh P, Wood TG;  
 PI  
 XX WPI; 2001-136591/14.  
 XX  
 XX Isolated antisense polynucleotide genetic construct for treatment of  
 PT colon cancer.  
 PT  
 XX Example 8; Col 43-44; 35pp; English.  
 PS  
 XX The present invention relates to methods for the treatment of colon  
 CC

CC cancer. The method involves inhibiting gastrin expression in colon cancer  
 CC cells using antisense construct. The present sequence is a human amidated  
 CC gastrin peptide. Gastrin is a peptide hormone that plays a role in the  
 CC initiation of colon tumours  
 XX  
 XX Sequence 17 AA;

Query Match 97.1%; Score 100; DB 4; Length 17;  
 Best Local Similarity 94.1%; Pred. NO. 8.5e-08; Indels 0; Gaps 0;  
 Mismatches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMP 17  
 :|||||  
 Db 1 QGPWLEEEERAYGWMP 17

RESULT 33  
 ADU48550  
 ID ADU48550 standard; protein; 17 AA.  
 XX

AC ADU48550;

XX 27-JAN-2005 (first entry)

XX Gastrin-17 amino acid sequence.

XX KGF; FGF; keratinocyte growth factor; gastrin-17; antilipemic;  
 KW antidiabetic; vasotropic; cerebroprotective; cardiant; antiarrhythmic;  
 KW antibacterial; immunosuppressive; antiinflammatory; gastrointestinal;  
 KW antitumor; hypotensive; neurotropic; neuroprotective; anorectic;  
 KW dermatological; endocrine; respiratory; hepatotropic; gene therapy;  
 KW cell therapy; fibroblast growth factor.  
 XX

XX Unidentified.

XX Key Location/Qualifiers  
 PT Modified-site 1 /note= "pyroglutamic acid"  
 FT

XX WO2004096853-A1.

XX 11-NOV-2004.

XX 30-APR-2004; 2004WO-CA000648.

XX 30-APR-2003; 2003US-0509068P.

XX (WARA-) WARATAH PHARM INC.

XX Brand SJ, Cruz A;

XX WPI; 2004-804727/79.

XX New pharmaceutical composition comprising a keratinocyte growth factor  
 PT (KGF) agonist and a gastrin compound, useful in treating or preventing  
 PT diabetes, hypertension, heart failure and obesity.  
 PT

XX Disclosure; SEQ ID NO 8; 58pp; English.

XX The invention relates to a pharmaceutical composition comprising a  
 CC keratinocyte growth factor (KGF) agonist and a gastrin compound that  
 CC provides beneficial effects relative to each compound alone, and  
 CC optionally a carrier, excipient, or vehicle. The composition provides  
 CC sustained beneficial effects, and is in a form that provides normal blood  
 CC glucose levels in a subject that persist for a prolonged period of time  
 CC after administration. The composition further comprises amounts of a KGF  
 CC agonist and a gastrin compound in a form for chronic or acute therapy of  
 CC a subject in need, where the amounts are suboptimal relative to the  
 CC amount of each compound administered alone for treatment of diabetes. The  
 CC beneficial effects are reduced or absent islet inflammation, decreased  
 CC disease progression, increased survival, or decreased symptoms of a  
 CC disease or condition, and/or are sustained beneficial effects that  
 CC persist for a prolonged period of time after termination of treatment.  
 CC

CC The composition is useful for the preparation of a medicament for the  
 CC treatment of a condition or disease, such as dyslipidaemia,  
 CC hyperglycaemia, severe hypoglycaemic episodes, stroke, left ventricular  
 CC hypertrophy, arrhythmia, bacteraemia, septicæmia, irritable bowel  
 CC syndrome, functional dyspepsia, diabetes, catabolic changes after  
 CC surgery, stress induced hyperglycaemia, gastric ulcers, myocardial  
 CC infarction, impaired glucose tolerance, hypertension, Alzheimer's disease  
 CC and other central and peripheral neurodegenerative conditions, chronic  
 CC heart failure, fluid retentive states, metabolic syndrome and related  
 CC diseases, and disorders and obesity. The composition is also used to  
 CC promote and/or enhance soft tissue growth and regeneration, such as in  
 CC epidermolysis bullosa, chemotherapy induced alopecia, male-pattern  
 CC baldness, hyaline membrane disease and hepatic cirrhosis. The present  
 CC sequence represents a little gastrin (gastrin-17) peptide sequence.

SQ Sequence 17 AA;

Query Match 97.1%; Score 100; DB 8; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.5e-08;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWDF 17

Db 1 EGPWLEEEERAYGWDF 17

RESULT 34

ADU24445

ID ADU24445 standard; peptide; 17 AA.

XX AC ADU24445;

XX 27-JAN-2005 (first entry)

XX DE Novel glutamyl cyclase (QC) inhibitor-related human peptide #13.

XX Alzheimer's disease; Down's syndrome; Huntington's disease;  
 KW glutamyl cyclase inhibitor; QC inhibitor; neuroprotective;  
 KW antiparkinsonian; neuroleptic; antipyretic; antidepressant; hypotensive;  
 KW eating-disorders-Gen; anticonvulsant; antialcoholic; antiaddictive;  
 KW hypnotic; CNS-Gen; endocrine-Gen; tranquiliser; antiulcer; cytostatic;  
 KW antiinflammatory; antipsoriatic; antirheumatic; antiarthritic;  
 KW antiarteriosclerotic; pyroglutamic acid; neuronal disease;  
 KW Parkinson's disease; Huntington's chorea; pathogenic psychotic condition;  
 KW schizophrenia; impaired food intake; sleep-wakefulness;  
 KW homeostatic regulation; energy metabolism; autonomic function;  
 KW hormonal balance; body fluid regulation; hypertension; fever;  
 KW sleep dysregulation; anorexia; anxiety related disorder; depression;  
 KW seizure; epilepsy; drug withdrawal; alcoholism;  
 KW neurodegenerative disorder; cognitive dysfunction; dementia; ulcer;  
 KW gastric cancer; neoplasia; inflammatory host response; cancer; melanoma;  
 KW malignant metastasis; psoriasis; rheumatoid arthritis; atherosclerosis;  
 KW leukocyte adhesion; human.

XX OS Homo sapiens.

XX US2004224875-A1.

XX 11-NOV-2004.

XX 05-MAY-2004; 2004US-00838993.

XX 05-MAY-2003; 2003US-0468014P.

XX (SCH/) SCHILLING S.

XX (NIES/) NIESTROJ A J.

XX (HEIS/) HEISER U.

XX (BUCH/) BUCHHOLZ M.

XX (DEMU/) DEMUTH H.

XX Schilling S, Niestroj AJ, Heiser U, Buchholz M, Demuth H;

XX WPI; 2004-813067/80.

XX Use of glutamyl cyclase inhibitor for the treatment of e.g. Alzheimer's  
 PT disease, Down syndrome, pathogenic psychotic conditions, schizophrenia  
 PT and Huntington's disease.

XX Disclosure; Page 11; 34pp; English.

XX This invention relates to a novel treatment of Alzheimer's disease,  
 PS Down's syndrome or Huntington's disease which involves administering a  
 CC glutamyl cyclase (QC) inhibitor. The invention may be useful for the  
 CC development of compounds with a nootropic, neuroprotective, hypotensive,  
 CC antiparkinsonian, neuroleptic, antipyretic, antidepressant, antialcoholic,  
 CC eating-disorders-Gen, anticonvulsant, antirheumatic, antiarthritic,  
 CC hypnotic, CNS-Gen, endocrine-Gen, tranquiliser, antiulcer, cytostatic,  
 CC antiinflammatory, antipsoriatic, antirheumatic, antiarthritic or  
 CC antiarteriosclerotic activity acting as glutamyl cyclase inhibitors.  
 CC Glutamyl cyclase catalyzes both the intramolecular cyclisation of N-  
 CC terminal glutamate residues into pyroglutamic acid with liberation of  
 CC ammonia and the intramolecular cyclisation of N-terminal glutamate  
 CC residues into pyroglutamic acid with liberation of water, the glutamyl  
 CC cyclase inhibitors are useful in the treatment of various neuronal  
 CC diseases. The composition containing a QC inhibitor is useful for the  
 CC treatment of neuronal disorders such as Alzheimer's disease, Down  
 CC syndrome, Parkinson's disease, Chorea Huntington, pathogenic psychotic  
 CC conditions, schizophrenia, impaired food intake, sleep-wakefulness,  
 CC impaired homeostatic regulation of energy metabolism, impaired autonomic  
 CC function, impaired hormonal balance, impaired regulation of body fluids,  
 CC hypertension, fever, sleep dysregulation, anorexia, anxiety related  
 CC disorders (including depression, seizures including epilepsy, drug  
 CC withdrawal and alcoholism), and neurodegenerative disorders (such as  
 CC cognitive dysfunction and dementia). The compositions may also be useful  
 CC for the treatment of ulcer, gastric cancer, neoplasia, inflammatory host  
 CC responses, cancer, melanoma, malignant metastasis, psoriasis, rheumatoid  
 CC arthritis, atherosclerosis and leukocyte adhesion and migration processes  
 CC in the endothelium. The present sequence is that of a peptide which is  
 CC related to the treatment method of the invention.

SQ Sequence 17 AA;

Query Match 97.1%; Score 100; DB 8; Length 17;

Best Local Similarity 94.1%; Pred. No. 8.5e-08;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWDF 17

Db 1 QGPWLEEEERAYGWDF 17

RESULT 35

ADU46719

ID ADU46719 standard; peptide; 17 AA.

XX AC ADU46719;

XX 10-FEB-2005 (first entry)

XX Gastrin 17, substrate of glutamyl cyclase.

XX Gastrin 17; glutamyl cyclase; nootropic; neuroprotective;  
 KW anticonvulsant; antiulcer; cytostatic; neuroleptic; antiinfertility;  
 KW antipsoriatic; antirheumatic; antiarthritic; antiarteriosclerotic; human.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 17

XX /note= "C-terminal amide"

XX WO2004098625-A2.

XX 18-NOV-2004.

XX 05-MAY-2004; 2004WO-EP004778.

XX 05-MAY-2003; 2003US-0468014P.  
 PR 05-MAY-2003; 2003US-0468043P.  
 PR 15-OCT-2003; 2003US-0512038P.  
 XX  
 PA (PROB-) PROBIODRUG AG.  
 XX  
 XX Demuth H, Hoffmann T, Niestroj AJ, Schilling S, Heiser U;  
 PI WPI; 2004-805062/79.  
 XX SWISSPROT; P01350.  
 DR  
 DR Use of effectors of glutamyl cyclase (QC) for treating diseases and/or  
 PT for modulating physiological processes based on the action of pGlu-  
 PT containing peptides.  
 PT  
 XX Disclosure; Page 31; 106pp; English.  
 PS  
 CC The present sequence is that of gastrin 17, a peptide that stimulates the  
 CC stomach mucosa to produce and secrete HCl and the pancreas to secrete  
 CC digestive enzymes. Gastrin 17 also stimulates smooth muscle contraction  
 CC and increases blood circulation and water secretion in the stomach and  
 CC intestine. The present invention shows that human glutamyl cyclase (QC,  
 CC EC-2.3.2.5) is capable of catalyzing the cyclisation of Gln and Glu to  
 CC pyroglutamate (pGlu), making the enzyme a target for drug development.  
 CC Gastrin 17 has Gln as its N-terminal residue, making it a substrate for  
 CC QC. The invention relates to the identification, screening and use of  
 CC effectors of QC for the preparation of a medicament for: (a) the  
 CC treatment of diseases that can be treated by modulation of QC activity in  
 CC vivo; and/or (b) the modulation of physiological processes based on the  
 CC action of pGlu-containing peptides caused by modulation of QC activity.  
 CC The QC effectors are used to alter the conversion of N-terminal Glu or  
 CC Gln residues to pGlu residues in a QC substrate such as gastrin 17. They  
 CC can be used to treat Alzheimer's disease, Down Syndrome, Huntington's  
 CC disease, Kennedy's disease, ulcer disease and gastric cancer with or  
 CC without Helicobacter pylori infections, pathogenic psychotic conditions,  
 CC schizophrenia, infertility, neoplasia, inflammatory host responses,  
 CC cancer, malign metastasis, melanoma, peoriasis, rheumatoid arthritis,  
 CC atherosclerosis, impaired humoral and cell-mediated immune responses,  
 CC leukocyte adhesion and migration processes in the endothelium, impaired  
 CC food intake, sleep-wakefulness, impaired homeostatic regulation of energy  
 CC metabolism, impaired autonomic function, impaired hormonal balance and  
 CC impaired regulation of body fluids. The effectors of QC are also useful  
 CC for: regulating and/or controlling male fertility; stimulating  
 CC gastrointestinal tract cell proliferation, preferably proliferation of  
 CC gastric mucosal cells, epithelial cells, acute acid secretion and for  
 CC differentiating acid-producing parietal cells and histamine-secreting  
 CC enterochromaffin-like cells (all claimed).  
 XX  
 XX Sequence 17 AA;  
 SQ  
 Query Match 97.1%; Score 100; DB 8; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.5e-08;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEERAYGWMDF 17  
 :|||||||  
 Db 1 QGPWLEEEERAYGWMDF 17  
 RESULT 36  
 ADV16302  
 ID ADV16302 standard; peptide; 17 AA.  
 XX  
 AC ADV16302;  
 XX  
 XX 10-FEB-2005 (first entry)  
 DT Human gastrin-17 mutant peptide - M14L.  
 DE  
 XX gastrin-34; diabetes mellitus; insulin dependent diabetes;  
 KW Gastrin receptor modulator; CCK receptor modulator; mutein.  
 XX

OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "Pyroglutamic acid, optionally absent"  
 FT Misc-difference 14 /note= "Wild-type Met substituted by Leu"  
 FT Modified-site 17 /note= "C-terminal amide"  
 FT  
 XX US2004229810-A1.  
 XX 18-NOV-2004.  
 PD  
 PD 03-DEC-2003; 2003US-00728082.  
 PF  
 XX 22-OCT-2002; 2002US-0420187P.  
 PR 21-OCT-2002; 2002US-0420399P.  
 PR 21-NOV-2002; 2002US-0428100P.  
 PR 22-NOV-2002; 2002US-0428562P.  
 PR 03-DEC-2002; 2002US-0430590P.  
 PR 22-OCT-2003; 2003US-00691123.  
 XX  
 XX (CRUZ/) CRUZ A.  
 XX  
 XX Cruz A;  
 PI WPI; 2005-037040/04.  
 DR  
 XX Pharmaceutical composition for treating subject with diabetes, has  
 PT gastrin compound having extended activity upon administration to subject  
 PT in comparison with native gastrin.  
 PT  
 XX Claim 2; SEQ ID NO 4; 24pp; English.  
 PS  
 XX The invention relates to a novel pharmaceutical composition comprising a  
 CC gastrin compound having an extended activity, upon administration to a  
 CC subject, in comparison with native gastrin. The compounds of the  
 CC invention may be useful for treating a subject having diabetes. This  
 CC involves measuring a physiological indicator of islet neogenesis and  
 CC fasting blood glucose (FBG). The method further involves decreasing  
 CC insulin dependency. Furthermore, the compounds may be useful for  
 CC maintaining an increase in gastrin serum level for an extended period of  
 CC time. The current sequence is that of the human gastrin-17 mutant peptide  
 CC of the invention which may act as a stimulator of the gastrin or CCK  
 CC receptor.  
 XX  
 XX Sequence 17 AA;  
 SQ  
 Query Match 97.1%; Score 100; DB 9; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.5e-08;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEERAYGWMDF 17  
 :|||||||  
 Db 1 EGPWLEEEERAYGWLDF 17  
 RESULT 37  
 ADW00243  
 ID ADW00243 standard; peptide; 17 AA.  
 XX  
 AC ADW00243;  
 XX  
 XX 24-MAR-2005 (first entry)  
 DT Human variant gastrin-17 (M14L) peptide.  
 XX  
 XX antidiabetic; gastrin receptor; cholecystokinin receptor;  
 KW gastrin receptor modulator; CCK receptor modulator; gastrin; diabetes;  
 KW fasting blood glucose; insulin.  
 XX

OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Modified-site 1  
 FT /note= "pyroglutamic acid"  
 FT Modified-site 17  
 FT /note= "amidated C-terminus"  
 XX  
 XX US2004266682-A1.  
 PN  
 XX 30-DEC-2004.  
 PD  
 XX  
 XX 21-NOV-2003; 2003US-00719450.  
 XX  
 XX 22-OCT-2002; 2002US-0420187P.  
 PR 22-OCT-2002; 2002US-0420399P.  
 PR 21-NOV-2002; 2002US-0428100P.  
 PR 22-NOV-2002; 2002US-0428562P.  
 PR 03-DEC-2002; 2002US-0430590P.  
 PR 22-OCT-2003; 2003US-00691123.  
 PR 14-NOV-2003; 2003US-0519933P.  
 XX  
 XX (CRUZ/) CRUZ A.  
 PA  
 XX  
 XX Cruz A;  
 PI  
 XX WPI; 2005-074216/08.  
 XX  
 XX Pharmaceutical composition useful for treating diabetes, comprises a  
 PT gastrin compound having an extended activity upon administration to a  
 PT subject in comparison with native gastrin.  
 PT  
 XX Disclosure; Page 5; 25pp; English.  
 PS  
 XX The invention relates to a pharmaceutical composition (I) comprising a  
 CC gastrin compound (C1) having an extended activity upon administration to  
 CC a subject in comparison with native gastrin. (I) or C1 is useful for  
 CC treating a subject having diabetes, which involves administering C1 or a  
 CC modified gastrin capable of covalently reacting with a serum protein,  
 CC where the frequency of administering the gastrin compound is less than  
 CC frequency of administration of a native gastrin. The method further  
 CC involves measuring a physiological indicator of islet neogenesis,  
 CC measuring fasting blood glucose (FBG), and decreasing insulin dependency.  
 CC The modified gastrin comprises a sequence of native gastrin capable of  
 CC binding to the gastrin/CKK receptor and an amino terminal cysteine or  
 CC lysine. (I) or C1 is useful for maintaining for an extended period of  
 CC time an increased gastrin serum level compared with the serum level of a  
 CC peptide having an amino acid sequence of a native gastrin, which involves  
 CC administering C1. (I) Contains gastrin compositions having longer active  
 CC function than native gastrin peptides, and has a longer half-life in  
 CC circulation in a subject. This sequence corresponds to the variant  
 CC gastrin-17(M14L) peptide used in the invention. (Note: this sequence  
 CC differs from sequence denoted as SEQ ID NO: 4 as given in the Sequence  
 CC Listing of the specification).  
 XX  
 XX Sequence 17 AA;  
 SQ  
 Query Match 97.1%; Score 100; DB 9; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.5e-08;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGFWLEEEEAEGWMDLF 17  
 Db 1 EGFWLEEEEAEGWLDLF 17  
 RESULT 38  
 ID ADZ71375  
 XX ADZ71375 standard; peptide; 17 AA.  
 AC  
 XX ADZ71375;  
 XX  
 XX 14-JUL-2005 (first entry)  
 DT

XX N-terminal glutamine peptide Gastrin 17.  
 DE  
 XX zollinger-ellison syndrome; gastrointestinal disease; neoplasm;  
 KW colorectal tumor; gastrointestinal tumor; Helicobacter pylori infection;  
 KW antibacterial; infection; Gastrin 17.  
 XX  
 OS Unidentified.  
 PN WO2005039548-A2.  
 XX  
 XX 06-MAY-2005.  
 PD  
 XX 15-OCT-2004; 2004WO-EP011630.  
 PF  
 XX 15-OCT-2003; 2003US-0512038P.  
 PR  
 XX (PROB-) PROBIODRUG AG.  
 PA  
 XX Schilling S, Hoffmann T, Niestroj AJ, Demuth H, Heiser U;  
 PI WPI; 2005-346574/35.  
 XX  
 XX Use of glutaminy cyclase effectors in the manufacture of a medicament  
 PT for modulating conversion of glutamic acid/glutamine residue to  
 PT pyroglutamic acid residue at the N-terminus of glutaminy cyclase  
 PT substrate in the treatment e.g. cancer.  
 PT  
 XX Disclosure; Page 32; 105pp; English.  
 PS  
 XX The invention relates to the use of a glutaminy cyclase effector (E1)  
 CC for modulating conversion of glutamic acid/glutamine residue to  
 CC pyroglutamic acid residue at the N-terminus of a glutaminy cyclase (QC)  
 CC substrate. The glutaminy cyclase effector is useful for treating a  
 CC condition mediated by modulation of QC enzyme activity e.g. Familial  
 CC British Dementia (FBD) and Familial Danish Dementia (FDD); ulcer disease  
 CC and duodenal cancer with or without Helicobacter pylori infections,  
 CC colorectal cancer, Zollinger-Ellison syndrome, gastric cancer, Alzheimer's  
 CC disease, Down's syndrome, pathogenic psychotic conditions, schizophrenia,  
 CC infertility, neoplasia, inflammatory host responses, cancer, malign  
 CC metastasis, psoriasis, rheumatoid arthritis, atherosclerosis, impaired  
 CC humoral and cell-mediated immunity responses, leukocyte adhesion and  
 CC migration processes in the endothelium, impaired food intake, sleep  
 CC wakefulness, impaired homeostatic regulation of energy metabolism,  
 CC impaired autonomic function, impaired hormonal balance and impaired  
 CC regulation of body fluids, for the preparation of contraceptive  
 CC medicaments for males. The amino acid sequence of an N-terminal glutamine  
 CC peptide Gastrin 17.  
 XX  
 XX Sequence 17 AA;  
 SQ  
 Query Match 97.1%; Score 100; DB 9; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.5e-08;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGFWLEEEEAEGWMDLF 17  
 Db 1 EGFWLEEEEAEGWMDLF 17  
 RESULT 39  
 ID AEB92577  
 XX AEB92577 standard; peptide; 17 AA.  
 XX  
 XX AEB92577;  
 XX  
 XX 20-OCT-2005 (first entry)  
 DT  
 XX Glutaminy cyclase inhibitor peptide #13.  
 DE  
 XX  
 XX Pharmaceutical; enzyme inhibition; neurological disease;  
 KW Alzheimer's disease; Down syndrome; Parkinson's disease;  
 KW Huntingtons chorea; psychotic disorder; schizophrenia; sleep disorder;  
 KW

KW metabolic disorder; hypertension; fever; anorexia nervosa;  
 KW anxiety disorder; depression; epilepsy; drug dependence; alcoholism;  
 KW neurodegenerative disease; cognitive disorder; dementia; neuroprotective;  
 KW nootropic; antiparkinsonian; anticonvulsant; neuroleptic; hypnotic;  
 KW endocrine-gen.; hypotensive; antipyretic; anabolic;  
 KW eating-disorders-gen.; tranquilizer; antidepressant; antiaddictive;  
 KW antialcoholic; antifertility; glutamyl cyclase inhibitor;  
 KW glutamyl-peptide cyclotransferase.

XX Synthetic.

XX WO2005075436-A2.

XX 18-AUG-2005.

XX 04-FEB-2005; 2005WO-BP001153.

XX 05-FEB-2004; 2004US-0542133P.

XX 05-MAY-2004; 2004US-00838993.

XX 08-DEC-2004; 2004US-0634364P.

XX (PROB-) PROBIODRUG AG.

XX Schilling S, Buchholz M, Niestroj AJ, Demuth H, Heiser U;

XX WPI; 2005-591611/60.

XX New imidazole derivatives are glutamyl cyclase inhibitors useful to  
 PT treat neuronal disorders e.g. Alzheimer's disease, Down syndrome,  
 PT Parkinson disease, Chorea Huntington, pathogenic psychotic conditions and  
 PT schizophrenia.

XX Disclosure; Page 55; 122pp; English.

XX The invention relates to imidazole derivatives and their salts,  
 CC stereoisomers and polymorphs. The invention also relates to a composition  
 CC comprising an imidazole optionally in combination with a carrier and/or  
 CC excipient. The imidazole derivatives are useful in the manufacture of a  
 CC medicament for the treatment of neurological diseases especially  
 CC Alzheimer's disease, Down syndrome, Parkinson's disease, Huntington's  
 CC chorea, psychotic disorders, schizophrenia, impaired food intake, sleep  
 CC disorders, impaired homeostatic regulation of energy metabolism,  
 CC hypertension, fever, anorexia nervosa, anxiety disorders, depression,  
 CC epilepsy, drug dependence, alcoholism and neurodegenerative diseases  
 CC including cognitive disorders and dementia. The imidazole derivatives are  
 CC also useful for stimulating the proliferation of myeloid progenitor cells  
 CC or to suppress male fertility. This sequence represents a glutamyl  
 CC cyclase inhibitor peptide used in the scope of the invention.

XX Sequence 17 AA;

Query Match 97.1%; Score 100; DB 9; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.5e-08;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17

DB 1 QGPWLEEEERAYGWMDF 17

RESULT 40

AAW31639

ID AAW31639 standard; peptide; 18 AA.

XX AAW31639;

XX 05-MAY-1998 (first entry)

DE Human glyastrin processing intermediate of gastrin.

XX Human; gastrin; inhibition; colon cancer; colorectal cancer; treatment;

KW prophylaxis; glyastrin.

XX

OS Synthetic.

XX Homo sapiens.

XX WO9738584-A1.

XX 23-OCT-1997.

XX 16-APR-1997; 97WO-US006528.

XX 18-APR-1996; 96US-00634546.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Singh P, Wood TG;

XX WPI; 1997-526130/48.

XX Inhibition of growth of colon cancer cells - by transfection of

XX anti:sense gastrin gene sequences.

XX Example 4; Page 52; 62pp; English.

XX The present sequence represents glyastrin, a processing intermediate of  
 CC gastrin derived through post-translational modification of the gastrin  
 CC gene (see AAT97434). A method has been developed of inhibiting the growth  
 CC of gastrin-expressing colon cancer cells. The method comprises reducing  
 CC gastrin expression of the cells by transfecting the cells to induce  
 CC antisense polynucleotides inhibiting gastrin expression in the cells. A  
 CC composition has also been developed for treating colon cancer, which  
 CC comprises an expression construct comprising a promoter functional in  
 CC eukaryotic cells and a polynucleotide encoding a gastrin gene positioned  
 CC antisense to and under the control of the promoter. The composition is  
 CC used for treating colorectal cancer, especially in humans. Antibodies  
 CC against gastrin are non-specific and cross-react with cholecystokinin.  
 CC Also, antibodies are not available against all precursor forms of  
 CC gastrin, and may often be antigenic themselves. The present method  
 CC provides an alternative that can be used for the treatment and  
 CC prophylaxis of colon-cancer cell growth

XX Sequence 18 AA;

Query Match 97.1%; Score 100; DB 2; Length 18;  
 Best Local Similarity 94.1%; Pred. No. 9e-08;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17

DB 1 QGPWLEEEERAYGWMDF 17

RESULT 41

AAV72381

ID AAV72381 standard; peptide; 18 AA.

XX AAV72381;

XX 24-APR-2001 (first entry)

DE Human progastrin derived peptide #3.

XX Human; cytostatic; antisense construct; progastrin; therapy;  
 KW colon cancer; tumour.

XX Homo sapiens.

XX US6165990-A.

XX 26-DEC-2000.

XX 15-MAY-1998; 98US-00079372.

XX 18-APR-1996; 96US-00634546.

XX

PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Singh P, Wood TG;

XX XW WPI; 2001-136591/14.

XX Isolated antisense polynucleotide genetic construct for treatment of colon cancer.

XX PS Disclosure; Col 39-40; 35pp; English.

XX CC The present invention relates to methods for the treatment of colon cancer. The method involves inhibiting gastrin expression in colon cancer cells using antisense construct. The present sequence is a human gastrin derived peptide. Gastrin is a peptide hormone that plays a role in the initiation of colon tumours

XX SQ Sequence 18 AA;

Query Match 97.1%; Score 100; DB 4; Length 18;  
Best Local Similarity 94.1%; Pred. No. 9e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEYAYGWDF 17

DB :|||||||||  
1 QGPWLEEEYAYGWDF 17

RESULT 42

AAW72385  
ID AAY72385 standard; peptide; 18 AA.

XX AC

XX AAY72385;

XX DT 24-APR-2001 (first entry)

XX DE Human gastrin peptide.

XX KW Human; cytostatic; antisense construct; gastrin; therapy;

XX KW colon cancer; tumour.

XX OS Homo sapiens.

XX XW US6165990-A.

XX PD 26-DEC-2000.

XX PF 15-MAY-1998; 98US-00079372.

XX PR 18-APR-1996; 96US-00634546.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Singh P, Wood TG;

XX DR WPI; 2001-136591/14.

XX Isolated antisense polynucleotide genetic construct for treatment of colon cancer.

XX PS Example 8; Col 41-42; 35pp; English.

XX CC The present invention relates to methods for the treatment of colon cancer. The method involves inhibiting gastrin expression in colon cancer cells using antisense construct. The present sequence is a human gastrin peptide. Gastrin is a peptide hormone that plays a role in the initiation of colon tumours

XX SQ Sequence 18 AA;

Query Match 97.1%; Score 100; DB 4; Length 18;  
Best Local Similarity 94.1%; Pred. No. 9e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEYAYGWDF 17  
DB :|||||||||  
1 QGPWLEEEYAYGWDF 17

RESULT 43

AAW31641  
ID AAW31641 standard; peptide; 21 AA.

XX AC

XX AAW31641;

XX DT 05-MAY-1998 (first entry)

XX DE Gastrin processing intermediate of gastrin.

XX KW Human; gastrin; inhibition; colon cancer; colorectal cancer; treatment; prophylaxis.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9738584-A1.

XX PD 23-OCT-1997.

XX PF 16-APR-1997; 97WO-US006528.

XX PR 18-APR-1996; 96US-00634546.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Singh P, Wood TG;

XX DR WPI; 1997-526130/48.

XX PT Inhibition of growth of colon cancer cells - by transfection of anti-sense gastrin gene sequences.

XX PS Disclosure; Page 52; 62pp; English.

XX CC The present sequence represents gastrin, a processing intermediate of gastrin derived through post-translational modification of the gastrin gene (see AAT97434). A method has been developed of inhibiting the growth of gastrin-expressing colon cancer cells. The method comprises reducing gastrin expression of the cells by transfecting the cells to induce antisense polynucleotides inhibiting gastrin expression in the cells. A composition has also been developed for treating colon cancer, which comprises an expression construct comprising a promoter functional in eukaryotic cells and a polynucleotide encoding a gastrin gene positioned antisense to and under the control of the promoter. The composition is used for treating colorectal cancer, especially in humans. Antibodies against gastrin are non-specific and cross-react with cholecystokinin. Also, antibodies are not available against all precursor forms of gastrin, and may often be antigenic themselves. The present method provides an alternative that can be used for the treatment and prophylaxis of colon-cancer cell growth

XX SQ Sequence 21 AA;

Query Match 97.1%; Score 100; DB 2; Length 21;  
Best Local Similarity 94.1%; Pred. No. 1.1e-07;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEYAYGWDF 17

DB :|||||||||  
5 QGPWLEEEYAYGWDF 21

RESULT 44

AAW72383  
ID AAY72383 standard; peptide; 21 AA.

XX

AC AAY72383;  
 XX  
 DT 24-APR-2001 (first entry)  
 XX  
 DE Human progastrin derived peptide #4.  
 XX  
 KW Human; cytostatic; antisense construct; progastrin; therapy;  
 KW colon cancer; tumour.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6165990-A.  
 XX  
 PD 26-DEC-2000.  
 XX  
 PF 15-MAY-1998; 98US-00079372.  
 XX  
 PR 18-APR-1996; 96US-00634546.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Singh P, Wood TG;  
 XX  
 XX WPI; 2001-136591/14.  
 XX  
 XX Isolated antisense polynucleotide genetic construct for treatment of  
 PT colon cancer.  
 PT  
 XX  
 PS Disclosure; Col 39-40; 35pp; English.  
 XX  
 CC The present invention relates to methods for the treatment of colon  
 CC cancer. The method involves inhibiting gastrin expression in colon cancer  
 CC cells using antisense construct. The present sequence is a human  
 CC progastrin derived peptide. Gastrin is a peptide hormone that plays a  
 CC role in the initiation of colon tumours  
 XX  
 SQ Sequence 21 AA;  
 Query Match 97.1%; Score 100; DB 4; Length 21;  
 Best Local Similarity 94.1%; Pred. No. 1.1e-07;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEERAYGWMDF 17  
 Db 5 QGPWLEEEERAYGWMDF 21  
 RESULT 45  
 ABR83022  
 ID ABR83022 standard; peptide; 33 AA.  
 XX  
 AC ABR83022;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 XX Gastrin-receptor binding ligand peptide.  
 DE  
 XX Cytotoxic; cytostatic; gene therapy; drug delivery; cancer; ligand;  
 KW gastrin.  
 KW  
 XX Synthetic.  
 OS  
 XX WO2003072754-A2.  
 XX  
 PN 04-SEP-2003.  
 XX  
 PD 27-FEB-2003; 2003WO-US0006344.  
 XX  
 PF 27-FEB-2002; 2002US-0360543P.  
 XX  
 PR 05-APR-2002; 2002US-0370189P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX

PI Tarasova NI, Michejda CJ, Dyba M, Cohran C;  
 XX  
 DR WPI; 2003-721769/68.  
 XX  
 PT New conjugate comprising a ligand, a linker and a cytotoxic agent, useful  
 PT for delivering drugs to specific cell populations, such as cancer cells,  
 PT and for treating cancer through the release of the cytotoxic agent.  
 XX  
 PS Claim 5; Page 35; 63pp; English.  
 XX  
 XX The invention relates to a conjugate comprising a ligand, a linker and a  
 CC cytotoxic agent. Also provided is a method of delivering a cytotoxic  
 CC agent in a cell-specific manner, that involves administering the  
 CC conjugate to a collection of cells comprising a receptor to which the  
 CC ligand of the conjugate binds; where the cytotoxic agent is administered  
 CC to the cells in a cell-specific manner. A composition comprising the  
 CC conjugate and a carrier and the methods are useful in delivering drugs to  
 CC specific cell populations, such as cancer cells, and in treating cancer  
 CC through the release of the cytotoxic agent. The present sequence  
 CC represents a specific example of a ligand peptide that the conjugate  
 CC comprises of  
 XX  
 XX Sequence 33 AA;  
 SQ  
 Query Match 97.1%; Score 100; DB 7; Length 33;  
 Best Local Similarity 94.1%; Pred. No. 1.8e-07;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGPWLEEEERAYGWMDF 17  
 Db 17 QGPWLEEEERAYGWMDF 33  
 RESULT 46  
 ADL92093  
 ID ADL92093 standard; peptide; 33 AA.  
 XX  
 AC ADL92093;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 XX Big gastrin-I S8, C11-sequence.  
 DE  
 XX harvesting; recombinant; host cell; N-terminal leader peptide;  
 KW pre-peptide; lantibiotic; post-translational modification;  
 KW pharmaceuticals; vaccine; immunogenic.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 8 /note= "This residue forms a thioether bond with residue  
 FT 11 to form a lanthionine ring"  
 FT Modified-site 11 /note= "This residue forms a thioether bond with residue  
 FT 8 to form a lanthionine ring"  
 FT  
 XX WO2003099862-A1.  
 PN  
 XX 04-DEC-2003.  
 PD  
 XX 26-MAY-2003; 2003WO-NL000389.  
 PF  
 PR 24-MAY-2002; 2002EP-00077060.  
 PR 07-FEB-2003; 2003US-00360101.  
 XX  
 XX (NANO-) APPLIED NANOSYSTEMS BV.  
 PA  
 XX Moll GN, Leenhouts CJ, Kuipers OF, Driessen AJM;  
 PI  
 XX WPI; 2004-042770/04.  
 DR  
 XX Harvesting a desired polypeptide produced by a recombinant host cell, for  
 PT

PT producing pharmaceuticals, comprises selecting a recombinant nucleic acid  
 PT comprising nucleic acid fragments encoding a leader peptide and the  
 PT polypeptide.

XX Claim 4; Page 54; 109pp; English.

XX The invention relates to a novel method for harvesting a (poly)peptide  
 CC produced by a recombinant host cell. The novel method involves selecting  
 CC a cell comprising a first nucleic acid encoding a leader peptide and a  
 CC second nucleic acid fragment encoding the desired (poly)peptide. The  
 CC first and second fragments are within the same open reading frame of the  
 CC first nucleic acid and the leader peptide is functionally equivalent to  
 CC an N-terminal leader peptide found with the pre-peptide of a lantibiotic.  
 CC The host cells and nucleic acids are useful for producing, harvesting and  
 CC post-translational modification of polypeptides. The polypeptides may be  
 CC used in the production of pharmaceuticals, e.g. as antigen for vaccine or  
 CC immunogenic composition. This sequence represents a polypeptide relating  
 CC to the novel method of the invention.

XX Sequence 33 AA;

Query Match 97.1%; Score 100; DB 8; Length 33;  
 Best Local Similarity 94.1%; Pred. No. 1.8e-07; Mismatches 0; Indels 0; Gaps 0;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMPF 17  
 :|||||  
 Db 17 QGPWLEEEEEEAYGWMPF 33

RESULT 47

ADW00233  
 ID ADW00233 standard; peptide; 33 AA.

XX ADW00233;

XX 24-MAR-2005 (first entry)

XX Human wild type gastrin-34 peptide.

XX antidiabetic; gastrin receptor; cholecystokinin receptor;  
 KW gastrin receptor modulator; CCK receptor modulator; Gastrin; diabetes;  
 KW fasting blood glucose; insulin.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FT Modified-site 33 /note= "amidated C-terminus"

XX US2004266682-A1.

XX 30-DEC-2004.

XX 21-NOV-2003; 2003US-00719450.

XX 22-OCT-2002; 2002US-0420187P.

XX 22-OCT-2002; 2002US-0420399P.

XX 21-NOV-2002; 2002US-0428100P.

XX 22-NOV-2002; 2002US-0428562P.

XX 03-DEC-2002; 2002US-0430590P.

XX 22-OCT-2003; 2003US-00691123.

XX 14-NOV-2003; 2003US-051933P.

XX (CRUZ/) CRUZ A.

XX Cruz A;

XX WPI; 2005-074216/08.

XX Pharmaceutical composition useful for treating diabetes, comprises a

PT Gastrin compound having an extended activity upon administration to a

PT subject in comparison with native gastrin.

XX Disclosure; SEQ ID NO 1; 25pp; English.

XX The invention relates to a pharmaceutical composition (I) comprising a  
 CC gastrin compound (Ci) having an extended activity upon administration to  
 CC a subject in comparison with native gastrin. (I) or Ci is useful for  
 CC treating a subject having diabetes, which involves administering Ci or a  
 CC modified gastrin capable of covalently reacting with a serum protein,  
 CC where the frequency of administering the gastrin compound is less than  
 CC frequency of administration of a native gastrin. The method further  
 CC involves measuring a physiological indicator of islet neogenesis,  
 CC measuring fasting blood glucose (FBG), and decreasing insulin dependency.  
 CC The modified gastrin comprises a sequence of native gastrin capable of  
 CC binding to the gastrin/CCK receptor and an amino terminal cysteine or  
 CC lysine. (I) or Ci is useful for maintaining for an extended period of  
 CC time an increased gastrin serum level compared with the serum level of a  
 CC peptide having an amino acid sequence of a native gastrin, which involves  
 CC administering Ci. (I) Contains gastrin compositions having longer active  
 CC function than native gastrin peptides, and has a longer half-life in  
 CC circulation in a subject. This sequence corresponds to amino acids 2-34  
 CC of the wild type gastrin-34 peptide used in the invention. (Note: this  
 CC sequence differs from sequence denoted as SEQ ID NO: 1 given on page 4 of  
 CC the disclosure of the specification).

XX Sequence 33 AA;

Query Match 97.1%; Score 100; DB 9; Length 33;  
 Best Local Similarity 94.1%; Pred. No. 1.8e-07;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMPF 17  
 :|||||  
 Db 17 QGPWLEEEEEEAYGWMPF 33

RESULT 48

AAR62734

ID AAR62734 standard; peptide; 34 AA.

XX AAR62734;

XX 25-MAR-2003 (revised)

DT 21-SEP-1995 (first entry)

XX Gastrin haptens.

XX Helper T cell epitope; universal immune stimulator; invasin; haptens;  
 KW gastrin; peptic ulcers; gastrin-stimulated tumours.

XX Homo sapiens.

XX WO9425060-A1.

XX 10-NOV-1994.

XX 28-APR-1994; 94WO-US004832.

XX 27-APR-1993; 93US-00057166.

XX 14-APR-1994; 94US-00229275.

XX (LADD/) LADD A E.

XX (WANG/) WANG C Y.

XX (ZAMB/) ZAMB T.

XX Ladd AE, Wang CY, Zamb T;

XX WPI; 1994-357910/44.

XX Immunogenic luteinising hormone releasing hormone peptide(s) - that  
 PT suppress LHRH activity in males and females.

XX Claim 27, 37; Page 96; 213pp; English.

CC Synthetic immunogenic peptides are provided in which a universal immune  
 CC stimulator is linked to a peptide or protein hapten containing B cell  
 CC and/or cytotoxic T lymphocyte epitopes, giving a product which causes  
 CC potent immune responses to the coupled peptide or protein. The stimulator  
 CC consists of (A) a promiscuous helper T cell epitope (Th) which elicits an  
 CC immune response to the coupled peptide in members of a heterogeneous  
 CC population expressing diverse HLA phenotypes, and (B) an adjuvant peptide  
 CC sequence from the invasive protein of Yersinia. Spacer amino acid  
 CC sequences (e.g. Gly-Gly) can be provided between the invasin and Th  
 CC domains and between the immune stimulator and hapten components. When the  
 CC hapten is LHRH, then optionally the invasin domain can be omitted from  
 CC the immune stimulator component. The present sequence is an example of a  
 CC gastrin hapten which can be bound to the immune stimulator to form a  
 CC vaccine for treating peptic ulcer disease or gastrin-stimulated tumours.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX

SQ Sequence 34 AA;

Query Match 97.1%; Score 100; DB 2; Length 34;  
 Best Local Similarity 94.1%; Pred. No. 1.9e-07;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17  
 :|||||  
 Db 18 QGPWLEEEERAYGWMDF 34

RESULT 49

AAW31638  
 ID AAW31638 standard; peptide; 34 AA.

AC AAW31638;

XX 05-MAY-1998 (first entry)

XX Amidated gastrin processing intermediate of gastrin.

XX Human; gastrin; inhibition; colon cancer; colorectal cancer; treatment;  
 XX prophylaxis; progastrin.

XX Synthetic.

OS Homo sapiens.

XX WO9738584-A1.

XX 23-OCT-1997.

XX 16-APR-1997; 97WO-US006528.

XX 18-APR-1996; 96US-00634546.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Singh P, Wood TG;

XX WPI; 1997-526130/48.

XX Inhibition of growth of colon cancer cells - by transfection of  
 PT anti-sense gastrin gene sequences.

XX Disclosure; Page 51; 62pp; English.

XX The present sequence represents an amidated gastrin, a processing  
 CC intermediate of gastrin derived through post-translational modification  
 CC of the gastrin gene (see AAT97434). A method has been developed of  
 CC inhibiting the growth of gastrin-expressing colon cancer cells. The  
 CC method comprises reducing gastrin expression of the cells by transfecting  
 CC the cells to induce antisense polynucleotides inhibiting gastrin  
 CC expression in the cells. A composition has also been developed for  
 CC treating colon cancer, which comprises an expression construct comprising  
 CC a promoter functional in eukaryotic cells and a polynucleotide encoding a  
 CC gastrin gene positioned antisense to and under the control of the  
 CC promoter. The composition is used for treating colorectal cancer,

CC especially in humans. Antibodies against gastrin are non-specific and  
 CC cross-react with cholecystokinin. Also, antibodies are not available  
 CC against all precursor forms of gastrin, and may often be antigenic  
 CC themselves. The present method provides an alternative that can be used  
 CC for the treatment and prophylaxis of colon-cancer cell growth  
 XX

SQ Sequence 34 AA;

Query Match 97.1%; Score 100; DB 2; Length 34;  
 Best Local Similarity 94.1%; Pred. No. 1.9e-07;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17  
 :|||||  
 Db 18 QGPWLEEEERAYGWMDF 34

RESULT 50

AAB91247

ID AAB91247 standard; peptide; 34 AA.

XX AAB91247;

XX 22-JUN-2001 (first entry)

XX Gastrin releasing peptide (GRP) SEQ ID NO:423.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl, thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity.

XX Disclosure; Page 336; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity in  
 CC vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention

SQ Sequence 34 AA;

Query Match 97.1%; Score 100; DB 4; Length 34;  
Best Local Similarity 94.1%; Pred. No. 1.9e-07;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEYGWMDP 17  
:|||||  
Db 18 QGPWLEEEEEEYGWMDP 34

Search completed: January 3, 2006, 09:18:48  
Job time : 212.619 secs

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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:05 ; Search time 12.8333 Seconds  
(without alignments)  
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Title: US-10-759-832-10  
Perfect score: 45  
Sequence: 1 SSPPPC 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents AA.\*  
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3: /cgm2\_6/ptodata/1/iaa/H-COMB.pep.\*  
4: /cgm2\_6/ptodata/1/iaa/PTUS-COMB.pep.\*  
5: /cgm2\_6/ptodata/1/iaa/RE-COMB.pep.\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	7	1	US-08-151-219-3
2	45	100.0	7	1	US-08-188-223-10
3	45	100.0	7	2	US-08-968-466-10
4	45	100.0	7	2	US-08-478-546B-10
5	45	100.0	7	4	PCT-US94-13205-3
6	45	100.0	7	4	PCT-US94-13205-3
7	45	100.0	16	1	US-08-151-219-1
8	45	100.0	16	4	PCT-US94-13205-1
9	45	100.0	17	1	US-08-188-223-6
10	45	100.0	17	2	US-08-968-466-6
11	45	100.0	17	2	US-08-478-546B-6
12	42	93.3	160	2	US-09-270-767-51037
13	42	93.3	160	2	US-09-270-767-51037
14	41	91.1	103	2	US-09-949-002-506
15	40	88.9	399	2	US-09-252-991A-18242
16	40	88.9	759	2	US-09-252-991A-29340
17	39	86.7	734	2	US-09-252-991A-33036
18	38	84.4	9	2	US-09-823-240A-8
19	38	84.4	100	2	US-09-673-395A-493
20	38	84.4	112	2	US-09-270-767-31687
21	38	84.4	112	2	US-09-270-767-46904
22	38	84.4	179	2	US-09-252-991A-26904
23	38	84.4	241	2	US-10-104-047-2317
24	38	84.4	511	2	US-09-252-991A-26078
25	38	84.4	574	2	US-09-252-991A-30868
26	38	84.4	806	2	US-09-949-016-7248
27	38	84.4	1274	2	US-09-095-443-2

28	37	82.2	6	1	US-08-151-219-5	Sequence 5, Appli
29	37	82.2	6	1	US-08-188-223-4	Sequence 4, Appli
30	37	82.2	6	2	US-08-968-466-4	Sequence 4, Appli
31	37	82.2	6	2	US-08-478-546B-4	Sequence 4, Appli
32	37	82.2	6	4	PCT-US94-13205-5	Sequence 5, Appli
33	37	82.2	6	4	US-09-823-240A-7	Sequence 7, Appli
34	37	82.2	9	4	PCT-US92-10432-2	Sequence 2, Appli
35	37	82.2	12	2	US-08-602-999A-256	Sequence 256, App
36	37	82.2	12	2	US-09-500-124-256	Sequence 256, App
37	37	82.2	15	1	US-08-151-219-4	Sequence 4, Appli
38	37	82.2	15	2	US-08-602-999A-433	Sequence 433, App
39	37	82.2	15	2	US-09-500-124-433	Sequence 433, App
40	37	82.2	15	2	US-09-413-564C-5	Sequence 5, Appli
41	37	82.2	15	4	PCT-US94-13205-4	Sequence 4, Appli
42	37	82.2	16	1	US-08-188-223-2	Sequence 2, Appli
43	37	82.2	16	2	US-08-968-466-2	Sequence 2, Appli
44	37	82.2	16	2	US-08-478-546B-2	Sequence 2, Appli
45	37	82.2	23	2	US-09-413-564C-9	Sequence 9, Appli
46	37	82.2	23	2	US-09-413-564C-33	Sequence 33, Appl
47	37	82.2	27	2	US-09-413-564C-34	Sequence 34, Appl
48	37	82.2	27	2	US-09-413-564C-41	Sequence 41, Appl
49	37	82.2	27	2	US-09-413-564C-43	Sequence 43, Appl
50	37	82.2	42	2	US-09-413-564C-11	Sequence 11, Appl
51	37	82.2	42	2	US-08-908-371B-12	Sequence 12, Appl
52	37	82.2	48	2	US-09-413-564C-10	Sequence 10, Appl
53	37	82.2	71	2	US-09-673-395A-251	Sequence 251, App
54	37	82.2	102	2	US-10-104-047-2024	Sequence 2024, Ap
55	37	82.2	109	2	US-10-104-047-3476	Sequence 3476, Ap
56	37	82.2	141	2	US-09-134-000C-5040	Sequence 5040, Ap
57	37	82.2	153	2	US-09-270-767-35906	Sequence 35906, A
58	37	82.2	153	2	US-09-270-767-51123	Sequence 51123, A
59	37	82.2	162	2	US-09-543-681A-5685	Sequence 5685, Ap
60	37	82.2	173	2	US-09-270-767-32051	Sequence 32051, A
61	37	82.2	173	2	US-09-270-767-47268	Sequence 47268, A
62	37	82.2	183	2	US-09-800-729-101	Sequence 101, App
63	37	82.2	198	2	US-09-489-039A-13679	Sequence 13679, A
64	37	82.2	216	2	US-09-252-991A-26935	Sequence 26935, A
65	37	82.2	235	2	US-09-252-991A-23626	Sequence 23626, A
66	37	82.2	252	2	US-09-800-729-133	Sequence 83, App
67	37	82.2	297	2	US-09-267-031-8	Sequence 8, Appli
68	37	82.2	297	2	US-10-104-047-2792	Sequence 2792, Ap
69	37	82.2	307	2	US-09-051-934-58	Sequence 58, Appl
70	37	82.2	311	2	US-09-087-134-15	Sequence 15, Appl
71	37	82.2	349	1	US-08-343-027A-12	Sequence 12, Appl
72	37	82.2	372	2	US-09-252-991A-20108	Sequence 20108, A
73	37	82.2	380	2	US-09-949-016-7909	Sequence 7909, Ap
74	37	82.2	393	2	US-09-432-470-2	Sequence 2, Appli
75	37	82.2	393	2	US-09-432-470-4	Sequence 4, Appli
76	37	82.2	419	2	US-09-248-796A-20956	Sequence 20956, A
77	37	82.2	419	2	US-09-949-016-6913	Sequence 6913, Ap
78	37	82.2	422	2	US-09-252-991A-30625	Sequence 30625, A
79	37	82.2	423	1	US-08-353-550-3	Sequence 3, Appli
80	37	82.2	423	1	US-08-551-687-3	Sequence 3, Appli
81	37	82.2	436	2	US-09-175-658B-21	Sequence 21, Appl
82	37	82.2	440	2	US-09-949-016-7809	Sequence 7809, Ap
83	37	82.2	441	2	US-09-623-828C-9	Sequence 9, Appli
84	37	82.2	465	2	US-09-627-986-1	Sequence 1, Appli
85	37	82.2	467	2	US-09-148-545-134	Sequence 134, App
86	37	82.2	467	2	US-09-907-794A-195	Sequence 195, App
87	37	82.2	467	2	US-09-905-125A-195	Sequence 195, App
88	37	82.2	467	2	US-09-902-775A-195	Sequence 195, App
89	37	82.2	467	2	US-09-906-700-195	Sequence 195, App
90	37	82.2	467	2	US-09-903-603A-195	Sequence 195, App
91	37	82.2	467	2	US-09-904-920A-195	Sequence 195, App
92	37	82.2	467	2	US-09-909-064-195	Sequence 195, App
93	37	82.2	467	2	US-09-905-381A-195	Sequence 195, App
94	37	82.2	467	2	US-09-906-618-195	Sequence 195, App
95	37	82.2	467	2	US-09-906-646-195	Sequence 195, App
96	37	82.2	467	2	US-09-621-011-134	Sequence 134, App
97	37	82.2	467	2	US-09-904-462-195	Sequence 195, App
98	37	82.2	467	2	US-09-902-736A-195	Sequence 195, App
99	37	82.2	467	2	US-09-906-722A-195	Sequence 195, App
100	37	82.2	469	1	US-08-363-215-1	Sequence 1, Appli

101	37	82.2	469	2	US-08-807-342B-6	Sequence 6, Appli	174	36	80.0	313	2	US-09-270-767-52410	Sequence 52410, A
102	37	82.2	473	1	US-08-363-215-2	Sequence 2, Appli	175	36	80.0	326	2	US-09-538-092-1019	Sequence 1019, Ap
103	37	82.2	473	2	US-08-807-342B-7	Sequence 7, Appli	176	36	80.0	343	2	US-09-949-016-11007	Sequence 11007, A
104	37	82.2	473	2	US-08-664-962B-4	Sequence 4, Appli	177	36	80.0	349	2	US-09-248-796A-20879	Sequence 20879, A
105	37	82.2	474	1	US-09-311-743-4	Sequence 4, Appli	178	36	80.0	351	2	US-10-029-217A-7	Sequence 7, Appli
106	37	82.2	474	1	US-08-353-550-8	Sequence 8, Appli	179	36	80.0	381	2	US-09-257-580-2	Sequence 2, Appli
107	37	82.2	474	1	US-08-551-687-8	Sequence 8, Appli	180	36	80.0	424	2	US-09-248-796A-24117	Sequence 24117, A
108	37	82.2	477	2	US-09-252-991A-24617	Sequence 24617, A	181	36	80.0	424	2	US-09-949-016-7642	Sequence 7642, Ap
109	37	82.2	479	2	US-09-949-016-6869	Sequence 6869, Ap	182	36	80.0	434	2	US-09-252-991A-30855	Sequence 30855, A
110	37	82.2	483	2	US-09-049-672A-5	Sequence 5, Appli	183	36	80.0	453	2	US-10-104-047-3019	Sequence 3019, Ap
111	37	82.2	487	2	US-09-800-729-1A5	Sequence 145, App	184	36	80.0	458	2	US-09-949-016-7534	Sequence 7534, Ap
112	37	82.2	490	2	US-09-949-016-7057	Sequence 7057, App	185	36	80.0	553	2	US-10-104-047-2655	Sequence 2655, Ap
113	37	82.2	500	2	US-09-949-016-7973	Sequence 7973, Ap	186	36	80.0	600	2	US-09-248-796A-23971	Sequence 23971, A
114	37	82.2	544	2	US-09-087-134-14	Sequence 14, Appl	187	36	80.0	634	2	US-09-295-744A-2	Sequence 2, Appli
115	37	82.2	583	2	US-09-949-016-6304	Sequence 6304, Ap	188	36	80.0	635	1	US-08-797-366-5	Sequence 5, Appli
116	37	82.2	616	2	US-09-949-016-6889	Sequence 6889, Ap	189	36	80.0	635	1	US-08-956-268-5	Sequence 5, Appli
117	37	82.2	616	2	US-09-949-016-7740	Sequence 7740, Ap	190	36	80.0	662	2	US-09-902-540-12594	Sequence 12594, A
118	37	82.2	616	2	US-09-830-902-3	Sequence 3, Appli	191	36	80.0	753	2	US-09-949-016-6676	Sequence 6676, Ap
119	37	82.2	622	2	US-09-949-016-9104	Sequence 9104, Ap	192	36	80.0	807	2	US-09-081-345-2	Sequence 2, Appli
120	37	82.2	627	2	US-09-252-991A-31696	Sequence 31696, A	193	36	80.0	807	2	US-09-822-295-2	Sequence 2, Appli
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122	37	82.2	635	2	US-08-176-320-2	Sequence 2, Appli	195	36	80.0	862	1	US-08-915-495-2	Sequence 2, Appli
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125	37	82.2	684	2	US-09-949-016-11299	Sequence 11299, A	198	36	80.0	864	2	US-09-949-016-7758	Sequence 7758, Ap
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128	37	82.2	2787	2	US-09-358-055B-15	Sequence 15, Appl	201	36	80.0	912	1	US-08-487-203A-8	Sequence 8, Appli
129	37	82.2	2787	2	US-09-893-238-15	Sequence 15, Appl	202	36	80.0	920	2	US-09-919-039-76	Sequence 76, Appl
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133	36	80.0	17	2	US-09-444-791A-19	Sequence 19, Appl	206	36	80.0	1466	6	5472939-6	Patent No. 5472939
134	36	80.0	23	1	US-08-268-251-36	Sequence 36, Appl	207	36	80.0	1537	6	5256642-5	Patent No. 5256642
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153	36	80.0	144	2	US-09-489-039A-11953	Sequence 11953, A	226	35	77.8	991	2	US-09-877-730-12	Sequence 12, Appl
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404	33	73.3	338	2	US-09-489-039A-11610	Sequence 11610, A	477	33	73.3	555	2	US-09-831-683B-12	Sequence 12, Appl
405	33	73.3	338	2	US-09-902-540-15883	Sequence 15883, A	478	33	73.3	559	2	US-10-116-370-2	Sequence 2, Appli
406	33	73.3	342	2	US-09-949-016-7625	Sequence 7625, Ap	479	33	73.3	562	2	US-10-104-047-3214	Sequence 3214, Ap
407	33	73.3	342	2	US-09-949-016-9110	Sequence 9110, Ap	480	33	73.3	562	2	US-09-949-016-10952	Sequence 10952, A
408	33	73.3	347	2	US-09-248-796A-19389	Sequence 19389, A	481	33	73.3	574	2	US-09-383-586-36	Sequence 36, Appl
409	33	73.3	347	2	US-08-126-505A-17	Sequence 17, Appl	482	33	73.3	574	2	US-09-823-038A-36	Sequence 36, Appl
410	33	73.3	348	2	US-09-270-767-46628	Sequence 46628, A	483	33	73.3	577	1	US-08-435-149-3	Sequence 3, Appli
411	33	73.3	354	2	US-09-583-110-4854	Sequence 4854, A	484	33	73.3	577	2	US-09-248-796A-18822	Sequence 18822, A
412	33	73.3	356	2	US-10-104-047-2028	Sequence 2028, Ap	485	33	73.3	578	2	US-08-981-392-13	Sequence 13, Appl
413	33	73.3	360	2	US-09-640-211A-624	Sequence 624, App	486	33	73.3	578	2	US-09-908-322-13	Sequence 13, Appl
414	33	73.3	364	2	US-09-107-433-4701	Sequence 4701, Ap	487	33	73.3	579	2	US-09-949-016-10483	Sequence 10483, A
415	33	73.3	365	2	US-09-902-540-10440	Sequence 10440, A	488	33	73.3	583	2	US-09-538-092-1071	Sequence 1071, Ap
416	33	73.3	371	2	US-09-533-029-86	Sequence 86, Appl	489	33	73.3	611	2	US-09-475-460A-32	Sequence 32, Appl
417	33	73.3	376	2	US-09-844-311-2	Sequence 19705, A	490	33	73.3	611	2	US-09-748-061A-32	Sequence 32, Appl
418	33	73.3	377	2	US-09-252-991A-19705	Sequence 19705, A	491	33	73.3	613	2	US-09-252-991A-19955	Sequence 19955, A
419	33	73.3	378	2	US-09-248-796A-18526	Sequence 18526, A	492	33	73.3	632	2	US-09-538-092-503	Sequence 503, App
420	33	73.3	381	2	US-09-014-240-2	Sequence 2, Appli	493	33	73.3	635	2	US-09-081-975-3	Sequence 3, Appli
421	33	73.3	381	2	US-09-844-311-4	Sequence 4, Appli	494	33	73.3	636	2	US-09-732-384-10	Sequence 10, Appl
422	33	73.3	383	2	US-09-252-991A-29706	Sequence 29706, A	495	33	73.3	642	2	US-08-872-855-10	Sequence 10, Appl
423	33	73.3	384	2	US-10-029-180-50	Sequence 50, Appl	496	33	73.3	664	2	US-09-248-796A-26707	Sequence 26707, A
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425	33	73.3	389	2	US-09-788-657-23	Sequence 23, Appl	498	33	73.3	666	2	US-09-270-767-62249	Sequence 62249, A
426	33	73.3	389	2	US-09-902-540-12890	Sequence 12890, A	499	33	73.3	673	2	US-09-196-387-8	Sequence 8, Appli
427	33	73.3	389	2	US-10-641-068-23	Sequence 23, Appl	500	33	73.3	673	2	US-09-841-835-8	Sequence 8, Appli
428	33	73.3	393	1	US-09-026-587-3	Sequence 3, Appli	501	33	73.3	675	1	US-08-386-435-10	Sequence 10, Appl
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431	33	73.3	393	2	US-09-823-240A-11	Sequence 11, Appl	504	33	73.3	701	2	US-09-370-368-10	Sequence 10, Appl
432	33	73.3	398	2	US-09-252-991A-19907	Sequence 19907, A	505	33	73.3	702	2	US-09-068-740A-4	Sequence 4, Appli
433	33	73.3	399	2	US-09-949-016-8459	Sequence 8459, Ap	506	33	73.3	704	2	US-10-104-047-3501	Sequence 3501, Ap
434	33	73.3	399	2	US-09-949-016-8460	Sequence 8460, Ap	507	33	73.3	713	2	US-08-872-855-5	Sequence 5, Appli
435	33	73.3	399	2	US-09-949-016-8461	Sequence 8461, Ap	508	33	73.3	715	2	US-09-902-540-9752	Sequence 9752, Ap
436	33	73.3	399	2	US-09-949-016-8462	Sequence 8462, Ap	509	33	73.3	717	2	US-08-872-855-9	Sequence 9, Appli
437	33	73.3	399	2	US-09-893-737-10	Sequence 10, Appl	510	33	73.3	720	2	US-08-872-855-4	Sequence 4, Appli
438	33	73.3	406	2	US-10-104-047-3010	Sequence 3010, Ap	511	33	73.3	721	2	US-08-872-855-7	Sequence 7, Appli
439	33	73.3	416	2	US-09-270-767-42942	Sequence 42942, A	512	33	73.3	721	2	US-08-981-392-5	Sequence 5, Appli
440	33	73.3	420	2	US-09-277-196-20	Sequence 20, Appl	513	33	73.3	721	2	US-09-270-767-46645	Sequence 46645, A
441	33	73.3	430	2	US-10-104-047-2361	Sequence 2361, Ap	514	33	73.3	721	2	US-09-908-322-5	Sequence 5, Appli
442	33	73.3	440	2	US-09-014-240-4	Sequence 4, Appli	515	33	73.3	721	2	US-09-310-685-12	Sequence 12, Appl
443	33	73.3	446	1	US-07-952-800-4	Sequence 4, Appli	516	33	73.3	722	2	US-08-981-392-12	Sequence 12, Appl
444	33	73.3	448	2	US-08-216-592A-2	Sequence 2, Appli	517	33	73.3	722	2	US-09-908-322-12	Sequence 12, Appl
445	33	73.3	457	2	US-09-902-540-11961	Sequence 11961, A	518	33	73.3	722	2	US-09-310-685-14	Sequence 14, Appl
446	33	73.3	466	2	US-09-248-796A-20516	Sequence 20516, A	519	33	73.3	723	2	US-09-068-740A-9	Sequence 9, Appli
447	33	73.3	469	2	US-09-252-991A-25490	Sequence 25490, A	520	33	73.3	723	2	US-09-423-753-27	Sequence 27, Appl
448	33	73.3	472	2	US-09-385-219A-8	Sequence 8, Appli	521	33	73.3	723	2	US-09-641-612-6	Sequence 6, Appli
449	33	73.3	472	2	US-09-248-796A-20611	Sequence 20611, A	522	33	73.3	724	2	US-09-949-016-9953	Sequence 9953, Ap
450	33	73.3	482	2	US-09-252-991A-31492	Sequence 31492, A	523	33	73.3	728	2	US-08-981-392-2	Sequence 2, Appli
451	33	73.3	482	2	US-09-949-016-9106	Sequence 9106, Ap	524	33	73.3	728	2	US-09-908-322-2	Sequence 2, Appli
452	33	73.3	489	2	US-09-559-622-3	Sequence 3, Appli	525	33	73.3	728	2	US-09-310-685-11	Sequence 11, Appl
453	33	73.3	490	2	US-09-039-555B-14	Sequence 14, Appl	526	33	73.3	729	2	US-08-872-855-8	Sequence 8, Appli
454	33	73.3	499	2	US-09-538-106-26	Sequence 26, Appl	527	33	73.3	793	1	US-08-720-484A-2	Sequence 2, Appli
455	33	73.3	506	2	US-09-949-016-7650	Sequence 7650, Ap	528	33	73.3	793	2	US-08-953-823A-2	Sequence 2, Appli
456	33	73.3	511	2	US-09-107-433-2904	Sequence 2904, Ap	529	33	73.3	793	2	US-09-293-505-16	Sequence 16, Appl
457	33	73.3	517	2	US-09-270-767-45655	Sequence 45655, A	530	33	73.3	793	2	US-09-293-505-17	Sequence 17, Appl
458	33	73.3	520	2	US-09-068-740A-3	Sequence 3, Appli	531	33	73.3	793	2	US-09-398-239-2	Sequence 2, Appli
459	33	73.3	520	2	US-09-270-767-45441	Sequence 45441, A	532	33	73.3	793	2	US-09-560-876A-2	Sequence 2, Appli
460	33	73.3	520	2	US-09-902-540-10545	Sequence 10545, A	533	33	73.3	793	2	US-09-060-939A-16	Sequence 16, Appl
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463	33	73.3	539	2	US-09-190-476B-2	Sequence 2, Appli	536	33	73.3	803	2	US-09-293-505-15	Sequence 15, Appl
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465	33	73.3	539	2	US-09-190-938B-2	Sequence 2, Appli	538	33	73.3	807	2	US-10-029-217A-2	Sequence 2, Appli

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540	33	73.3	822	2	US-09-248-796A-20139	Sequence 20139, A	613	32	71.1	15	2	US-09-500-124-428	Sequence 428, App
541	33	73.3	840	2	US-09-949-016-7029	Sequence 7029, Ap	614	32	71.1	15	2	US-09-500-124-429	Sequence 429, App
542	33	73.3	901	2	US-09-248-796A-20495	Sequence 20495, A	615	32	71.1	15	2	US-09-500-124-453	Sequence 453, App
543	33	73.3	904	2	US-09-976-594-615	Sequence 615, App	616	32	71.1	16	1	US-08-477-509B-17	Sequence 17, Appl
544	33	73.3	915	2	US-09-252-991A-22344	Sequence 22344, A	617	32	71.1	16	1	US-08-477-509B-18	Sequence 18, Appl
545	33	73.3	928	2	US-09-320-878-13	Sequence 13, Appl	618	32	71.1	16	1	US-08-844-312-8	Sequence 8, Appl
546	33	73.3	928	2	US-09-141-908-14	Sequence 14, Appl	619	32	71.1	16	1	US-08-844-312-10	Sequence 10, Appl
547	33	73.3	928	2	US-09-657-440-13	Sequence 13, Appl	620	32	71.1	16	1	US-08-844-312-11	Sequence 11, Appl
548	33	73.3	928	2	US-09-793-708-13	Sequence 13, Appl	621	32	71.1	16	2	US-08-482-085B-17	Sequence 17, Appl
549	33	73.3	935	2	US-10-029-217A-31	Sequence 31, Appl	622	32	71.1	16	2	US-08-482-085B-18	Sequence 18, Appl
550	33	73.3	935	2	US-10-029-217A-32	Sequence 32, Appl	623	32	71.1	16	2	US-09-444-791A-17	Sequence 17, Appl
551	33	73.3	945	2	US-09-248-796A-15743	Sequence 15743, A	624	32	71.1	18	2	US-09-444-791A-18	Sequence 18, Appl
552	33	73.3	949	2	US-09-196-387-10	Sequence 10, Appl	625	32	71.1	18	2	US-08-602-999A-409	Sequence 409, App
553	33	73.3	949	2	US-09-841-835-10	Sequence 10, Appl	626	32	71.1	18	2	US-09-500-124-409	Sequence 409, App
554	33	73.3	1025	2	US-09-834-309-5	Sequence 5, Appl	627	32	71.1	18	2	US-09-119-507B-16	Sequence 16, Appl
555	33	73.3	1027	2	US-09-902-540-11750	Sequence 11750, A	628	32	71.1	18	2	US-09-119-507B-17	Sequence 17, Appl
556	33	73.3	1050	2	US-09-428-711A-16	Sequence 16, Appl	629	32	71.1	18	2	US-08-897-556A-16	Sequence 16, Appl
557	33	73.3	1055	2	US-09-412-545-2	Sequence 2, Appl	630	32	71.1	18	2	US-08-897-556A-17	Sequence 17, Appl
558	33	73.3	1065	2	US-09-949-016-6541	Sequence 6541, Ap	631	32	71.1	18	2	US-09-547-693-16	Sequence 16, Appl
559	33	73.3	1065	2	US-09-771-161A-239	Sequence 239, App	632	32	71.1	18	2	US-09-547-693-17	Sequence 17, Appl
560	33	73.3	1073	2	US-09-949-016-9771	Sequence 9771, Ap	633	32	71.1	18	2	US-09-547-693-190	Sequence 193, App
561	33	73.3	1241	2	US-09-248-796A-18397	Sequence 18397, A	634	32	71.1	18	2	US-09-547-693-193	Sequence 4, Appl
562	33	73.3	1290	2	US-09-248-796A-20654	Sequence 20654, A	635	32	71.1	19	1	US-08-660-789-4	Sequence 4, Appl
563	33	73.3	1297	2	US-09-540-245A-17	Sequence 17, Appl	636	32	71.1	19	2	US-09-074-114-4	Sequence 1, Appl
564	33	73.3	1297	2	US-10-289-776-17	Sequence 17, Appl	637	32	71.1	19	2	US-09-119-507B-1	Sequence 1, Appl
565	33	73.3	1298	1	US-08-690-473-2	Sequence 2, Appl	638	32	71.1	19	2	US-09-119-507B-28	Sequence 28, Appl
566	33	73.3	1298	2	US-09-259-821A-2	Sequence 2, Appl	639	32	71.1	19	2	US-09-119-507B-113	Sequence 113, App
567	33	73.3	1298	2	US-08-843-659-2	Sequence 2, Appl	640	32	71.1	19	2	US-09-119-507B-115	Sequence 115, App
568	33	73.3	1298	2	US-09-825-288A-2	Sequence 2, Appl	641	32	71.1	19	2	US-08-897-556A-1	Sequence 1, Appl
569	33	73.3	1327	2	US-09-196-387-2	Sequence 2, Appl	642	32	71.1	19	2	US-08-897-556A-28	Sequence 28, Appl
570	33	73.3	1327	2	US-09-841-835-2	Sequence 2, Appl	643	32	71.1	19	2	US-09-547-693-1	Sequence 1, Appl
571	33	73.3	1327	2	US-09-972-115A-8	Sequence 8, Appl	644	32	71.1	19	2	US-09-547-693-28	Sequence 28, Appl
572	33	73.3	1402	2	US-09-248-796A-14503	Sequence 14503, A	645	32	71.1	19	2	US-09-547-693-143	Sequence 143, App
573	33	73.3	1495	2	US-08-522-726B-1	Sequence 1, Appl	646	32	71.1	19	2	US-09-547-693-146	Sequence 146, App
574	33	73.3	1495	2	US-09-337-384-1	Sequence 1, Appl	647	32	71.1	19	2	US-09-547-693-149	Sequence 149, App
575	33	73.3	1540	2	US-09-949-016-11382	Sequence 11382, A	648	32	71.1	19	2	US-09-547-693-150	Sequence 150, App
576	33	73.3	1540	2	US-09-949-016-11383	Sequence 11383, A	649	32	71.1	19	2	US-09-547-693-152	Sequence 152, App
577	33	73.3	1706	1	US-08-459-568-2	Sequence 2, Appl	650	32	71.1	19	2	US-09-547-693-153	Sequence 153, App
578	33	73.3	1706	1	US-08-399-411-2	Sequence 2, Appl	651	32	71.1	19	2	US-09-547-693-217	Sequence 217, App
579	33	73.3	1706	2	US-08-516-859A-2	Sequence 2, Appl	652	32	71.1	19	2	US-09-547-693-218	Sequence 218, App
580	33	73.3	1706	2	US-09-586-472-2	Sequence 2, Appl	653	32	71.1	19	2	US-09-547-693-219	Sequence 219, App
581	33	73.3	1706	2	US-09-528-706-2	Sequence 2, Appl	654	32	71.1	19	2	US-09-547-693-220	Sequence 220, App
582	33	73.3	1706	2	US-10-024-450-2	Sequence 2, Appl	655	32	71.1	19	2	US-09-547-693-221	Sequence 221, App
583	33	73.3	1719	1	US-08-459-568-4	Sequence 4, Appl	656	32	71.1	19	2	US-09-547-693-222	Sequence 222, App
584	33	73.3	1719	1	US-08-399-411-4	Sequence 4, Appl	657	32	71.1	19	2	US-09-547-693-223	Sequence 223, App
585	33	73.3	1719	2	US-08-516-859A-4	Sequence 4, Appl	658	32	71.1	19	2	US-09-547-693-224	Sequence 224, App
586	33	73.3	1719	2	US-09-586-472-4	Sequence 4, Appl	659	32	71.1	19	2	US-09-547-693-225	Sequence 225, App
587	33	73.3	1719	2	US-09-528-706-4	Sequence 4, Appl	660	32	71.1	20	2	US-08-602-999A-132	Sequence 132, App
588	33	73.3	1719	2	US-10-024-450-4	Sequence 4, Appl	661	32	71.1	20	2	US-08-602-999A-357	Sequence 357, App
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590	33	73.3	4861	2	US-09-919-497-70	Sequence 70, Appl	663	32	71.1	20	2	US-09-500-124-132	Sequence 132, App
591	32-5	72.2	220	2	US-09-252-991A-17636	Sequence 17636, A	664	32	71.1	20	2	US-09-500-124-357	Sequence 357, App
592	32	71.1	5	1	US-08-477-509B-9	Sequence 9, Appl	665	32	71.1	20	2	US-09-885-722A-11	Sequence 11, Appl
593	32	71.1	5	2	US-08-482-085B-9	Sequence 9, Appl	666	32	71.1	21	2	US-09-270-767-60070	Sequence 60070, A
594	32	71.1	5	2	US-09-444-791A-9	Sequence 9, Appl	667	32	71.1	23	1	US-08-268-251-37	Sequence 37, Appl
595	32	71.1	5	2	US-09-119-507B-3	Sequence 3, Appl	668	32	71.1	23	1	US-08-268-251-47	Sequence 47, Appl
596	32	71.1	5	2	US-08-897-556A-3	Sequence 3, Appl	669	32	71.1	23	1	US-09-270-767-34404	Sequence 34404, A
597	32	71.1	5	2	US-08-897-556A-105	Sequence 105, App	670	32	71.1	23	1	US-09-270-767-49621	Sequence 49621, A
598	32	71.1	5	2	US-09-547-693-3	Sequence 3, Appl	671	32	71.1	23	4	PCT-US93-01112-37	Sequence 37, Appl
599	32	71.1	5	2	US-09-547-693-216	Sequence 216, App	672	32	71.1	23	4	PCT-US93-01112-40	Sequence 40, Appl
600	32	71.1	6	2	US-09-119-507B-117	Sequence 117, App	673	32	71.1	23	4	PCT-US93-01112-47	Sequence 47, Appl
601	32	71.1	10	2	US-09-119-507B-37	Sequence 37, Appl	674	32	71.1	23	4	PCT-US93-01112-47	Sequence 47, Appl
602	32	71.1	10	2	US-08-897-556A-37	Sequence 37, Appl	675	32	71.1	24	2	US-09-547-693-185	Sequence 185, App
603	32	71.1	10	2	US-09-547-693-37	Sequence 37, Appl	676	32	71.1	24	2	US-09-270-767-38705	Sequence 38705, A
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606	32	71.1	12	2	US-09-547-693-16	Sequence 16, App	679	32	71.1	24	2	US-09-270-767-54575	Sequence 54575, A
607	32	71.1	12	2	US-09-547-693-162	Sequence 162, App	680	32	71.1	25	2	US-09-270-767-37791	Sequence 37791, A
608	32	71.1	15	2	US-08-602-999A-346	Sequence 346, App	681	32	71.1	25	2	US-09-270-767-53008	Sequence 53008, A
609	32	71.1	15	2	US-08-602-999A-428	Sequence 428, App	682	32	71.1	27	2	US-09-544-664B-10	Sequence 10, Appl
610	32	71.1	15	2	US-08-602-999A-429	Sequence 429, App	683	32	71.1	29	2	US-09-270-767-38381	Sequence 38381, A
611	32	71.1	15	2	US-08-602-999A-453	Sequence 453, App	684	32	71.1	29	2	US-09-270-767-53598	Sequence 53598, A

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686	32	71.1	30	2	US-09-270-767-39792	Sequence 39792, A	759	32	71.1	107	2	US-09-270-767-33886	Sequence 33886, A
687	32	71.1	31	2	US-09-270-767-55009	Sequence 55009, A	760	32	71.1	107	2	US-09-270-767-49103	Sequence 49103, A
688	32	71.1	31	2	US-09-270-767-45298	Sequence 45298, A	761	32	71.1	107	2	US-10-178-213-269	Sequence 269, App
689	32	71.1	32	2	US-09-270-767-32021	Sequence 32021, A	762	32	71.1	109	2	US-09-252-991A-28987	Sequence 28987, A
690	32	71.1	32	2	US-09-270-767-42238	Sequence 42238, A	763	32	71.1	109	2	US-09-621-976-4213	Sequence 4213, Ap
691	32	71.1	33	2	US-09-270-767-58260	Sequence 58260, A	764	32	71.1	111	2	US-09-485-421A-3	Sequence 3, Appl
692	32	71.1	33	2	US-09-270-767-43927	Sequence 43927, A	765	32	71.1	112	1	US-08-446-919A-5	Sequence 5, Appl
693	32	71.1	34	2	US-09-270-767-57328	Sequence 57328, A	766	32	71.1	113	2	US-09-248-796A-23989	Sequence 23989, A
694	32	71.1	35	2	US-09-471-276-1402	Sequence 1402, Ap	767	32	71.1	114	2	US-09-621-976-6804	Sequence 6804, Ap
695	32	71.1	36	2	US-09-270-767-35113	Sequence 35113, A	768	32	71.1	114	2	US-09-270-767-40084	Sequence 40084, A
696	32	71.1	36	2	US-09-270-767-50330	Sequence 50330, A	769	32	71.1	114	2	US-09-270-767-55300	Sequence 55300, A
697	32	71.1	37	2	US-09-270-767-46422	Sequence 46422, A	770	32	71.1	115	2	US-09-205-258-627	Sequence 627, App
698	32	71.1	38	2	US-09-547-693-180	Sequence 180, App	771	32	71.1	115	2	US-09-270-767-41272	Sequence 41272, A
699	32	71.1	38	2	US-09-547-693-181	Sequence 181, App	772	32	71.1	115	2	US-09-270-767-56488	Sequence 56488, A
700	32	71.1	39	2	US-09-547-693-131	Sequence 131, App	773	32	71.1	115	2	US-10-004-860-627	Sequence 627, App
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702	32	71.1	47	1	US-08-660-789-6	Sequence 6, Appl	775	32	71.1	117	2	US-09-489-039A-10431	Sequence 10431, A
703	32	71.1	47	2	US-09-074-114-6	Sequence 6, Appl	776	32	71.1	117	2	US-09-107-433-2883	Sequence 2883, Ap
704	32	71.1	47	4	PCT-US93-05640-36	Sequence 36, Appl	777	32	71.1	118	2	US-09-765-815-8	Sequence 8, Appl
705	32	71.1	51	2	US-09-513-999C-4356	Sequence 4356, Ap	778	32	71.1	120	2	US-09-489-039A-7728	Sequence 7728, Ap
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707	32	71.1	56	2	US-09-270-767-46613	Sequence 46613, A	780	32	71.1	121	2	US-09-270-767-61497	Sequence 61497, A
708	32	71.1	56	2	US-10-001-887-137	Sequence 137, App	781	32	71.1	122	2	US-09-800-729-132	Sequence 132, App
709	32	71.1	57	2	US-09-935-916B-35	Sequence 35, Appl	782	32	71.1	122	2	US-09-800-729-185	Sequence 185, App
710	32	71.1	57	2	US-09-513-999C-4630	Sequence 4630, Ap	783	32	71.1	126	2	US-09-252-991A-21726	Sequence 21726, A
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712	32	71.1	58	2	US-09-270-767-55843	Sequence 55843, A	785	32	71.1	128	2	US-09-370-838-97	Sequence 97, Appl
713	32	71.1	61	2	US-09-621-976-4941	Sequence 4941, Ap	786	32	71.1	128	2	US-09-311-021-200	Sequence 200, App
714	32	71.1	66	2	US-09-513-999C-6811	Sequence 6811, Ap	787	32	71.1	128	2	US-09-854-133-97	Sequence 97, Appl
715	32	71.1	67	2	US-09-248-796A-25852	Sequence 25852, A	788	32	71.1	130	2	US-09-583-110-4170	Sequence 4170, Ap
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718	32	71.1	70	2	US-09-471-276-1482	Sequence 1482, Ap	791	32	71.1	132	2	US-09-489-039A-9920	Sequence 9920, Ap
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721	32	71.1	74	2	US-09-547-693-133	Sequence 133, App	794	32	71.1	136	2	US-09-621-976-6751	Sequence 6751, Ap
722	32	71.1	74	2	US-09-513-999C-6742	Sequence 6742, Ap	795	32	71.1	136	2	US-09-270-767-45958	Sequence 45958, A
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754	32	71.1	102	2	US-09-270-767-50886	Sequence 50886, A	827	32	71.1	166	1	US-09-252-991A-16776	Sequence 16776, A
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757	32	71.1	104	2	US-09-252-991A-32823	Sequence 32823, A	830	32	71.1	167	2	US-09-640-211A-838	Sequence 838, App

831	32	71.1	169	2	US-09-252-991A-18456	Sequence 18456, A	904	32	71.1	247	2	US-09-976-594-781	Sequence 781, App
832	32	71.1	169	2	US-09-252-991A-18456	Sequence 14212, A	905	32	71.1	247	2	US-09-919-039-309	Sequence 309, App
833	32	71.1	172	2	US-09-252-991A-23050	Sequence 23050, A	906	32	71.1	248	2	US-09-252-991A-28640	Sequence 28640, A
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844	32	71.1	189	2	US-09-270-767-39457	Sequence 39457, A	917	32	71.1	274	2	US-10-104-047-3279	Sequence 3379, Ap
845	32	71.1	189	2	US-09-270-767-54674	Sequence 54674, A	918	32	71.1	277	2	US-10-104-047-3279	Sequence 3379, Ap
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852	32	71.1	205	2	US-09-543-681A-8287	Sequence 8287, Ap	925	32	71.1	294	2	US-09-949-002-429	Sequence 429, App
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855	32	71.1	208	2	US-10-104-047-3920	Sequence 3920, Ap	928	32	71.1	302	4	PCT-US91-02714-21	Sequence 21, Appl
856	32	71.1	209	2	US-10-188-495-85	Sequence 85, Appl	929	32	71.1	303	2	US-08-818-112-92	Sequence 92, Appl
857	32	71.1	209	2	US-09-270-767-41925	Sequence 41925, A	930	32	71.1	303	2	US-08-818-111-93	Sequence 93, Appl
858	32	71.1	209	2	US-10-188-495-42	Sequence 42, Appl	931	32	71.1	303	2	US-09-056-556-92	Sequence 92, Appl
859	32	71.1	212	2	US-09-270-767-46591	Sequence 46591, A	932	32	71.1	303	2	US-09-072-596-93	Sequence 93, Appl
860	32	71.1	213	2	US-09-248-796A-16185	Sequence 16185, A	933	32	71.1	303	2	US-09-072-967-92	Sequence 92, Appl
861	32	71.1	216	2	US-09-252-991A-28120	Sequence 28120, A	934	32	71.1	303	2	US-10-193-003-93	Sequence 93, Appl
862	32	71.1	221	2	US-09-949-016-9330	Sequence 9330, Ap	935	32	71.1	307	2	US-10-084-843-92	Sequence 92, Appl
863	32	71.1	223	2	US-09-009-816-4	Sequence 4, Appl	936	32	71.1	307	2	US-09-902-540-16403	Sequence 16403, A
864	32	71.1	224	2	US-09-252-991A-16953	Sequence 16953, A	937	32	71.1	309	1	US-08-191-866D-2	Sequence 2, Appl
865	32	71.1	225	2	US-10-188-495-83	Sequence 83, Appl	938	32	71.1	309	1	US-08-185-949B-2	Sequence 2, Appl
866	32	71.1	226	2	US-10-188-495-40	Sequence 40, Appl	939	32	71.1	311	2	US-09-248-796A-14776	Sequence 14776, A
867	32	71.1	227	2	US-09-270-767-42070	Sequence 42070, A	940	32	71.1	312	2	US-09-252-991A-20753	Sequence 20753, A
868	32	71.1	231	2	US-08-480-594-37	Sequence 37, Appl	941	32	71.1	312	2	US-10-104-047-3588	Sequence 3588, Ap
869	32	71.1	235	1	US-08-616-844-37	Sequence 37, Appl	942	32	71.1	314	2	US-09-640-211A-2179	Sequence 2179, Ap
870	32	71.1	235	1	US-08-599-654-37	Sequence 37, Appl	943	32	71.1	316	2	US-09-248-796A-21697	Sequence 21697, A
871	32	71.1	235	1	US-08-485-573-37	Sequence 37, Appl	944	32	71.1	317	2	US-09-949-016-9806	Sequence 9806, Ap
872	32	71.1	235	1	US-08-944-868A-37	Sequence 37, Appl	945	32	71.1	319	2	US-09-902-540-9739	Sequence 9739, Ap
873	32	71.1	235	2	US-08-944-423A-37	Sequence 37, Appl	946	32	71.1	324	2	US-09-252-991A-16622	Sequence 16622, A
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876	32	71.1	235	2	US-08-944-495-12	Sequence 12, Appl	949	32	71.1	330	2	US-09-270-767-49148	Sequence 49148, A
877	32	71.1	235	2	US-09-126-640-12	Sequence 12, Appl	950	32	71.1	332	2	US-09-252-991A-19457	Sequence 19457, A
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879	32	71.1	235	2	US-08-925-588-12	Sequence 12, Appl	952	32	71.1	335	2	US-09-595-386-5	Sequence 5, Appl
880	32	71.1	235	2	US-08-925-767-37	Sequence 37, Appl	953	32	71.1	335	2	US-09-993-525-5	Sequence 5, Appl
881	32	71.1	235	2	US-08-840-767-49	Sequence 49, Appl	954	32	71.1	335	2	US-09-949-016-11210	Sequence 11210, A
882	32	71.1	235	2	US-09-096-776B-5	Sequence 5, Appl	955	32	71.1	345	2	US-09-248-796A-25189	Sequence 25189, A
883	32	71.1	235	2	US-08-288-292A-12	Sequence 12, Appl	956	32	71.1	345	2	US-10-104-047-3496	Sequence 3496, Ap
884	32	71.1	235	2	US-09-372-044-12	Sequence 12, Appl	957	32	71.1	350	2	US-09-248-796A-21542	Sequence 21542, A
885	32	71.1	235	2	US-09-923-522-5	Sequence 5, Appl	958	32	71.1	351	2	US-09-524-162-2	Sequence 2, Appl
886	32	71.1	235	2	US-08-825-486-12	Sequence 12, Appl	959	32	71.1	365	2	US-09-113-309-2	Sequence 2, Appl
887	32	71.1	235	2	US-08-826-248-12	Sequence 12, Appl	960	32	71.1	365	2	US-09-521-109-2	Sequence 2, Appl
888	32	71.1	236	1	US-08-112-208C-11	Sequence 11, Appl	961	32	71.1	365	2	US-09-562-332-2	Sequence 2, Appl
889	32	71.1	236	1	US-08-248-819A-11	Sequence 11, Appl	962	32	71.1	365	2	US-09-949-016-6436	Sequence 6436, Ap
890	32	71.1	236	1	US-08-607-369-22	Sequence 22, Appl	963	32	71.1	366	2	US-09-377-285B-20	Sequence 20, Appl
891	32	71.1	236	1	US-08-337-846A-11	Sequence 11, Appl	964	32	71.1	366	2	US-10-192-381-20	Sequence 20, Appl
892	32	71.1	236	1	US-08-856-531-11	Sequence 11, Appl	965	32	71.1	367	2	US-09-009-816-2	Sequence 2, Appl
893	32	71.1	236	1	US-08-856-034-11	Sequence 11, Appl	966	32	71.1	368	2	US-10-104-047-3645	Sequence 3645, Ap
894	32	71.1	236	1	US-09-137-048-9	Sequence 9, Appl	967	32	71.1	371	2	US-08-586-165-3	Sequence 3, Appl
895	32	71.1	236	2	US-08-927-326-11	Sequence 11, Appl	968	32	71.1	376	2	US-09-949-016-6504	Sequence 6504, Ap
896	32	71.1	236	2	US-09-379-820A-11	Sequence 11, Appl	969	32	71.1	378	2	US-09-560-761B-18	Sequence 18, Appl
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898	32	71.1	238	2	US-09-270-767-34310	Sequence 34310, A	971	32	71.1	381	2	US-09-949-016-6287	Sequence 6287, Ap
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988 32 71.1 418 1 US-09-227-420-1  
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998 32 71.1 426 2 US-08-925-588-4  
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## ALIGNMENTS

RESULT 1  
US-08-151-219-3  
; Sequence 3, Application US/08151219  
; Patent No. 5468494  
; GENERAL INFORMATION:  
; APPLICANT: Gevas, Philip C.  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Karr, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Scibienski, Robert  
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS: 5  
; ADDRESSEE: Dimitrios T. Drivas, White and Case  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/151,219  
; FILING DATE: 12-NOV-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Drivas, Dimitrios T.  
; REGISTRATION NUMBER: 32,218  
; REFERENCE/DOCKET NUMBER: 1102865-028  
; TELEPHONE: (212) 819-8286  
; TELEFAX: (212) 354-8113  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal  
US-08-151-219-3  
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RESULT 2  
US-08-188-223-10  
; Sequence 10, Application US/08188223  
; Patent No. 5688506  
; GENERAL INFORMATION:  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Scibienski, Robert  
; TITLE OF INVENTION: Immunogens Against Gonadotropin  
; TITLE OF INVENTION: Releasing Hormone  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dimitrios T. Drivas, Esq.  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2787  
; COMPUTER READABLE FORM:  
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; COMPUTER: IBM PC compatible  
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; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/188,223  
; FILING DATE: 27-JAN-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Drivas Esq., Dimitrios T.  
; REGISTRATION NUMBER: 32,218  
; REFERENCE/DOCKET NUMBER: 1102865-300  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-819-8286  
; TELEFAX: 212-354-8113  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
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US-08-188-223-10  
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US-08-968-466-10  
; Sequence 10, Application US/08968466  
; Patent No. 6132720  
; GENERAL INFORMATION:

APPLICANT: Grimes, Stephen  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: Immunogens Against Gonadotropin  
TITLE OF INVENTION: Releasing Hormone  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Dimitrios T. Drivas, Esq.  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/968,466  
FILING DATE: 27-JAN-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas Esq., Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-300  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-819-8286  
TELEFAX: 212-354-8113  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
FRAGMENT TYPE: C-terminal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..7  
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US-08-968-466-10

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Qy 1 SSPPPPC 7  
Db 1 SSPPPPC 7

RESULT 4  
US-08-478-546B-10  
Sequence 10, Application US/08478546B  
Patent No. 6303123  
GENERAL INFORMATION:  
APPLICANT: Grimes, Stephen  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: Methods for the Treatment of Hormone-Dependent  
TITLE OF INVENTION: Tumors with Immunogens against Gonadotropin Releasing Hormone  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Dimitrios T. Drivas, Esq.  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,546B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/188,223  
FILING DATE: 27-JAN-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas Esq., Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-300  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-819-8286  
TELEFAX: 212-354-8113  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: C-terminal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..7  
OTHER INFORMATION: /note= "spacer"  
US-08-478-546B-10

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Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
Db 1 SSPPPPC 7

RESULT 5  
US-09-076-372-3  
Sequence 3, Application US/09076372  
Patent No. 6548066  
GENERAL INFORMATION:  
APPLICANT: Michaeli, Dov  
APPLICANT: Caplin, Martyn E.  
APPLICANT: Watson, Susan A.  
APPLICANT: Grimes, Stephen  
TITLE OF INVENTION: Immunogenic Compositions  
TITLE OF INVENTION: to the CCK-B/gastrin Receptor and Methods for  
TITLE OF INVENTION: the Treatment of Tumors  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Dimitrios T. Drivas, White & Case LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/076,372  
FILING DATE: 12-MAY-1998  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/046,201  
FILING DATE: 12-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas, Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-0032

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 819-8200  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-076-372-3

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QY 1 SSPPPPC 7  
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DB 1 SSPPPPC 7

RESULT 6  
PCT-US94-13205-3  
Sequence 3, Application PC/TUS9413205  
GENERAL INFORMATION:  
APPLICANT: Gevas, Philip C.  
APPLICANT: Grimes, Stephen  
APPLICANT: Karr, Stephen  
APPLICANT: Michaeli, Dov  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, White and Case  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 100036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/13205  
FILING DATE: 12-NOV-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas, Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-028  
TELEPHONE: (212) 819-8286  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
PCT-US94-13205-3

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Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
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QY 1 SSPPPPC 7  
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DB 1 SSPPPPC 7  
RESULT 7  
US-08-151-219-1  
Sequence 1, Application US/08151219  
Patent No. 5468494  
GENERAL INFORMATION:  
APPLICANT: Gevas, Philip C.  
APPLICANT: Grimes, Stephen  
APPLICANT: Karr, Stephen  
APPLICANT: Michaeli, Dov  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, White and Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 100036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/151,219  
FILING DATE: 12-NOV-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas, Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-028  
TELEPHONE: (212) 819-8286  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-151-219-1

Query Match 100.0%; Score 45; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 10 SSPPPPC 16

RESULT 8  
PCT-US94-13205-1  
Sequence 1, Application PC/TUS9413205  
GENERAL INFORMATION:  
APPLICANT: Gevas, Philip C.  
APPLICANT: Grimes, Stephen  
APPLICANT: Karr, Stephen  
APPLICANT: Michaeli, Dov  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, White and Case

STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 100036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/13205  
FILING DATE: 12-NOV-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas, Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-028  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 819-8286  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
PCT-US94-13205-1

Query Match 100.0%; Score 45; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7  
Db 10 SSPPPPC 16

RESULT 9  
US-08-188-223-6  
Sequence 6, Application US/08188223  
Patent No. 5688506  
GENERAL INFORMATION:  
APPLICANT: Grimes, Stephen  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: Immunogens Against Gonadotropin  
TITLE OF INVENTION: Releasing Hormone  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, Esq.  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,223  
FILING DATE: 27-JAN-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas Esq., Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-300  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-819-8286

TELEFAX: 212-354-8113  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
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US-08-188-223-6

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Best Local Similarity 100.0%; Pred. No. 3.6;  
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Qy 1 SSPPPPC 7  
Db 11 SSPPPPC 17

RESULT 10  
US-08-968-466-6  
Sequence 6, Application US/08968466  
Patent No. 6132720  
GENERAL INFORMATION:  
APPLICANT: Grimes, Stephen  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: Immunogens Against Gonadotropin  
TITLE OF INVENTION: Releasing Hormone  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, Esq.  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/968,466  
FILING DATE: 27-JAN-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas Esq., Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-300  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-819-8286  
TELEFAX: 212-354-8113  
INFORMATION FOR SEQ ID NO: 6:  
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LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
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Query Match 100.0%; Score 45; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSPPPPC 7
Db 11 SSPPPPC 17
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US-08-478-546B-6
; Sequence 6, Application US/08478546B
; Patent No. 6303123
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Methods for the Treatment of Hormone-Dependent
; TITLE OF INVENTION: Tumors with Immunogens against Gonadotropin Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,546B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
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; LOCATION: 1
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; OTHER INFORMATION: /note= "pyroglutamic acid"
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; NAME/KEY: Region
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; LOCATION: 1..10
; OTHER INFORMATION: /note= "immunomimic"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 11..17
; OTHER INFORMATION: /note= "spacer"
; US-08-478-546B-6
Query Match 100.0%; Score 45; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSPPPPC 7
Db 11 SSPPPPC 17
RESULT 12
US-09-270-767-35820
; Sequence 35820, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35820
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-35820
Query Match 93.3%; Score 42; DB 2; Length 160;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSPPPPC 7
Db 28 ASPPPPC 34
RESULT 13
US-09-270-767-51037
; Sequence 51037, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51037
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-51037
Query Match 93.3%; Score 42; DB 2; Length 160;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSPPPPC 7
Db 28 ASPPPPC 34
```

```
RESULT 14
US-09-949-002-506
; Sequence 506, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 506
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-506

Query Match      91.1%; Score 41; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SPPTPC 7
Db      72 SPPTPC 77

RESULT 15
US-09-252-991A-18242
; Sequence 18242, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18242
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18242

Query Match      88.9%; Score 40; DB 2; Length 399;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 SSPPPPC 7
Db      45 SRPPPPC 51

RESULT 16
US-09-252-991A-29340
; Sequence 29340, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
```

```
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29340
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29340

Query Match      88.9%; Score 40; DB 2; Length 759;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 SSPPPPC 7
Db      748 SRPPPPC 754

RESULT 17
US-09-252-991A-33036
; Sequence 33036, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 33036
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-33036

Query Match      86.7%; Score 39; DB 2; Length 734;
Best Local Similarity 71.4%; Pred. No. 6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SSPPPPC 7
Db      127 AAPPPPC 133

RESULT 18
US-09-823-240A-8
; Sequence 8, Application US/09823240A
; Patent No. 6716597
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
; APPLICANT: James E. Bear
; APPLICANT: Jurgen Wehland
; APPLICANT: Joseph Loureiro
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; TITLE OF INVENTION: Motility
; FILE REFERENCE: M00656.70064.US
; CURRENT APPLICATION NUMBER: US/09/823,240A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/194,564
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 9
```

```
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: Misc feature
/ LOCATION: (9)...(9)
/ OTHER INFORMATION: Xaa is any amino acid
US-09-823-240A-8

Query Match      84.4%; Score 38; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPDPCC 7
Db 1 APPDPC 6

RESULT 19
US-09-673-395A-493
; Sequence 493, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 493
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-395A-493

Query Match      84.4%; Score 38; DB 2; Length 100;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPDPCC 7
Db 86 TPDPCC 91

RESULT 20
US-09-270-767-31687
; Sequence 31687, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31687
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-31687

Query Match      84.4%; Score 38; DB 2; Length 112;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPDPCC 7
Db 12 TPDPCC 17

RESULT 21
US-09-270-767-46904
; Sequence 46904, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46904
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-46904

Query Match      84.4%; Score 38; DB 2; Length 112;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPDPCC 7
Db 7 APPDPC 12

RESULT 22
US-09-252-991A-26904
; Sequence 26904, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26904
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26904

Query Match      84.4%; Score 38; DB 2; Length 179;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPDPCC 7
Db 12 TPDPCC 17

RESULT 23
US-10-104-047-2317
; Sequence 2317, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
```

; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2317  
; LENGTH: 241  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-2317

Query Match 84.4%; Score 38; DB 2; Length 241;  
Best Local Similarity 83.3%; Pred. No. 3.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7  
:|||||  
Db 213 TTPPPC 218

RESULT 24  
US-09-252-991A-26078  
; Sequence 26078, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 26078  
; LENGTH: 511  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-26078

Query Match 84.4%; Score 38; DB 2; Length 511;  
Best Local Similarity 83.3%; Pred. No. 5.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7  
:|||||  
Db 430 APPPPC 435

RESULT 25  
US-09-252-991A-30868  
; Sequence 30868, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 30868  
; LENGTH: 574  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-30868

Query Match 84.4%; Score 38; DB 2; Length 574;  
Best Local Similarity 83.3%; Pred. No. 6.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7  
:|||||  
Db 291 TTPPPC 296

RESULT 26  
US-09-949-016-7248  
; Sequence 7248, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7248  
; LENGTH: 806  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7248

Query Match 84.4%; Score 38; DB 2; Length 806;  
Best Local Similarity 83.3%; Pred. No. 8.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7  
:|||||  
Db 786 NPPPPC 791

RESULT 27  
US-09-095-443-2  
; Sequence 2, Application US/09095443  
; Patent No. 6342593  
; GENERAL INFORMATION:  
; APPLICANT: Plowman, Gregory  
; APPLICANT: Peles, Eior  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT  
; TITLE OF INVENTION: OF ALP RELATED DISORDERS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/095,443  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:

```
,
, ATTORNEY/AGENT INFORMATION:
, NAME: Divvas, Dmitrios T.
, REGISTRATION NUMBER: 32,218
, REFERENCE/DOCKET NUMBER: 1102865-028
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (212) 819-8286
, TELEFAX: (212) 354-8113
, INFORMATION FOR SEQ ID NO: 5:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 6 amino acids
, TYPE: amino acid
, TOPOLOGY: linear
, MOLECULE TYPE: peptide
, HYPOTHEetical: NO
, ANTI-SENSE: NO
, FRAGMENT TYPE: N-terminal
,
```

US-08-968-466-4  
; Sequence 4, Application US/08968466  
; Patent No. 6132720  
; GENERAL INFORMATION:  
; APPLICANT: Grimes, Stephen

APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: Immunogens Against Gonadotropin  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, Esq.  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/968,466  
FILING DATE: 27-JAN-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas Esq., Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-300  
TELEPHONE: 212-819-8286  
TELEFAX: 212-354-8113  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
FRAGMENT TYPE: C-terminal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /note= "spacer"  
US-08-968-466-4

Query Match 82.2%; Score 37; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
DB 2 PPPPC 6

RESULT 31  
US-08-478-546B-4  
Sequence 4, Application US/08478546B  
Patent No. 6303123  
GENERAL INFORMATION:  
APPLICANT: Grimes, Stephen  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: Methods for the Treatment of Hormone-Dependent  
Tumors with Immunogens against Gonadotropin Releasing Hormone  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, Esq.  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,546B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/188,223  
FILING DATE: 27-JAN-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas Esq., Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-300  
TELEPHONE: 212-819-8286  
TELEFAX: 212-354-8113  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: C-terminal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /note= "spacer"  
US-08-478-546B-4

Query Match 82.2%; Score 37; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
DB 2 PPPPC 6

RESULT 32  
PCT-US94-13205-5  
Sequence 5, Application PC/TUS9413205  
GENERAL INFORMATION:  
APPLICANT: Gevas, Philip C.  
APPLICANT: Grimes, Stephen  
APPLICANT: Karr, Stephen  
APPLICANT: Michaeli, Dov  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
AGAINST HUMAN GASTRIN 17  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, White and Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 100036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/13205  
FILING DATE: 12-NOV-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas, Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-028  
TELEPHONE: (212) 819-8286  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:

```
;
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
PCT-US94-13205-5
```

```
Query Match 82.2%; Score 37; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 3 PPPPC 7
DB 2 PPPPC 6
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## RESULT 33

```
US-09-823-240A-7
; Sequence 7, Application US/09823240A
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```
; Patent No. 6716597
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; GENERAL INFORMATION:
```

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; APPLICANT: Frank B. Gertler
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; APPLICANT: James E. Bear
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; APPLICANT: Jurgen Wehland
```

```
; APPLICANT: Joseph Loureiro
```

```
; TITLE OF INVENTION: Methods and Products for Regulating Cell
```

```
; TITLE OF INVENTION: Motility
```

```
; FILE REFERENCE: M00656.70064.US
```

```
; CURRENT APPLICATION NUMBER: US/09/823,240A
```

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; CURRENT FILING DATE: 2001-03-30
```

```
; PRIOR APPLICATION NUMBER: 60/194,564
```

```
; PRIOR FILING DATE: 2000-04-03
```

```
; NUMBER OF SEQ ID NOS: 14
```

```
; SOFTWARE: FastSeq for Windows Version 3.0
```

```
; SEQ ID NO 7
```

```
; LENGTH: 9
```

```
; TYPE: PRT
```

```
; ORGANISM: Homo sapien
```

```
; FEATURE:
```

```
; NAME/KEY: Misc_feature
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```
; LOCATION: (9)...(9)
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```
; OTHER INFORMATION: Xaa is any amino acid
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```
US-09-823-240A-7
```

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Query Match 82.2%; Score 37; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 3 PPPPC 7
DB 2 PPPPC 6
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## RESULT 34

```
PCT-US92-10432-2
```

```
; Sequence 2, Application PC/TUS9210432
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: New England Medical Center
```

```
; APPLICANT: Hospitals, Inc.
```

```
; TITLE OF INVENTION: Infant Formula and Infant
```

```
; TITLE OF INVENTION: Formula Additives
```

```
; NUMBER OF SEQUENCES: 2
```

```
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Fish & Richardson
```

```
; STREET: 225 Franklin Street
```

```
; CITY: Boston
```

```
; STATE: Massachusetts
```

```
; COUNTRY: U.S.A.
```

```
; ZIP: 02110-2804
```

```
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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;
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10432
; FILING DATE: 19921203
; CLASSIFICATION:
```

```
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: 07/802,338
```

```
; FILING DATE: 04 December 1991
```

```
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Paul T. Clark
```

```
; REGISTRATION NUMBER: 30,162
```

```
; REFERENCE/DOCKET NUMBER: 00398/059W01
```

```
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (617) 542-5070
```

```
; TELEFAX: (617) 542-8906
```

```
; TELEX: 200154
```

```
; INFORMATION FOR SEQ ID NO: 2:
```

```
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 9
```

```
; TYPE: AMINO ACID
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```
; TOPOLOGY: linear
```

```
PCT-US92-10432-2
```

```
Query Match 82.2%; Score 37; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 3 PPPPC 7
DB 5 PPPPC 9
```

## RESULT 35

```
US-08-602-999A-256
```

```
; Sequence 256, Application US/08602999A
```

```
; Patent No. 6184205
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: SPARKS, Andrew B.
```

```
; APPLICANT: KAY, Brian K.
```

```
; APPLICANT: THORN, Judith M.
```

```
; APPLICANT: QUILLIAM, Lawrence A.
```

```
; APPLICANT: DER, Channing J.
```

```
; APPLICANT: FOWLKES, Dana M.
```

```
; APPLICANT: RIDER, James E.
```

```
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
```

```
; TITLE OF INVENTION: ISOLATING AND USING SAME
```

```
; NUMBER OF SEQUENCES: 467
```

```
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Pennie & Edmonds
```

```
; STREET: 1155 Avenue of the Americas
```

```
; CITY: New York
```

```
; STATE: New York
```

```
; COUNTRY: U.S.A.
```

```
; ZIP: 10036-2711
```

```
; COMPUTER READABLE FORM:
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```
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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```
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

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; CURRENT APPLICATION DATA:
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```
; APPLICATION NUMBER: US/08/602,999A
```

```
; FILING DATE: 16-FEB-1996
```

```
; CLASSIFICATION: 435
```

```
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Misrock, S. Leslie
```

```
; REGISTRATION NUMBER: 18,872
```

```
; REFERENCE/DOCKET NUMBER: 1101-202
```

```
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (212) 790-9090
```

```
; TELEFAX: (212) 869-9741/8864
```

```
; TELEX: 66141 PENNIE
```

; INFORMATION FOR SEQ ID NO: 256:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-256

Query Match 82.2%; Score 37; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7  
Db 7 PPPPC 11

RESULT 36  
US-09-500-124-256  
; Sequence 256, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 256:

SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-256

Query Match 82.2%; Score 37; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7  
Db 7 PPPPC 11

Db 7 PPPPC 11

RESULT 37

US-08-151-219-4  
; Sequence 4, Application US/08151219  
; Patent No. 5468494  
; GENERAL INFORMATION:  
; APPLICANT: Gevas, Philip C.  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Karr, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Scibienski, Robert  
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Dimitrios T. Drivas, White and Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 100036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/151,219  
FILING DATE: 12-NOV-1993  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Drivas, Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-028  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 819-8286  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-151-219-4

Query Match 82.2%; Score 37; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7  
Db 11 PPPPC 15

RESULT 38

US-08-602-999A-433  
; Sequence 433, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME

NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mirock, S. Lealie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 433:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-433

Query Match 82.2%; Score 37; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
Db 6 PPPPC 10

RESULT 39  
US-09-500-124-433  
; Sequence 433, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: O'ILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Lealie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 433:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-433

Query Match 82.2%; Score 37; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
Db 6 PPPPC 10

RESULT 40  
US-09-413-564C-5  
; Sequence 5, Application US/09413564C  
; Patent No. 6716428  
; GENERAL INFORMATION:  
; APPLICANT: The Ohio State University Research Foundation  
; APPLICANT: Stevens, Vernon  
; TITLE OF INVENTION: Antigenic modification of polypeptides  
; FILE REFERENCE: URF 2-056 AVI  
; CURRENT APPLICATION NUMBER: US/09/413,564C  
; CURRENT FILING DATE: 2002-08-27  
; PRIOR APPLICATION NUMBER: 09/413,564  
; PRIOR FILING DATE: 1999-10-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PPT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(15)  
US-09-413-564C-5

Query Match 82.2%; Score 37; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7  
Db 11 PPPPC 15

RESULT 41  
PCT-US94-13205-4  
; Sequence 4, Application PC/TUS9413205  
; GENERAL INFORMATION:  
; APPLICANT: Gevas, Philip C.  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Karr, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Scibienski, Robert  
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
; AGAINST HUMAN GASTRIN 17  
; NUMBER OF SEQUENCES: 5

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Dimitrios T. Drivas, White and Case  
;; STREET: 1155 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 10036  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US94/13205  
;; FILING DATE: 12-NOV-1993  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Drivas, Dimitrios T.  
;; REGISTRATION NUMBER: 32,218  
;; REFERENCE/DOCKET NUMBER: 1102865-028  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 819-8286  
;; TELEFAX: (212) 354-8113  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 15 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHEetical: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: N-terminal  
;; PCT-US94-13205-4

Query Match 82.2%; Score 37; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7  
Db 11 PPPPC 15

RESULT 42  
US-08-188-223-2  
; Sequence 2, Application US/08188223  
; Patent No. 5688506  
; GENERAL INFORMATION:  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Scibienski, Robert  
; TITLE OF INVENTION: Immunogens Against Gonadotropin  
; TITLE OF INVENTION: Releasing Hormone  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dimitrios T. Drivas, Esq.  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2787  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/188,223  
; FILING DATE: 27-JAN-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Drivas Esq., Dimitrios T.  
; REGISTRATION NUMBER: 32,218  
; REFERENCE/DOCKET NUMBER: 1102865-300

;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212-819-8286  
;; TELEFAX: 212-354-8113  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 16 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHEtical: YES  
;; FEATURE:  
;; NAME/KEY: Region  
;; LOCATION: 1..10  
;; OTHER INFORMATION: /note= "immunomimic"  
;; FEATURE:  
;; NAME/KEY: Region  
;; LOCATION: 11..16  
;; OTHER INFORMATION: /note= "spacer"  
;; FEATURE:  
;; NAME/KEY: Modified-site  
;; LOCATION: 1  
;; OTHER INFORMATION: /label= pglu  
;; OTHER INFORMATION: /note= "pyroglutamic acid (5-oxoproline)"  
;; US-08-188-223-2

Query Match 82.2%; Score 37; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7  
Db 12 PPPPC 16

RESULT 43  
US-08-968-466-2  
; Sequence 2, Application US/08968466  
; Patent No. 6132720  
; GENERAL INFORMATION:  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Scibienski, Robert  
; TITLE OF INVENTION: Immunogens Against Gonadotropin  
; TITLE OF INVENTION: Releasing Hormone  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dimitrios T. Drivas, Esq.  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2787  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/968,466  
; FILING DATE: 27-JAN-1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Drivas Esq., Dimitrios T.  
; REGISTRATION NUMBER: 32,218  
; REFERENCE/DOCKET NUMBER: 1102865-300  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-819-8286  
; TELEFAX: 212-354-8113  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

```
/
/ HYPOTHETICAL: YES
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 1..10
/ OTHER INFORMATION: /note= "immunomimic"
/
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 11..16
/ OTHER INFORMATION: /note= "spacer"
/
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 1
/ OTHER INFORMATION: /label= pGlu
/ OTHER INFORMATION: /note= "pyroglutamic acid (5-oxoprolinone)"
US-08-968-466-2

Query Match 82.2%; Score 37; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
Db 12 PPPPC 16

RESULT 44
US-08-478-546B-2
; Sequence 2, Application US/08478546B
; Patent No. 6303123
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Sciblenki, Robert
; TITLE OF INVENTION: Methods for the Treatment of Hormone-Dependent
; TITLE OF INVENTION: Tumors with Immunogens against Gonadotropin Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,546B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 1
; OTHER INFORMATION: /note= Xaa
; OTHER INFORMATION: /note= "pyroglutamic acid"
```

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/
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 1..10
/ OTHER INFORMATION: /note= "immunomimic"
/
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 11..16
/ OTHER INFORMATION: /note= "spacer"
US-08-478-546B-2

Query Match 82.2%; Score 37; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
Db 12 PPPPC 16

RESULT 45
US-09-413-564C-9
; Sequence 9, Application US/09413564C
; Patent No. 6716428
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; APPLICANT: Stevens, Vernon
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564C
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(23)
US-09-413-564C-9

Query Match 82.2%; Score 37; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
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RESULT 46
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; Sequence 33, Application US/09413564C
; Patent No. 6716428
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; APPLICANT: Stevens, Vernon
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564C
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Synthetic
; FEATURE:
; NAME/KEY: PEPTIDE
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; LOCATION: (1)..(27)
; OTHER INFORMATION: conjugated to diphtheria toxoid
US-09-413-564C-33

Query Match      82.2%; Score 37; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7
Db 4 PPPPC 8

RESULT 47
US-09-413-564C-34
; Sequence 34, Application US/09413564C
; Patent No. 6716428
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564C
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
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; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: conjugated to Diphtheria toxoid
US-09-413-564C-34

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7
Db 4 PPPPC 8

RESULT 48
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; Sequence 41, Application US/09413564C
; Patent No. 6716428
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; APPLICANT: The Ohio State University Research Foundation
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564C
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 43
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US-09-413-564C-41

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7
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Db 4 PPPPC 8

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; Patent No. 6716428
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564C
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
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US-09-413-564C-43

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Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7
Db 4 PPPPC 8

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; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564C
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
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; ORGANISM: Homo sapiens
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; NAME/KEY: PEPTIDE
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US-09-413-564C-11

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Qy 3 PPPPC 7
Db 38 PPPPC 42

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Listing first 1000 summaries

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#### SUMMARIES

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100	37	69.8				

101	37	69.8	700	2	US-09-976-594-67	Sequence 67, Appl	174	34	64.2	103	2	US-08-894-173-76	Sequence 76, Appl
102	37	69.8	700	2	US-09-538-092-893	Sequence 893, App	175	34	64.2	103	2	US-09-398-193-76	Sequence 76, Appl
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105	37	69.8	741	2	US-09-949-016-10694	Sequence 10694, A	178	34	64.2	109	2	US-08-894-173-96	Sequence 96, Appl
106	37	69.8	751	2	US-09-402-929-2	Sequence 2, Appl	179	34	64.2	109	2	US-09-398-193-96	Sequence 96, Appl
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109	36	67.9	99	2	US-09-828-648-7	Sequence 7, Appl	182	34	64.2	122	2	US-09-248-796A-14432	Sequence 14432, A
110	36	67.9	210	2	US-09-252-991A-22805	Sequence 22805, A	183	34	64.2	162	2	US-09-640-211A-2204	Sequence 2204, Ap
111	36	67.9	365	2	US-09-107-532A-6590	Sequence 6590, Ap	184	34	64.2	170	2	US-09-640-211A-1156	Sequence 1156, Ap
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117	35	66.0	61	2	US-09-640-211A-2310	Sequence 2310, Ap	190	34	64.2	226	2	US-09-533-029-88	Sequence 88, Appl
118	35	66.0	61	2	US-09-640-211A-2324	Sequence 2324, Ap	191	34	64.2	243	2	US-09-270-767-32265	Sequence 32265, A
119	35	66.0	126	2	US-09-640-211A-2359	Sequence 2359, Ap	192	34	64.2	243	2	US-09-270-767-47482	Sequence 47482, A
120	35	66.0	62	2	US-09-640-211A-2139	Sequence 2139, Ap	193	34	64.2	308	1	US-09-533-029-32	Sequence 32, Appl
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124	35	66.0	85	2	US-09-640-211A-869	Sequence 869, App	197	34	64.2	275	2	US-09-533-029-62	Sequence 62, Appl
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142	35	66.0	529	2	US-09-712-363-175	Sequence 5223, Ap	215	34	64.2	453	2	US-09-612-473-5	Sequence 5, Appl
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145	35	66.0	569	2	US-10-314-881-5	Sequence 5, Appl	218	34	64.2	637	2	US-09-489-039A-10817	Sequence 10817, A
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152	35	66.0	576	2	US-09-298-404-21	Sequence 21, Appl	225	33	62.3	14	2	US-09-561-490B-24	Sequence 24, Appl
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154	35	66.0	576	2	US-09-298-404-23	Sequence 23, Appl	227	33	62.3	42	1	US-08-691-814B-45	Sequence 45, Appl
155	35	66.0	760	2	US-08-928-941D-29	Sequence 29, Appl	228	33	62.3	63	2	US-09-640-211A-2348	Sequence 2348, Ap
156	35	66.0	760	2	US-09-280-590A-29	Sequence 29, Appl	229	33	62.3	125	2	US-09-621-976-4822	Sequence 4822, Ap
157	35	66.0	761	2	US-08-928-941D-1	Sequence 29, Appl	230	33	62.3	126	2	US-08-772-440-10	Sequence 10, Appl
158	35	66.0	761	2	US-08-928-941D-1	Sequence 1, Appl	231	33	62.3	150	2	US-09-205-258-775	Sequence 775, App
159	35	66.0	761	2	US-08-928-941D-1	Sequence 1, Appl	232	33	62.3	150	2	US-10-004-860-775	Sequence 775, App
160	35	66.0	893	2	US-08-892-398-1	Sequence 1, Appl	233	33	62.3	176	2	US-08-772-440-8	Sequence 8, Appl
161	34	64.2	55	2	US-10-104-047-3504	Sequence 3504, Ap	234	33	62.3	180	2	US-08-772-440-31	Sequence 31, Appl
162	34	64.2	55	2	US-09-640-211A-2333	Sequence 2333, Ap	235	33	62.3	192	2	US-09-543-681A-7846	Sequence 7846, Ap
163	34	64.2	57	2	US-09-640-211A-2334	Sequence 2334, Ap	236	33	62.3	197	2	US-09-902-540-13013	Sequence 13013, A
164	34	64.2	57	2	US-09-640-211A-2286	Sequence 2286, Ap	237	33	62.3	199	2	US-08-772-440-13	Sequence 13, Appl
165	34	64.2	58	2	US-09-640-211A-2344	Sequence 2344, Ap	238	33	62.3	208	2	US-09-640-211A-2250	Sequence 2250, Ap
166	34	64.2	61	2	US-09-640-211A-2314	Sequence 2314, Ap	239	33	62.3	214	2	US-09-949-016-7312	Sequence 7312, Ap
167	34	64.2	61	2	US-09-640-211A-2331	Sequence 2331, Ap	240	33	62.3	218	2	US-09-252-991A-31618	Sequence 31618, A
168	34	64.2	62	2	US-09-640-211A-2361	Sequence 2361, Ap	241	33	62.3	224	2	US-09-640-211A-919	Sequence 919, App
169	34	64.2	62	2	US-09-640-211A-2321	Sequence 2321, Ap	242	33	62.3	236	2	US-09-902-540-15119	Sequence 15119, A
170	34	64.2	64	2	US-09-640-211A-2303	Sequence 2303, Ap	243	33	62.3	244	2	US-08-772-440-2	Sequence 2, Appl
171	34	64.2	67	2	US-09-640-211A-2346	Sequence 2346, Ap	244	33	62.3	247	2	US-08-311-731A-118	Sequence 118, App
172	34	64.2	78	2	US-09-640-211A-2240	Sequence 2240, Ap	245	33	62.3	257	2	US-09-543-681A-4193	Sequence 4193, Ap
173	34	64.2	94	2	US-09-640-211A-2153	Sequence 2153, Ap	246	33	62.3	275	2	US-09-489-039A-8651	Sequence 8651, Ap

247	33	62.3	303	1	US-08-286-819A-23	Sequence 23, Appl	320	33	62.3	3878	2	US-09-914-259-11	Sequence 11, Appl
248	33	62.3	303	2	US-08-980-357-23	Sequence 23, Appl	321	32.5	61.3	168	2	US-10-000-489-88	Sequence 88, Appl
249	33	62.3	303	2	US-09-357-375-23	Sequence 23, Appl	322	32.5	61.3	168	2	US-10-000-489-90	Sequence 90, Appl
250	33	62.3	304	2	US-09-270-767-44979	Sequence 44979, A	323	32	60.4	10	2	US-09-640-211A-2318	Sequence 2318, Ap
251	33	62.3	312	2	US-09-636-382A-15	Sequence 15, Appl	324	32	60.4	14	2	US-09-640-211A-2319	Sequence 2319, Ap
252	33	62.3	316	2	US-09-902-540-10498	Sequence 10498, A	325	32	60.4	16	2	US-08-729-416C-18	Sequence 18, Appl
253	33	62.3	327	2	US-09-533-028-68	Sequence 68, Appl	326	32	60.4	16	2	US-09-433-353-18	Sequence 18, Appl
254	33	62.3	329	2	US-09-489-039A-9812	Sequence 9812, Ap	327	32	60.4	18	2	US-09-640-211A-2317	Sequence 2317, Ap
255	33	62.3	337	2	US-09-489-039A-10149	Sequence 10149, A	328	32	60.4	20	2	US-09-640-211A-2316	Sequence 2316, Ap
256	33	62.3	335	2	US-09-134-000C-6438	Sequence 6438, Ap	329	32	60.4	31	2	US-09-640-211A-2297	Sequence 2297, Ap
257	33	62.3	363	2	US-09-902-540-15970	Sequence 15970, A	330	32	60.4	35	2	US-09-079-372-11	Sequence 11, Appl
258	33	62.3	365	2	US-10-104-047-3375	Sequence 3375, Ap	331	32	60.4	41	2	US-09-640-211A-2296	Sequence 2296, Ap
259	33	62.3	369	2	US-09-108-020-40	Sequence 40, Appl	332	32	60.4	50	2	US-09-640-211A-2301	Sequence 2301, Ap
260	33	62.3	369	2	US-09-685-296-40	Sequence 40, Appl	333	32	60.4	50	2	US-09-640-211A-2327	Sequence 2327, Ap
261	33	62.3	372	2	US-09-252-991A-22962	Sequence 22962, A	334	32	60.4	53	2	US-09-640-211A-2290	Sequence 2290, Ap
262	33	62.3	392	2	US-09-489-039A-12900	Sequence 12900, A	335	32	60.4	53	2	US-09-640-211A-2302	Sequence 2302, Ap
263	33	62.3	397	2	US-10-243-468-8	Sequence 8, Appl	336	32	60.4	53	2	US-09-640-211A-2328	Sequence 2328, Ap
264	33	62.3	411	2	US-09-328-352-5684	Sequence 5684, Ap	337	32	60.4	59	2	US-09-513-999C-5172	Sequence 5172, Ap
265	33	62.3	413	2	US-10-243-468-9	Sequence 9, Appl	338	32	60.4	61	2	US-09-621-976-6403	Sequence 6403, Ap
266	33	62.3	427	2	US-09-350-841A-1603	Sequence 9, Appl	339	32	60.4	70	2	US-09-079-372-2	Sequence 2, Appl
267	33	62.3	462	2	US-08-486-099-117	Sequence 1603, Ap	340	32	60.4	78	2	US-09-640-211A-2289	Sequence 2289, Ap
268	33	62.3	462	2	US-08-486-099-117	Sequence 117, App	341	32	60.4	90	2	US-09-673-809-34	Sequence 24, Appl
269	33	62.3	462	2	US-08-360-107A-127	Sequence 127, App	342	32	60.4	90	2	US-09-673-809-103	Sequence 103, App
270	33	62.3	462	2	US-08-484-223B-117	Sequence 127, App	343	32	60.4	90	2	US-09-673-809-105	Sequence 105, App
271	33	62.3	462	2	US-08-919-597-117	Sequence 117, App	344	32	60.4	91	2	US-09-252-991A-17783	Sequence 17783, A
272	33	62.3	462	2	US-08-475-668A-117	Sequence 117, App	345	32	60.4	96	2	US-09-640-211A-2225	Sequence 2225, Ap
273	33	62.3	462	2	US-08-485-551A-117	Sequence 117, App	346	32	60.4	99	2	US-09-513-999C-4288	Sequence 4288, Ap
274	33	62.3	462	2	US-08-471-913A-117	Sequence 117, App	347	32	60.4	103	2	US-09-640-211A-2224	Sequence 2224, Ap
275	33	62.3	462	2	US-08-485-264A-117	Sequence 117, App	348	32	60.4	108	2	US-09-640-211A-2140	Sequence 2140, Ap
276	33	62.3	462	2	US-08-474-349A-117	Sequence 117, App	349	32	60.4	110	2	US-09-640-211A-2158	Sequence 2158, Ap
277	33	62.3	462	2	US-08-470-896-117	Sequence 117, App	350	32	60.4	122	1	US-08-266-451B-18	Sequence 18, Appl
278	33	62.3	462	2	US-08-485-546A-117	Sequence 117, App	351	32	60.4	122	1	US-08-748-725-18	Sequence 18, Appl
279	33	62.3	462	2	US-08-487-266A-117	Sequence 117, App	352	32	60.4	124	1	US-09-252-991A-17879	Sequence 17879, A
280	33	62.3	462	2	US-08-484-741-117	Sequence 117, App	353	32	60.4	124	1	US-09-513-999C-4287	Sequence 4287, Ap
281	33	62.3	477	2	US-09-252-991A-17047	Sequence 17047, A	354	32	60.4	125	2	US-09-640-211A-2231	Sequence 2231, Ap
282	33	62.3	489	2	US-09-393-171-7	Sequence 7, Appl	355	32	60.4	125	2	US-09-640-211A-2231	Sequence 2231, Ap
283	33	62.3	495	2	US-09-252-991A-23393	Sequence 23393, A	356	32	60.4	135	2	US-09-513-999C-7880	Sequence 7880, Ap
284	33	62.3	502	2	US-09-489-039A-13376	Sequence 13376, A	357	32	60.4	137	2	US-09-513-999C-4291	Sequence 4291, Ap
285	33	62.3	527	2	US-08-369-822C-25	Sequence 25, Appl	358	32	60.4	139	2	US-09-513-999C-8121	Sequence 8121, Ap
286	33	62.3	527	2	US-08-582-776C-40	Sequence 40, Appl	359	32	60.4	145	1	US-08-170-179-32	Sequence 32, Appl
287	33	62.3	542	2	US-08-434-831B-37	Sequence 37, Appl	360	32	60.4	148	2	US-09-134-000C-4507	Sequence 4507, Ap
288	33	62.3	542	2	US-09-667-365-1903	Sequence 1903, Ap	361	32	60.4	150	2	US-09-640-211A-2134	Sequence 2134, Ap
289	33	62.3	543	2	US-09-529-093A-2	Sequence 2, Appl	362	32	60.4	155	2	US-09-640-211A-2128	Sequence 2128, Ap
290	33	62.3	543	2	US-09-529-154-2	Sequence 2, Appl	363	32	60.4	156	2	US-09-513-999C-4289	Sequence 4289, Ap
291	33	62.3	543	2	US-10-185-182A-2	Sequence 2, Appl	364	32	60.4	162	2	US-09-640-211A-2130	Sequence 2130, Ap
292	33	62.3	574	2	US-09-252-991A-18858	Sequence 18858, A	365	32	60.4	169	2	US-09-640-211A-1144	Sequence 1144, Ap
293	33	62.3	575	2	US-08-913-805A-2	Sequence 2, Appl	366	32	60.4	181	2	US-09-013-077A-13	Sequence 13, Appl
294	33	62.3	575	2	US-08-913-805A-10	Sequence 10, Appl	367	32	60.4	182	1	US-08-127-954-135	Sequence 135, App
295	33	62.3	575	2	US-09-442-629-2	Sequence 2, Appl	368	32	60.4	182	1	US-08-127-954-136	Sequence 136, App
296	33	62.3	575	2	US-09-442-629-10	Sequence 10, Appl	369	32	60.4	182	1	US-08-127-954-137	Sequence 137, App
297	33	62.3	575	2	US-09-971-773-24	Sequence 24, Appl	370	32	60.4	182	1	US-08-127-954-138	Sequence 138, App
298	33	62.3	579	2	US-09-369-247-61	Sequence 61, Appl	371	32	60.4	182	1	US-08-127-954-139	Sequence 139, App
299	33	62.3	579	2	US-10-062-548-61	Sequence 61, Appl	372	32	60.4	182	1	US-08-127-954-140	Sequence 140, App
300	33	62.3	592	2	US-10-438-339-8	Sequence 8, Appl	373	32	60.4	182	1	US-08-127-954-141	Sequence 141, App
301	33	62.3	619	2	US-10-104-047-3354	Sequence 3354, Ap	374	32	60.4	182	1	US-08-127-954-142	Sequence 142, App
302	33	62.3	660	2	US-09-583-110-4478	Sequence 4478, Ap	375	32	60.4	182	1	US-08-127-954-143	Sequence 143, App
303	33	62.3	663	2	US-09-107-532A-6861	Sequence 6861, Ap	376	32	60.4	182	1	US-08-127-954-144	Sequence 144, App
304	33	62.3	664	2	US-09-107-433A-3490	Sequence 3490, Ap	377	32	60.4	182	1	US-08-127-954-145	Sequence 145, App
305	33	62.3	776	2	US-09-523-849-34	Sequence 34, Appl	378	32	60.4	182	1	US-08-127-954-146	Sequence 146, App
306	33	62.3	1360	2	US-10-162-012-34	Sequence 34, Appl	379	32	60.4	182	1	US-08-127-954-147	Sequence 147, App
307	33	62.3	1363	2	US-09-375-248-19	Sequence 19, Appl	380	32	60.4	182	1	US-08-127-954-148	Sequence 148, App
308	33	62.3	1382	2	US-10-087-782A-31	Sequence 31, Appl	381	32	60.4	182	1	US-08-127-954-149	Sequence 149, App
309	33	62.3	1500	2	US-09-323-472A-2	Sequence 2, Appl	382	32	60.4	182	1	US-08-127-954-150	Sequence 150, App
310	33	62.3	1500	2	US-09-323-472A-12	Sequence 12, Appl	383	32	60.4	182	1	US-08-127-954-151	Sequence 151, App
311	33	62.3	1500	2	US-09-323-472A-14	Sequence 14, Appl	384	32	60.4	182	1	US-08-127-954-152	Sequence 152, App
312	33	62.3	1500	2	US-09-585-077C-2	Sequence 2, Appl	385	32	60.4	182	1	US-08-127-954-153	Sequence 153, App
313	33	62.3	1500	2	US-09-585-077C-4	Sequence 4, Appl	386	32	60.4	182	1	US-08-127-954-154	Sequence 154, App
314	33	62.3	1500	2	US-09-585-077C-12	Sequence 12, Appl	387	32	60.4	182	1	US-08-127-954-155	Sequence 155, App
315	33	62.3	1500	2	US-09-585-077C-14	Sequence 14, Appl	388	32	60.4	182	1	US-08-127-954-156	Sequence 156, App
316	33	62.3	1500	2	US-09-538-092-1051	Sequence 1051, Ap	389	32	60.4	182	1	US-08-127-954-157	Sequence 157, App
317	33	62.3	2291	1	US-08-286-819A-29	Sequence 29, Appl	390	32	60.4	182	1	US-08-127-954-158	Sequence 158, App
318	33	62.3	2291	2	US-08-360-357-29	Sequence 29, Appl	391	32	60.4	182	1	US-08-127-954-159	Sequence 159, App
319	33	62.3	2291	2	US-09-357-375-29	Sequence 29, Appl	392	32	60.4	182	1	US-08-127-954-160	Sequence 160, App



539	32	60.4	544	2	US-10-011-833A-118	Sequence 118, App	612	31	58.5	118	2	US-09-270-767-55077	Sequence 55077, A
540	32	60.4	544	2	US-10-006-041A-118	Sequence 118, App	613	31	58.5	120	2	US-09-270-767-59011	Sequence 59011, A
541	32	60.4	544	2	US-10-012-064A-118	Sequence 118, App	614	31	58.5	120	2	US-09-513-999C-4280	Sequence 4280, Ap
542	32	60.4	546	2	US-09-949-016-8921	Sequence 8921, Ap	615	31	58.5	147	2	US-09-134-000C-5950	Sequence 5951, Ap
543	32	60.4	546	2	US-09-949-016-8922	Sequence 8922, Ap	616	31	58.5	170	2	US-09-902-540-15177	Sequence 15177, A
544	32	60.4	546	2	US-09-949-016-8923	Sequence 8923, Ap	617	31	58.5	184	2	US-09-270-767-44296	Sequence 44296, A
545	32	60.4	546	2	US-09-949-016-8924	Sequence 8924, Ap	618	31	58.5	185	2	US-09-252-931A-21225	Sequence 21225, A
546	32	60.4	546	2	US-09-949-016-8925	Sequence 8925, Ap	619	31	58.5	202	2	US-09-543-681A-7852	Sequence 7852, Ap
547	32	60.4	557	2	US-09-710-279-1486	Sequence 1486, Ap	620	31	58.5	204	2	US-10-104-047-2253	Sequence 2253, Ap
548	32	60.4	558	2	US-09-134-001C-4178	Sequence 4178, Ap	621	31	58.5	205	2	US-09-248-796A-18009	Sequence 18009, A
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550	32	60.4	570	2	US-09-949-016-9928	Sequence 9928, Ap	623	31	58.5	237	2	US-09-640-211A-2212	Sequence 2212, Ap
551	32	60.4	570	2	US-09-949-016-9929	Sequence 9929, Ap	624	31	58.5	280	2	US-09-489-039A-9395	Sequence 9395, Ap
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553	32	60.4	570	2	US-09-949-016-9931	Sequence 9931, Ap	626	31	58.5	282	2	US-09-845-713A-2	Sequence 2, Appli
554	32	60.4	570	2	US-09-949-016-9932	Sequence 9932, Ap	627	31	58.5	288	2	US-09-252-931A-23714	Sequence 23714, A
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556	32	60.4	574	2	US-09-142-623-13	Sequence 13, Appli	629	31	58.5	289	2	US-08-481-985B-79	Sequence 79, Appl
557	32	60.4	575	2	US-09-971-773-23	Sequence 23, Appli	630	31	58.5	289	2	US-08-370-476-79	Sequence 79, Appl
558	32	60.4	588	2	US-09-949-016-7290	Sequence 7290, Ap	631	31	58.5	290	1	US-08-484-905-80	Sequence 80, Appl
559	32	60.4	594	2	US-08-729-416C-7	Sequence 7, Appli	632	31	58.5	290	2	US-08-481-985B-80	Sequence 80, Appl
560	32	60.4	594	2	US-08-729-416C-17	Sequence 17, Appli	633	31	58.5	292	2	US-08-370-476-80	Sequence 80, Appl
561	32	60.4	594	2	US-09-433-353-7	Sequence 7, Appli	634	31	58.5	314	2	US-09-636-382A-2	Sequence 2, Appli
562	32	60.4	594	2	US-09-433-353-17	Sequence 17, Appli	635	31	58.5	336	2	US-09-252-931A-16707	Sequence 16707, A
563	32	60.4	598	1	US-08-455-543A-41	Sequence 41, Appli	636	31	58.5	338	2	US-09-710-279-1756	Sequence 1756, Ap
564	32	60.4	598	1	US-08-223-305C-41	Sequence 41, Appli	637	31	58.5	338	2	US-09-949-016-6176	Sequence 6176, Ap
565	32	60.4	598	1	US-08-149-097D-33	Sequence 33, Appli	638	31	58.5	339	2	US-09-949-016-8636	Sequence 8636, Ap
566	32	60.4	613	2	US-09-508-264A-3	Sequence 3, Appli	639	31	58.5	343	1	US-08-599-171A-28	Sequence 28, Appl
567	32	60.4	658	2	US-08-895-590-10	Sequence 10, Appli	640	31	58.5	343	1	US-08-646-590B-28	Sequence 28, Appl
568	32	60.4	666	2	US-09-422-869-18	Sequence 18, Appli	641	31	58.5	343	2	US-09-069-226-28	Sequence 28, Appl
569	32	60.4	672	2	US-09-422-869-2	Sequence 2, Appli	642	31	58.5	343	2	US-09-412-184-28	Sequence 28, Appl
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572	32	60.4	680	2	US-09-670-827-4	Sequence 4, Appli	645	31	58.5	362	2	US-09-949-016-8242	Sequence 8242, Ap
573	32	60.4	680	2	US-09-827-949-4	Sequence 4, Appli	646	31	58.5	364	2	US-08-914-372C-11	Sequence 11, Appl
574	32	60.4	690	2	US-09-252-931A-29429	Sequence 29429, A	647	31	58.5	364	2	US-09-543-681A-6003	Sequence 6003, Ap
575	32	60.4	765	2	US-08-275-252A-19	Sequence 19, Appli	648	31	58.5	386	2	US-09-603-703B-2578	Sequence 2578, Ap
576	32	60.4	792	2	US-08-444-818-70	Sequence 70, Appli	649	31	58.5	406	2	US-09-134-001C-3202	Sequence 3202, Ap
577	32	60.4	811	2	US-09-949-016-6199	Sequence 6199, Ap	650	31	58.5	415	2	US-09-489-039A-10072	Sequence 10072, A
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580	32	60.4	1129	2	US-09-902-540-13875	Sequence 13875, A	653	31	58.5	437	2	US-09-252-931A-26020	Sequence 26020, A
581	32	60.4	1148	2	US-09-538-092-156	Sequence 156, App	654	31	58.5	468	2	US-09-252-931A-27684	Sequence 27684, A
582	32	60.4	1620	1	US-08-542-363-2	Sequence 2, Appli	655	31	58.5	476	2	US-09-252-931A-27684	Sequence 27684, A
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584	32	60.4	1620	2	US-09-670-827-2	Sequence 2, Appli	657	31	58.5	510	2	US-09-248-796A-15003	Sequence 15003, A
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591	31.5	59.4	904	2	US-09-964-899-49	Sequence 49, Appli	664	31	58.5	528	2	US-09-010-147B-20	Sequence 20, Appl
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593	31	58.5	8	2	US-08-335-733D-53	Sequence 53, Appli	666	31	58.5	537	2	US-08-604-333-4	Sequence 4, Appli
594	31	58.5	8	2	US-08-335-733D-55	Sequence 55, Appli	667	31	58.5	537	2	US-09-110-618-4	Sequence 4, Appli
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597	31	58.5	53	2	US-09-640-211A-2313	Sequence 2313, Ap	670	31	58.5	537	2	US-09-577-806-4	Sequence 4, Appli
598	31	58.5	63	2	US-09-673-395A-336	Sequence 336, App	671	31	58.5	560	1	US-09-621-502-8	Sequence 8, Appli
599	31	58.5	63	2	US-09-673-395A-599	Sequence 599, App	672	31	58.5	560	1	US-08-647-484-2	Sequence 2, Appli
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601	31	58.5	64	2	US-10-004-860-387	Sequence 387, App	674	31	58.5	560	1	US-08-805-118-4	Sequence 4, Appli
602	31	58.5	83	1	US-08-332-562A-91	Sequence 91, Appli	675	31	58.5	560	1	US-09-391-958-4	Sequence 4, Appli
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604	31	58.5	104	1	US-08-481-985B-81	Sequence 81, Appli	677	31	58.5	560	2	PCT-US96-05752-2	Sequence 2805, Ap
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607	31	58.5	111	2	US-08-488-446-72	Sequence 72, Appli	680	31	58.5	587	1	US-07-955-905A-23	Sequence 23, Appl
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686	31	58.5	623	2	US-09-854-731-4	Sequence 4, Appli	759	30	56.6	22	1	US-08-488-351A-70	Sequence 70, Appli
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689	31	58.5	628	2	US-09-107-532A-7123	Sequence 7123, Ap	762	30	56.6	57	1	US-08-488-351A-96	Sequence 96, Appl
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712	31	58.5	1281	2	US-09-949-016-10444	Sequence 10444, A	785	30	56.6	207	2	US-09-438-185A-592	Sequence 592, App
713	31	58.5	1351	2	US-09-548-473B-1	Sequence 1, Appli	786	30	56.6	208	2	US-09-270-767-41023	Sequence 41023, A
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717	31	58.5	1665	2	US-09-858-664A-2	Sequence 2, Appli	790	30	56.6	237	1	US-09-121-211-15	Sequence 15, Appli
718	31	58.5	1665	2	US-10-274-978-2	Sequence 2, Appli	791	30	56.6	237	2	US-09-787-328B-10	Sequence 10, Appl
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729	30	56.6	18	2	US-09-052-888-69	Sequence 69, Appl	802	30	56.6	280	2	US-09-252-991A-26771	Sequence 26771, A
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733	30	56.6	18	2	US-09-723-947-69	Sequence 69, Appl	806	30	56.6	292	2	US-09-303-040-4	Sequence 4, Appli
734	30	56.6	18	2	US-09-724-127-69	Sequence 69, Appl	807	30	56.6	292	2	US-09-538-092-546	Sequence 546, App
735	30	56.6	18	2	US-09-723-931-69	Sequence 69, Appl	808	30	56.6	302	2	US-09-107-532A-624	Sequence 624, Ap
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833	30	56.6	348	2	US-09-252-991A-31001	Sequence 31001, A	906	30	56.6	673	2	US-09-990-444-52	Sequence 52, Appl
834	30	56.6	349	2	US-09-248-796A-14572	Sequence 14572, A	907	30	56.6	673	2	US-09-997-333-52	Sequence 52, Appl
835	30	56.6	356	2	US-09-949-016-6179	Sequence 6179, Ap	908	30	56.6	673	2	US-09-992-598-52	Sequence 52, Appl
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846	30	56.6	370	2	US-10-006-041A-315	Sequence 315, App	919	30	56.6	781	2	US-09-902-540-12692	Sequence 9899, Ap
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851	30	56.6	376	2	US-10-243-468-32	Sequence 32, Appl	924	30	56.6	812	2	US-08-991-761A-7	Sequence 7, Appl
852	30	56.6	381	2	US-09-248-796A-19357	Sequence 19357, A	925	30	56.6	836	2	US-10-272-459-40	Sequence 40, Appl
853	30	56.6	384	2	US-09-711-164-384	Sequence 384, App	926	30	56.6	883	2	US-10-188-495-72	Sequence 72, Appl
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859	30	56.6	422	1	US-08-485-938A-34	Sequence 34, Appl	932	30	56.6	947	2	US-09-871-889A-1	Sequence 1, Appl
860	30	56.6	442	2	US-09-328-352-5748	Sequence 5748, Ap	933	30	56.6	947	2	US-09-871-889A-1	Sequence 1, Appl
861	30	56.6	464	2	US-09-902-540-10156	Sequence 10156, A	934	30	56.6	980	2	US-10-272-459-41	Sequence 41, Appl
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863	30	56.6	500	2	US-09-326-203A-17	Sequence 17, Appl	936	30	56.6	1091	6	5516630-2	Patent No. 5516630
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865	30	56.6	515	2	US-08-961-083-22	Sequence 22, Appl	938	30	56.6	1119	2	US-09-396-651B-2	Sequence 2, Appl
866	30	56.6	515	2	US-09-536-784-22	Sequence 22, Appl	939	30	56.6	1140	2	US-09-651-656-21	Sequence 21, Appl
867	30	56.6	515	2	US-09-765-272A-22	Sequence 22, Appl	940	30	56.6	1140	2	US-09-650-855-21	Sequence 21, Appl
868	30	56.6	515	2	US-09-765-272A-22	Sequence 22, Appl	941	30	56.6	1175	2	US-09-252-991A-25044	Sequence 25044, A
869	30	56.6	516	1	US-08-762-106-8	Sequence 8, Appl	942	30	56.6	1203	2	US-09-489-039A-12326	Sequence 12326, A
870	30	56.6	516	2	US-08-745-404-2	Sequence 2, Appl	943	30	56.6	1304	2	US-09-489-039A-13449	Sequence 13449, A
871	30	56.6	516	2	US-09-320-774-8	Sequence 8, Appl	944	30	56.6	1376	2	US-09-252-991A-30344	Sequence 30344, A
872	30	56.6	521	2	US-08-657-749D-6	Sequence 6, Appl	945	30	56.6	1380	2	US-09-252-991A-25722	Sequence 25722, A
873	30	56.6	524	2	US-08-657-749D-4	Sequence 4, Appl	946	30	56.6	1400	2	US-09-764-176-7	Sequence 7, Appl
874	30	56.6	527	1	US-08-762-106-9	Sequence 9, Appl	947	30	56.6	1674	1	US-08-968-542C-12	Sequence 12, Appl
875	30	56.6	527	1	US-09-320-774-9	Sequence 9, Appl	948	30	56.6	1674	2	US-09-554-467A-12	Sequence 12, Appl
876	30	56.6	528	2	US-09-489-039A-13077	Sequence 13077, A	949	30	56.6	1698	2	US-09-902-540-12813	Sequence 12813, A
877	30	56.6	538	2	US-09-583-110-3055	Sequence 3055, Ap	950	30	56.6	1936	2	US-10-152-886-1	Sequence 1, Appl
878	30	56.6	550	2	US-09-252-991A-21295	Sequence 21295, A	951	30	56.6	1939	2	US-10-152-886-43	Sequence 43, Appl
879	30	56.6	551	2	US-09-194-145-2	Sequence 2, Appl	952	30	56.6	2227	2	US-08-475-886-2	Sequence 2, Appl
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883	30	56.6	552	2	US-08-745-404-3	Sequence 3, Appl	956	30	56.6	2227	2	US-09-171-387-2	Sequence 2, Appl
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887	30	56.6	562	2	US-09-437-568A-4	Sequence 4, Appl	960	30	56.6	2227	2	US-09-653-499-6	Sequence 6, Appl
888	30	56.6	568	2	US-10-418-036-6	Sequence 6, Appl	961	30	56.6	2227	2	US-10-104-966-12	Sequence 12, Appl
889	30	56.6	570	2	US-09-107-433-4627	Sequence 4627, Ap	962	30	56.6	2227	2	US-10-135-988-2	Sequence 2, Appl
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891	30	56.6	579	2	US-09-270-767-45302	Sequence 45302, A	964	30	56.6	2227	2	US-09-929-953-12	Sequence 12, Appl
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893	30	56.6	594	2	US-09-949-002-537	Sequence 537, App	966	30	56.6	3852	2	US-10-025-225-4	Sequence 4, Appl
894	30	56.6	598	2	US-09-866-028-69	Sequence 69, Appl	967	30	56.6	4302	2	US-08-658-136-5	Sequence 5, Appl
895	30	56.6	598	2	US-09-944-457-69	Sequence 69, Appl	968	30	56.6	4302	2	US-09-052-469-8	Sequence 8, Appl
896	30	56.6	598	2	US-09-944-584-69	Sequence 69, Appl	969	30	56.6	4302	2	US-08-422-582-8	Sequence 8, Appl
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898	30	56.6	620	2	US-09-945-587-69	Sequence 69, Appl	971	30	56.6	4303	1	US-08-460-751-2	Sequence 2, Appl
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902	30	56.6	646	2	US-09-720-317A-26	Sequence 26, Appl	975	30	56.6	4339	2	US-08-422-582-6	Sequence 6, Appl
903	30	56.6	658	2	US-09-720-317A-24	Sequence 24, Appl	976	30	56.6	4339	2	US-09-052-262-6	Sequence 6, Appl

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978 30 56.6 4588 2 US-10-025-225-8 Sequence 8, Appli  
979 30 56.6 4589 2 US-10-025-225-2 Sequence 2, Appli  
980 29.5 55.7 123 2 US-09-513-999C-5964 Sequence 5964, Ap  
981 29.5 55.7 135 2 US-09-621-976-5492 Sequence 5492, Ap  
982 29.5 55.7 285 2 US-09-902-540-15481 Sequence 15481, A  
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987 29 54.7 12 1 US-08-260-582-47 Sequence 47, Appl  
988 29 54.7 12 1 US-08-260-582-48 Sequence 48, Appl  
989 29 54.7 12 4 PCT-US95-05471-47 Sequence 47, Appl  
990 29 54.7 12 4 PCT-US95-05471-48 Sequence 48, Appl  
991 29 54.7 19 1 US-08-310-912A-30 Sequence 30, Appl  
992 29 54.7 19 2 US-08-841-089-30 Sequence 30, Appl  
993 29 54.7 19 2 US-09-301-085-30 Sequence 30, Appl  
994 29 54.7 19 4 PCT-US95-04570-30 Sequence 30, Appl  
995 29 54.7 19 4 PCT-US95-04589-30 Sequence 30, Appl  
996 29 54.7 22 2 US-08-940-095-64 Sequence 64, Appl  
997 29 54.7 22 2 US-08-940-093-64 Sequence 64, Appl  
998 29 54.7 22 2 US-08-940-096-64 Sequence 64, Appl  
999 29 54.7 22 2 US-09-465-719-64 Sequence 64, Appl  
1000 29 54.7 22 2 US-09-453-605-64 Sequence 64, Appl

## ALIGNMENTS

RESULT 1  
US-08-151-219-2  
; Sequence 2, Application US/08151219  
; Patent No. 5468494  
; GENERAL INFORMATION:  
; APPLICANT: Gevas, Philip C.  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Karr, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Scibienski, Robert  
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dimitrios T. Drivas, White and Case  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/151.219  
; FILING DATE: 12-NOV-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Drivas, Dimitrios T.  
; REGISTRATION NUMBER: 32,218  
; REFERENCE/DOCKET NUMBER: 1102865-028  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 819-8286  
; TELEFAX: (212) 354-8113  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal  
US-08-151-219-2  
Query Match 100.0%; Score 53; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EGPWLEEE 9  
Db 1 EGPWLEEE 9  
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RESULT 2  
PCT-US94-13205-2  
; Sequence 2, Application PC/TUS9413205  
; GENERAL INFORMATION:  
; APPLICANT: Gevas, Philip C.  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Karr, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Scibienski, Robert  
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dimitrios T. Drivas, White and Case  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/13205  
; FILING DATE: 12-NOV-1993  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Drivas, Dimitrios T.  
; REGISTRATION NUMBER: 32,218  
; REFERENCE/DOCKET NUMBER: 1102865-028  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 819-8286  
; TELEFAX: (212) 354-8113  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
PCT-US94-13205-2  
Query Match 100.0%; Score 53; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EGPWLEEE 9  
Db 1 EGPWLEEE 9  
|||||  
RESULT 3  
US-08-652-971-10  
; Sequence 10, Application US/08652971  
; Patent No. 5814507  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill

APPLICANT: Lasky, Laurence A.  
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd.  
CITY: South San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,971  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: P1033  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 952-3216  
TELEFAX: (415) 952-9881  
TELEX: 910 371-7168  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-652-971-10

Query Match 100.0%; Score 53; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9  
DB 1 EGPWLEEEE 9

RESULT 4  
US-08-991-258A-10  
Sequence 10, Application US/08991258A  
Patent No. 5928887  
GENERAL INFORMATION:  
APPLICANT: Cheng, Jill  
APPLICANT: Lasky, Laurence A.  
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT, LLP  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/991,258A  
FILING DATE: 17-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/652,971  
FILING DATE: 24-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-63478-3/WHI/MTK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-991-258A-10

Query Match 100.0%; Score 53; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9  
DB 1 EGPWLEEEE 9

RESULT 5  
US-08-769-399-10  
Sequence 10, Application US/08769399  
Patent No. 5976852  
GENERAL INFORMATION:  
APPLICANT: Cheng, Jill  
APPLICANT: Lasky, Laurence A.  
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd.  
CITY: South San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/769,399  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: P1033  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 225-3216  
TELEFAX: (415) 952-9881  
TELEX: 910 371-7168  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-769-399-10

Query Match 100.0%; Score 53; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.01;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9  
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 Db 1 EGPWLEEE 9

## RESULT 6

US-08-991-953A-10  
 ; Sequence 10, Application US/08991953A  
 ; Patent No. 6083748  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheng, Jill  
 ; APPLICANT: Lasky, Laurence A.  
 ; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
 ; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT, LLP  
 ; STREET: 4 Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/991,953A  
 ; FILING DATE: 16-DEC-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/652,971  
 ; FILING DATE: 24-MAY-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dreger, Walter H.  
 ; REGISTRATION NUMBER: 24,190  
 ; REFERENCE/DOCKET NUMBER: A-63478-3/WHI/MTK  
 ; TELEPHONE: (415) 781-1989  
 ; TELEFAX: (415) 398-3249  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 12 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-991-953A-10

Query Match 100.0%; Score 53; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.01;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9  
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 Db 1 EGPWLEEE 9

## RESULT 7

US-08-151-219-4  
 ; Sequence 4, Application US/08151219  
 ; Patent No. 5468494  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gevas, Philip C.  
 ; APPLICANT: Grimes, Stephen  
 ; APPLICANT: Karr, Stephen  
 ; APPLICANT: Michaeli, Dov  
 ; APPLICANT: Scibienski, Robert  
 ; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS

; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dimitrios T. Drivas, White and Case  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 100036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/151,219  
 ; FILING DATE: 12-NOV-1993  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Drivas, Dimitrios T.  
 ; REGISTRATION NUMBER: 32,218  
 ; REFERENCE/DOCKET NUMBER: 1102865-028  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 819-8286  
 ; TELEFAX: (212) 354-8113  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE: N-terminal  
 ; US-08-151-219-4

Query Match 100.0%; Score 53; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9  
 |||||  
 Db 1 EGPWLEEE 9

## RESULT 8

PCT-US94-13205-4  
 ; Sequence 4, Application PC/TUS9413205  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gevas, Philip C.  
 ; APPLICANT: Grimes, Stephen  
 ; APPLICANT: Karr, Stephen  
 ; APPLICANT: Michaeli, Dov  
 ; APPLICANT: Scibienski, Robert  
 ; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
 ; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dimitrios T. Drivas, White and Case  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 100036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/13205  
 ; FILING DATE: 12-NOV-1993  
 ; CLASSIFICATION:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; PCT-US94-13205-4
;
Query Match 100.0%; Score 53; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 1 EGPWLEEE 9

RESULT 9
US-08-151-219-1
; Sequence 1, Application US/08151219
; Patent No. 5468494
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,219
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-151-219-1
```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; PCT-US94-13205-4
;
Query Match 100.0%; Score 53; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 1 EGPWLEEE 9

RESULT 10
PCT-US94-13205-1
; Sequence 1, Application PC/TUS9413205
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13205
; FILING DATE: 12-NOV-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; PCT-US94-13205-1
;
Query Match 100.0%; Score 53; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 1 EGPWLEEE 9

RESULT 11
US-09-174-216-4
; Sequence 4, Application US/09174216A
; Patent No. 6335176
; GENERAL INFORMATION:
; APPLICANT: Inglesse, James
; APPLICANT: Glickman, Joseph Fraser
; TITLE OF INVENTION: Incorporation of Phosphorylation Sites
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; FILE REFERENCE: 1073.050  
; CURRENT APPLICATION NUMBER: US/09/174.216A  
; CURRENT FILING DATE: 1998-10-16  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Designed  
; OTHER INFORMATION: peptide to act as kinase substrate  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-09-174-216-4

Query Match 100.0%; Score 53; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EGPWLEEEE 9  
Db 1 EGPWLEEEE 9  
|||||

RESULT 12  
US-09-623-548A-422  
; Sequence 422, Application US/09623548A  
; Patent No. 6849714  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623.548A  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 422  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-623-548A-422

Query Match 100.0%; Score 53; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EGPWLEEEE 9  
Db 1 EGPWLEEEE 9  
|||||

RESULT 13  
US-09-657-276-422  
; Sequence 422, Application US/09657276

; Patent No. 6887470  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/657.276  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 422  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-657-276-422

Query Match 100.0%; Score 53; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EGPWLEEEE 9  
Db 1 EGPWLEEEE 9  
|||||

RESULT 14  
US-08-446-692-75  
; Sequence 75, Application US/08446692  
; Patent No. 5759551  
; GENERAL INFORMATION:  
; APPLICANT: Ladd, Anna  
; APPLICANT: Wang, Chang Yi  
; APPLICANT: Zamb, Timothy  
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Maria C.H. Lin  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10154-0053  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,692  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maria C.H. Lin  
; REGISTRATION NUMBER: 29,323  
; REFERENCE/DOCKET NUMBER: 1151-4146 US2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)415-8745

```
; TELFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-75

Query Match          94.3%; Score 50; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 0.033;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
   :|||||||
Db 1 QGPWLEEE 9

RESULT 15
US-08-488-351A-75
; Sequence 75, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-351A-75

Query Match          94.3%; Score 50; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 0.033;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
   :|||||||
Db 1 QGPWLEEE 9

US-08-446-692-74
; Sequence 74, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-74

Query Match          94.3%; Score 50; DB 1; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.048;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
   :|||||||
Db 1 QGPWLEEE 9

RESULT 17
US-08-488-351A-74
; Sequence 74, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
```

```

; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488.351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-488-351A-74

Query Match 94.3%; Score 50; DB 1; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.048;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 1 QGPWLEEE 9

RESULT 18
US-09-079-372-17
; Sequence 17, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-372-10

Query Match 94.3%; Score 50; DB 2; Length 18;
Best Local Similarity 88.9%; Pred. No. 0.051;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 1 QGPWLEEE 9

RESULT 19
US-09-079-372-10
; Sequence 10, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-372-10

Query Match 94.3%; Score 50; DB 2; Length 18;
Best Local Similarity 88.9%; Pred. No. 0.051;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 1 QGPWLEEE 9
```

```
Db          1 QGPWLEEE 9

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-372-12

Query Match          94.3%; Score 50; DB 2; Length 21;
Best Local Similarity 88.9%; Pred. No. 0.059;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy          1 EGPWLEEE 9
           :|||||||
Db          5 QGPWLEEE 13

RESULT 22
US-10-360-101-170
; Sequence 170, Application US/10360101
; Patent No. 6861236
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 33
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: S8,C11-sequence of Big Gastrin-1
US-10-360-101-170

Query Match          94.3%; Score 50; DB 2; Length 33;
Best Local Similarity 88.9%; Pred. No. 0.096;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy          1 EGPWLEEE 9
           :|||||||
Db          17 QGPWLEEE 25

RESULT 23
US-08-446-692-69
; Sequence 69, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Y1
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
```

```
Db          1 QGPWLEEE 9

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-372-15

Query Match          94.3%; Score 50; DB 2; Length 18;
Best Local Similarity 88.9%; Pred. No. 0.051;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy          1 EGPWLEEE 9
           :|||||||
Db          1 QGPWLEEE 9

RESULT 21
US-09-079-372-12
; Sequence 12, Application US/09079372
; Patent No. 616590
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-372-15

Query Match          94.3%; Score 50; DB 2; Length 18;
Best Local Similarity 88.9%; Pred. No. 0.051;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy          1 EGPWLEEE 9
           :|||||||
Db          1 QGPWLEEE 9

RESULT 21
US-09-079-372-12
; Sequence 12, Application US/09079372
; Patent No. 616590
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/446,692
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-446-692-69

Query Match 94.3%; Score 50; DB 1; Length 34;
Best Local Similarity 88.9%; Pred. No. 0.099;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 18 QGPWLEEE 26

RESULT 24
US-08-488-351A-69
; Sequence 69, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Y1
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
```

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; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-488-351A-69

Query Match 94.3%; Score 50; DB 1; Length 34;
Best Local Similarity 88.9%; Pred. No. 0.099;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 18 QGPWLEEE 26

RESULT 25
US-09-079-372-9
; Sequence 9, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-372-9

Query Match 94.3%; Score 50; DB 2; Length 34;
Best Local Similarity 88.9%; Pred. No. 0.099;
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Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
:|||||  
Db 18 QGPWLEEE 26

RESULT 26  
US-09-079-372-16  
; Sequence 16, Application US/09079372  
; Patent No. 6165990  
; GENERAL INFORMATION:  
; APPLICANT: Singh, Pomila  
; APPLICANT: Wood, T.  
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN  
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079,372  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/634,546  
; FILING DATE: 18-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hodgins, Daniel S.  
; REGISTRATION NUMBER: 31,026  
; REFERENCE/DOCKET NUMBER: UTSG:220  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-09-079-372-16

Query Match 94.3%; Score 50; DB 2; Length 34;  
Best Local Similarity 88.9%; Pred. No. 0.099;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
:|||||  
Db 18 QGPWLEEE 26

RESULT 27  
US-09-623-548A-423  
; Sequence 423, Application US/09623548A  
; Patent No. 6849714  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623,548A

; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 423  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-623-548A-423

Query Match 94.3%; Score 50; DB 2; Length 34;  
Best Local Similarity 88.9%; Pred. No. 0.099;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
:|||||  
Db 18 QGPWLEEE 26

RESULT 28  
US-09-657-276-423  
; Sequence 423, Application US/09657276  
; Patent No. 6887470  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/657,276  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 423  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-657-276-423

Query Match 94.3%; Score 50; DB 2; Length 34;  
Best Local Similarity 88.9%; Pred. No. 0.099;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
:|||||  
Db 18 QGPWLEEE 26

RESULT 29  
US-09-079-372-8  
; Sequence 8, Application US/09079372

```
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-372-8

Query Match 94.3%; Score 50; DB 2; Length 35;
Best Local Similarity 88.9%; Pred. No. 0.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 18 QGPWLEEE 26

RESULT 30
; Sequence 100, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
```

```
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-446-692-100

Query Match 94.3%; Score 50; DB 1; Length 47;
Best Local Similarity 88.9%; Pred. No. 0.14;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 36 QGPWLEEE 44

RESULT 31
; US-08-488-351A-100
; Sequence 100, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
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; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-446-692-95

Query Match 94.3%; Score 50; DB 1; Length 69;
Best Local Similarity 88.9%; Pred. No. 0.21;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 18 QGPWLEEE 26

RESULT 35
US-08-488-351A-95
; Sequence 95, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Y1
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-488-351A-95

Query Match 94.3%; Score 50; DB 1; Length 69;
Best Local Similarity 88.9%; Pred. No. 0.21;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 18 QGPWLEEE 26

RESULT 36
US-09-079-372-7
; Sequence 7, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-372-7

Query Match 94.3%; Score 50; DB 2; Length 74;
Best Local Similarity 88.9%; Pred. No. 0.22;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 55 QGPWLEEE 63
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RESULT 37
US-09-079-372-14
; Sequence 14, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-372-14

Query Match 94.3%; Score 50; DB 2; Length 100;
Best Local Similarity 88.9%; Pred. No. 0.31;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGFWLEEE 9
Db 75 QGFWLEEE 83

RESULT 38
US-09-949-016-11739
; Sequence 11739, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11739
; LENGTH: 122
; TYPE: PRT
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; ORGANISM: Human
US-09-949-016-11739

Query Match 94.3%; Score 50; DB 2; Length 122;
Best Local Similarity 88.9%; Pred. No. 0.38;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGFWLEEE 9
Db 97 QGFWLEEE 105

RESULT 39
US-09-174-263-2
; Sequence 2, Application US/09174263
; Patent No. 6319898
; GENERAL INFORMATION:
; APPLICANT: Davies, J.
; APPLICANT: Walters, B.
; APPLICANT: Saxena, G.
; TITLE OF INVENTION: METHOD FOR INHIBITING EUKARYOTIC PROTEIN KINASES
; FILE REFERENCE: 9993-007
; CURRENT APPLICATION NUMBER: US/09/174,263
; CURRENT FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Biotinylated peptide substrate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa=Biotin-Glu
US-09-174-263-2

Query Match 90.6%; Score 48; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEEE 9
Db 2 GPWLEEE 9

RESULT 40
US-08-446-692-76
; Sequence 76, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Y1
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
```

```
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-76

Query Match      84.9%; Score 45; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EGPWLEEE 8
Db      1 QGPWLEEE 8

RESULT 41
US-08-488-351A-76
; Sequence 76, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-351A-76

Query Match      84.9%; Score 45; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EGPWLEEE 8
Db      1 QGPWLEEE 8

RESULT 42
US-08-127-351-3
; Sequence 3, Application US/08127351
; Patent No. 5449761
; GENERAL INFORMATION:
; APPLICANT: BELINKA Jr, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,351
; FILING DATE: 28-SEP-1993
; CLASSIFICATION: 534
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-127-351-3

Query Match      84.9%; Score 45; DB 1; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.32;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 EGPWLEEE 9
Db      2 EGPWLEEE 10

RESULT 43
US-08-480-367B-3
; Sequence 3, Application US/08480367B
```

Patent No. 5578288  
; GENERAL INFORMATION:  
; APPLICANT: BELINKA JR, BENJAMIN A.  
; APPLICANT: COUGHLIN, DANIEL J.  
; APPLICANT: ALVAREZ, VERNON L.  
; APPLICANT: WOOD, RICHARD  
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LOWE, PRICE, LeBLANC & BECKER  
; STREET: 99 Canal Center Plaza, Suite 300  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480.367B  
; FILING DATE: 07-06-95  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Villacorta, Gilberto M.  
; REGISTRATION NUMBER: 34,038  
; REFERENCE/DOCKET NUMBER: 2654-002A  
; TELEPHONE: (703) 684-1111  
; TELEFAX: (703) 684-1124  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-480-367B-3

Query Match 84.9%; Score 45; DB 1; Length 17;  
Best Local Similarity 88.9%; Pred. No. 0.32;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
DB 2 EGPWLFEE 10

RESULT 44  
US-08-487-221A-3  
; Sequence 3, Application US/08487221A  
; Patent No. 5593656  
; GENERAL INFORMATION:  
; APPLICANT: BELINKA JR, BENJAMIN A.  
; APPLICANT: COUGHLIN, DANIEL J.  
; APPLICANT: ALVAREZ, VERNON L.  
; APPLICANT: WOOD, RICHARD  
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &  
; ADDRESSEE: NEUSTADT, P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480.370  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/127,351  
; FILING DATE: 28-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Villacorta, Gilberto M.  
; REGISTRATION NUMBER: 34,038  
; REFERENCE/DOCKET NUMBER: 4980-004-44  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000

OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487.221A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/127,351  
; FILING DATE: 28-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Villacorta, Gilberto M.  
; REGISTRATION NUMBER: 34,038  
; REFERENCE/DOCKET NUMBER: 4980-004-44  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-487-221A-3

Query Match 84.9%; Score 45; DB 1; Length 17;  
Best Local Similarity 88.9%; Pred. No. 0.32;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9  
DB 2 EGPWLFEE 10

RESULT 45  
US-08-480-370-3  
; Sequence 3, Application US/08480370  
; Patent No. 5609847  
; GENERAL INFORMATION:  
; APPLICANT: BELINKA JR, BENJAMIN A.  
; APPLICANT: COUGHLIN, DANIEL J.  
; APPLICANT: ALVAREZ, VERNON L.  
; APPLICANT: WOOD, RICHARD  
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &  
; ADDRESSEE: NEUSTADT, P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480.370  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/127,351  
; FILING DATE: 28-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Villacorta, Gilberto M.  
; REGISTRATION NUMBER: 34,038  
; REFERENCE/DOCKET NUMBER: 4980-004-44  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000

; TELEFAX: (703) 413-2220  
 ; TELEX: 248855 OPAT UR  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 17 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 ; US-09-480-370-3

Query Match 84.9%; Score 45; DB 1; Length 17;  
 Best Local Similarity 88.9%; Pred. No. 0.32; Indels 1; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 EGPWLEEE 9  
 |||||  
 Db 2 EGPWLFEE 10

## RESULT 46

US-09-902-540-15521  
 ; Sequence 15521, Application US/09902540  
 ; Patent No. 6833447  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Wisland, Roger C.  
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
 ; FILE REFERENCE: 38-10(15849)B  
 ; CURRENT APPLICATION NUMBER: US/09/902,540  
 ; CURRENT FILING DATE: 2001-07-10  
 ; PRIOR APPLICATION NUMBER: 60/217,883  
 ; PRIOR FILING DATE: 2000-07-10  
 ; NUMBER OF SEQ ID NOS: 16825  
 ; SEQ ID NO 15521  
 ; LENGTH: 542  
 ; TYPE: PRT  
 ; ORGANISM: Myxococcus xanthus  
 ; US-09-902-540-15521

Query Match 79.2%; Score 42; DB 2; Length 542;  
 Best Local Similarity 66.7%; Pred. No. 39; Indels 1; Gaps 0;  
 Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

Qy 1 EGPWLEEE 9  
 |||||  
 Db 299 EGPWVSDEE 307

## RESULT 47

US-09-533-029-40  
 ; Sequence 40, Application US/09533029  
 ; Patent No. 6664446  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Heard, Jacqueline  
 ; APPLICANT: Brown, Pierre  
 ; APPLICANT: Riechmann, Jose-Luis  
 ; APPLICANT: Keddie, James  
 ; APPLICANT: Pineda, Omaira  
 ; APPLICANT: Adam, Luc  
 ; APPLICANT: Samaha, Raymond  
 ; APPLICANT: Zhang, James  
 ; APPLICANT: Yu, Guo-Liang  
 ; APPLICANT: Ratcliffe, Oliver  
 ; APPLICANT: Pilgrim, Marsha  
 ; APPLICANT: Jiang, Cai-Zhong  
 ; APPLICANT: Reuber, Lynne  
 ; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES  
 ; FILE REFERENCE: MBI-010  
 ; CURRENT APPLICATION NUMBER: US/09/533,029  
 ; CURRENT FILING DATE: 2000-03-22  
 ; EARLIER APPLICATION NUMBER: 60/125,814

; EARLIER FILING DATE: 1999-03-23  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 40  
 ; LENGTH: 273  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:  
 ; OTHER INFORMATION: G239  
 ; US-09-533-029-40

Query Match 77.4%; Score 41; DB 2; Length 273;  
 Best Local Similarity 66.7%; Pred. No. 28; Indels 1; Gaps 0;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9  
 :|||  
 Db 22 KGPWTEED 30

## RESULT 48

US-09-270-767-42702  
 ; Sequence 42702, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 42702  
 ; LENGTH: 447  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 ; FEATURE:  
 ; OTHER INFORMATION: Xaa means any amino acid  
 ; US-09-270-767-42702

Query Match 73.6%; Score 39; DB 2; Length 447;  
 Best Local Similarity 85.7%; Pred. No. 1e+02; Indels 0; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEE 9  
 |||||  
 Db 36 PWLEQEE 42

## RESULT 49

US-08-416-478A-7  
 ; Sequence 7, Application US/08416478A  
 ; Patent No. 5773578  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hercend, Thierry  
 ; APPLICANT: Triebel, Frederic  
 ; TITLE OF INVENTION: New Proteins Produced By Human  
 ; APPLICANT: Lymphocytes, DNA Sequences Encoding These Proteins And  
 ; TITLE OF INVENTION: Their Pharmaceutical And Biological Uses  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
 ; STREET: 419 Seventh Street, N.W., Suite 400  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/416,478A
; FILING DATE: 04-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,644
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: HERCEND=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 470 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-416-478A-7

Query Match 73.6%; Score 39; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPWLEEE 9
DB 367 GPWLEAQE 374

RESULT 50
US-08-474-988B-7
; Sequence 7, Application US/08/4988B
; Patent No. 5874250
; GENERAL INFORMATION:
; APPLICANT: Hercend, Thierry
; APPLICANT: Triebel, Frederic
; TITLE OF INVENTION: NEW PROTEINS PRODUCED BY HUMAN
; TITLE OF INVENTION: LYMPHOCYTES, DNA SEQUENCES ENCODING THESE PROTEINS AND
; TITLE OF INVENTION: THEIR PHARMACEUTICAL AND BIOLOGICAL USES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,988B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/416,478
; FILING DATE: 04-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,644
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: HERCEND=1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 470 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; US-08-474-988B-7

Query Match 73.6%; Score 39; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPWLEEE 9
DB 367 GPWLEAQE 374

Search completed: January 3, 2006, 09:19:46
Job time : 23.5 secs
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